

CG/914088

GenCore version: 5.1.6  
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Protein - protein search, using sw model

Run on: November 5, 2003, 17:11:03 : Search time 21 Seconds  
(without alignments)  
41.215 Million cell updates/sec

File: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDQVMDVD 9

Scoring table: R:OSUM62  
Gapop 10.0 , Gapext 0.5

searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 753

Minimum DB seq length: 3

Maximum DB seq length: 3

Post processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 761\*

1: pir1\*

2: pir2\*

3: pir3\*

4: pir4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	36.2	6	2 PT0604	T-cell receptor be
2	17	36.2	6	2 PT0657	T-cell receptor be
3	17	36.2	7	2 PT0543	T-cell receptor be
4	17	36.2	8	2 A28713	thymic humoral fac
5	16	34.0	9	2 A37027	macrophage chemot
6	16	34.0	9	2 A60427	macrophage cytotox
7	14	29.8	4	2 PT0271	Ig heavy chain CRD
8	14	29.8	7	2 S29735	polysphosphate-gluc
9	14	29.8	8	2 PT0537	T-cell receptor be
10	14	29.8	9	2 B39841	dextranuclease (EC
11	14	29.8	9	2 D44787	CalHMramide 13
12	14	29.8	9	2 A56029	N-methylpurine DNA
13	13	27.7	4	2 A41890	protein D - Escher
14	13	27.7	6	2 B35640	cerebellar degener
15	13	27.7	7	2 PC2370	probable H-transp
16	13	27.7	8	2 PT0279	Ig heavy chain CRD
17	13	27.7	8	2 S66296	Na+-transporting A
18	13	27.7	9	2 B45796	dihydrofolateamide S
19	13	27.7	9	2 A61230	caldesmonin, car
20	13	27.7	9	2 D48186	ATPase R1 subunit
21	13	27.7	9	2 C60070	gastrin - domestic
22	12	25.5	5	2 B31836	25k protein - Rick
23	12	25.5	5	2 PT0699	T-cell receptor be
24	12	25.5	5	2 PT0703	T-cell receptor be
25	12	25.5	6	2 PC4392	whey glycoprotein
26	12	25.5	6	2 A20186	fatty acid synthas
27	12	25.5	6	2 PT0720	T-cell receptor be
28	12	25.5	6	2 PT0589	T-cell receptor be
29	12	25.5	7	2 S20446	glucanase - Pseudom

30	12	25.5	7	2 B39127	phosphotransferase
31	12	25.5	7	2 PT0611	T-cell receptor be
32	12	25.5	7	2 PT0523	T-cell receptor be
33	12	25.5	7	2 PT0665	T-cell receptor be
34	12	25.5	7	2 PT0567	T-cell receptor be
35	12	25.5	7	2 PT0689	T-cell receptor be
36	12	25.5	7	2 PT0688	T-cell receptor be
37	12	25.5	8	2 E60588	sperm-activating p
38	12	25.5	8	2 G60588	urine glycopeptide
39	12	25.5	8	2 XGHUEU	Ig heavy chain CRD
40	12	25.5	8	2 PT0298	T-cell receptor be
41	12	25.5	8	2 PT0623	T-cell receptor be
42	12	25.5	8	2 PT0547	T-cell receptor be
43	12	25.5	8	2 PT0724	T-cell receptor be
44	12	25.5	8	2 PT0725	T-cell receptor be
45	12	25.5	8	2 A25836	L-serine ammonia

ALIGNMENTS

RESULT 1

PT0604

T-cell receptor beta chain V-D-J region (111-1A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0604

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0604

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGG 4

Db 4 DGG 6

RESULT 2

PT0657

T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0657

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0657

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGG 4

Db 4 DGG 6







Matches	27	Conservative	17	Mismatches	67	Indels	07	Gaps	07
27	7	END 9							
07	4	END 6							

Protein 1:  
 P1470  
 Protein R, transporting two-sector ATPase [EC 3.6.3.14, alpha chain (similarity)] - Bac  
 N. Arbutus: name: unidentified 78K protein  
 Organism: *Paecilomyces*  
 Cited in: Apr 1997: sequence\_revision\_20Apr1997: text: change 03 Jun 2003  
 Accession: P02170  
 A: Masuno, K.; Miyamoto, T.; Yamaguchi, Y.; Sayed, M.A.; Kawano, T.; Hatada, S.  
 Biosci. Biotechnol. Biochem. 59, 231-237, 1995  
 Article: Identification of DNA-binding proteins changed after infection of sporulation  
 A: Reference: P02169, NCBI:55218.207 PMID:758522  
 A: Accession: P02170  
 A: Status: preliminary  
 A: Molecule type: Protein  
 A: Residues: 7 <MAS>  
 Keywords: ATP biosynthesis; hydrolase

Query Match	27/77	Score 137.08	Length 77
Best local similarity	50.0%	Pred. No. 2 6e+05	
Matches	27	Conservative	17
		Mismatches	67
		Indels	07
		Gaps	07

07 - MVD 6  
 17 - MVD 4

Search completed: November 5, 2003, 12:14:16  
 Job time: 1.12 Secs

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SW protein-protein search, using sw model

Run on: November 5, 2003, 17:14:37, server time 11:00:00  
Working directory: /usr/local/gencore/workdir  
Input file: us-09-914-088-1

Output file: /usr/local/gencore/output  
Output file: /usr/local/gencore/output

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CC eutotids II, Brassicales; Brassicaceae; Brassica.
CX NCBI_TaxID:3738;
RN [1]
RP SEQUENCE
RC STRAIN:CV, TAPAZ, TISSUE=Tapetum;
RX MEDLINE=99149116; PubMed=12420521;
RA Hernandez-Pinzon I., Ross J.H.E., Baines K.A., Darand A.B.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipoproteins in the biosynthesis of the
RT pollen coat of Brassica napus";
RI Planta 202:588-598(1999);
CC [1] FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE BLAD PLANT, A TAPETUM-
CC SPECIFIC PLASMA-LIPID ORGANELLE
CC TISSUE SPECIFICITY: TAPETUM OF ANthers.
PT MONT. TER 8
RC TISSUE SPECIFICITY: TAPETUM OF ANthers.
SQ SEQUENCE 9 AA, 939 MW, 9031AA452CAB04L CR054;

Query Match 34.8%; Score 16; DB 1; Length 8;
Best local Similarity 60.0%; Pred. No. 1; 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQG 4
DB 1 EQG 4

RESULT 4
CC NAME STANDARD; PRT; 9 AA;
AC P44167;
DT 01-MAR-1992 (Rel. 21; Created)
DT 01-MAR-1992 (Rel. 21; Last sequence update)
DT 01-MAR-1992 (Rel. 21; Last annotation update)
DE Gastrin/cholecystokinin-like peptide OI
OS Nephrops norvegicus (Norway lobster)
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Emdacostraca; Eucaridra; Decapoda; Pleocyemata; Astacoidea;
CC Nephropoidea; Nephropidae; Nephrops.
CX NCBI_TaxID:6542;
RN [1]
RP SEQUENCE
RC TISSUE=Stomach;
RX MEDLINE=92042847; PubMed=1147394;
RA Patel P., Kojal G., Sedlmayer D., Keller P., von Willebrand A.;
RT "Structure and biological activity of a processed and hydrolyzed
RT peptide identified with antibodies to human cholecystokinin";
RI Biochem. J. 323:123-129(1997);
CC [1] FUNCTION: MAY CONTROL DIGESTIVE ENZYSES IN THE GASTRIC
CC [1] SIMILARITY: BELONGS TO THE GASTRIN-RELEASING PEPTIDE
TR PIR: S47421; S47422.
KW Homo sapiens.
SQ SEQUENCE 9 AA, 1038 MW, 60E07ACAB0408H CR064.

Query Match 31.9%; Score 15; DB 1; Length 9;
Best local Similarity 75.0%; Pred. No. 1; 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQG 4
DB 1 EQG 5

RESULT 4
CC NAME STANDARD; PRT; 9 AA;
AC P41674;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 01-NOV-1995 (Rel. 32; Last annotation update)
DE Call. FMSamide 13.
OS Calliphora vomitoria (Blue blowfly)
CC Eukaryota; Metazoa; Arthropoda; Hymenoptera; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscophorida; Calliphoridae.

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CC Calliphoridae; Calliphora.
CX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196117; PubMed=1549595;
RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe NH2
RT neuropeptides (designated calliphramide) from the blowfly
RT Calliphora vomitoria";
RA Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992);
CC [1] SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: D44787; D44787;
KW Neuropeptide; Amidation.
PT MODRES 9
SQ SEQUENCE 9 AA, 1028 MW, 22D10E99C87AB6D8 CR064;

Query Match 29.9%; Score 14; DB 1; Length 9;
Best local Similarity 66.7%; Pred. No. 1; 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQG 3
DB 1 EQG 5

RESULT 5
CC NAME STANDARD; PRT; 8 AA;
ID GCLR_HUMAN
AC P02729;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE
RX MEDLINE=9202313; PubMed=5126895;
RA Loe C.J., Weiss J.B.;
RT "Identification in urine of a low molecular weight highly polar
RT glycopeptide containing cysteinyl galactose";
RI Biochem. J. 323:253-257(1997);
CC [1] FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03189; XGHUEU.
DR GO: GO:0005576; C: C:extracellular; NAS.
KW Glycoprotein.
PT CARBOHYD
SQ SEQUENCE 8 AA, 855 MW, C2E87AA:FSB1EB1E CR064;

Query Match 25.8%; Score 12; DB 1; Length 8;
Best local Similarity 100.0%; Pred. No. 1; 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DG 3
DB 6 DG 7

RESULT 6
CC NAME STANDARD; PRT; 9 AA;
ID FAR6_MACRS
AC P83279;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)

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DE EXPEPTIDE-like neuropeptide FLP6 (DCKNENRFPamide).  
 CC Macrobathrus rosenbergii (Glans fresh water planaria).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eucaridacea; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonidae; Palaemonidae; Macrobathridae.  
 CC NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RP TISSUE=Eye stalk.  
 RP MEDLINE=2110794; PubMed=11179518  
 RA Steinbocker S.T., Saitoh-Chokku W., Ishiyasu S., Paoletti R.L.  
 RA Saitoh-Chokku W., Paoletti R.L.  
 RA "The more novel FNPamide-like neuropeptide sequences from the  
 RA eye stalk of the giant freshwater plan Macrobathrus rosenbergii".  
 RA Peptides 22(19):1972007.  
 CC [1]  
 CC [1] MASS SPECTROMETRY: MW:1080.7; METHOD=VALDI.  
 CC [1] SIMILARITY: BELONGS TO THE FNP (FNPAMIDE) RELATED PEPTIDE  
 CC FAMILY.  
 CC GO: 0403022.9; Peptide hormone stimulating pathway; ICA.  
 CC KW Neuroptidae; Amidation.  
 CC MOD RES 9  
 CC SEQUENCE 9 AA: 1081 MW; 26807294547874 CRC64.  
 Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DB 3  
 DB 1  
 DB 1  
 DB 1

RESULT 9  
 JF02 MOUSE  
 ID JF02 MOUSE STANDARD: PNT: 9 AA.  
 AC P38640;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P32) (fragment).  
 CS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Fibroblast;  
 RP MEDLINE=9500907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RA "Separation and sequencing of familial and novel murine proteins  
 RA using preparative two-dimensional gel electrophoresis".  
 RA Electrophoresis 15(7):745(1994).  
 CC [1] MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.  
 CC NON\_TER 9  
 CC SEQUENCE 9 AA: 1102 MW; 7573EAB56D05B1AAB CRC64;

Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 MOD 9  
 DB 1  
 DB 1  
 DB 1

RESULT 9  
 JF02 MOUSE  
 ID JF02 MOUSE STANDARD: PNT: 9 AA.  
 AC P38640;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P32) (fragment).  
 CS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Fibroblast;  
 RP MEDLINE=9500907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RA "Separation and sequencing of familial and novel murine proteins  
 RA using preparative two-dimensional gel electrophoresis".  
 RA Electrophoresis 15(7):745(1994).  
 CC [1] MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.  
 CC NON\_TER 9  
 CC SEQUENCE 9 AA: 1102 MW; 7573EAB56D05B1AAB CRC64;

DE EXPEPTIDE-like neuropeptide FLP6 (DCKNENRFPamide).  
 CC Macrobathrus rosenbergii (Glans fresh water planaria).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eucaridacea; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonidae; Palaemonidae; Macrobathridae.  
 CC NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RP TISSUE=Skin secretion;  
 RP MEDLINE=2110794; PubMed=11179518  
 RA Steinbocker S.T., Wabnitz P.A., Waugh R.J., Bowse J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RA "The structure of new peptides from the Australian red tree frog  
 RA 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RA of evolutionary trends of amphibians".  
 RA Aust. J. Chem. 49:955-963(1996).  
 RN [2]  
 RP SEQUENCE.  
 RP TISSUE=Skin secretion;  
 RP Wabnitz P.A., Bowse J.H., Tyler M.J., Wallace J.C.;  
 RP "Peptides from the skin glands of the Australian tree frog  
 RP Litoria rubella: Comparison with the skin peptides from Litoria  
 RP rubella".  
 RN Aust. J. Chem. 52:639-645(1999).  
 CC [1] FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC [1] SUBCELLULAR LOCATION: Secreted.  
 CC [1] TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC [1] PM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-  
 CC terminal amidation.  
 CC [1] MASS SPECTROMETRY: MW=933; METHOD=FAE.  
 CC Amphibian defense peptide; Amidation.  
 CC MOD RES 9  
 CC SEQUENCE 9 AA: 884 MW; 2C2D77255AA72728 CRC64;  
 Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 25.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 MOD 8  
 DB 1  
 DB 1  
 DB 1

RESULT 9  
 JF02 MOUSE  
 ID JF02 MOUSE STANDARD: PNT: 9 AA.  
 AC P38640;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P32) (fragment).  
 CS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Fibroblast;  
 RP MEDLINE=9500907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RA "Separation and sequencing of familial and novel murine proteins  
 RA using preparative two-dimensional gel electrophoresis".  
 RA Electrophoresis 15(7):745(1994).  
 CC [1] MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.  
 CC NON\_TER 9  
 CC SEQUENCE 9 AA: 1102 MW; 7573EAB56D05B1AAB CRC64;



OC Hypocnemycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
 RX NCBI TaxID=332;  
 RA [1]

RA Aviclad G., Markus Z.,  
 RP SEQUENCE.  
 RT Identification of a peptide inhibitor of lactose oxidase from  
 RL Dactylium dendroides.  
 RJ Fed. Proc. 31:447-447(1972).  
 CC ! FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE  
 CC LACTOSE OXIDASE APPEZYM. IT MAY INACTIVATE THE ENZYME BY  
 CC BINDING TO ITS PROSTHETIC COPPER GROUP.  
 ER PIP: A01341; XEYDGD  
 KW Copper; Metalloenzyme inhibitor.  
 SQ SEQUENCE 5 AA; 406 MW; 75B01A56D57D60 CPG64.

Query Match 23.4% Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQ 4  
 DB 2 GQ 3

## RESULT 14

CHIL\_PAT STANDARD; PRT: 5 AA;  
 AC 15-DEC-1998 (Rel. 37, Created);  
 DT 15-DEC-1998 (Rel. 37, Last sequence update);  
 DT 15-DEC-1998 (Rel. 37, Last annotation update);  
 DE Unknown protein from 2D-page of heart tissue. Spot 116 (Fragment).  
 CS Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Molelesta; Eumetazoa;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Molelesta; Eumetazoa;  
 CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI TaxID=10114;  
 RN 1;  
 RP SEQUENCE;  
 RC STRAIN=Missouri; TISSUE=Heart;  
 PA Li X., Li, P., Pfleger K., Schell G., Rogli z-Zhang X., Saitov G.,  
 RA Cuihui P.,  
 RL Submitted (SEP-1998) to the SWISS PROT data bank.  
 CC ! MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.I. OF THIS UNKNOWN  
 CC PROTEIN IS 4.5, ITS MW IS 42 KDa.  
 ER INSURE 3 2 CR AL  
 RI NON RES 7  
 SQ SEQUENCE 5 AA; 475 MW; 6860B54115A628 CPG64;

Query Match 23.4% Score 11; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQ 4  
 DB 5 GQ 7

## RESULT 15

ALL7\_CARMA STANDARD; PRT: 8 AA;  
 AC 08-NOV-2000 (Rel. 39, Created);  
 DT 30-MAY-2000 (Rel. 39, Last sequence update);  
 DT 30-MAY-2000 (Rel. 39, Last annotation update);  
 DE Carcinustatin.  
 CS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eucaridacea; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 CX NCBI TaxID=6759;  
 RN 1;  
 RP SEQUENCE;  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX WEDLINE=98:21193; PubMed=9461295;  
 RA Dave H., Johnsen A.H., Maestro J. L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC !- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC !- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Allatostatin; Multigene family.  
 FT MOD.RES 8 8 AMIDATION (POTENTIAL).  
 SQ SEQUENCE 8 AA; 858 MW; C8287955AB46D865 CPG64;

Query Match 23.4% Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQ 4  
 DB 2 GQ 3

Search completed: November 5, 2003, 17:13:17  
 Job time : 12 secs





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RS Zea mays (Maize).
AC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Rubrales;
AC PACCAN clade; Ranunculales; Ranunculaceae; Zed.
CX NCBI_TaxID=4577;
EP SEQUENCE FROM N.A.
RC STRAIN=CV, C123;
RA Cheng A.S., Catala K.S., Jung Y., Jolani Y., Smith G.S., Tinney S.,
RA Vondra M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR2002) to the EMBL/GenBank/CCRC databases
DR EMBL; AY094310; AAC21836.1;
FT NON_TER
SQ SEQUENCE 9 AA, 977 MW, 50554.22CBIAAAS CR64,
Query Match 40.4%, Score 19, DB 10, Length 9;
Best Local Similarity 42.9%, Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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DB 2 KODVVC 8
RESULT 3
C90265 PRELIMINARY; PRT; 4 AA.
ID C90265
DT 01-OCT-2000 (TREMURel. 15, Created;
DT 01-OCT-2000 (TREMURel. 15, Last sequence update;
DT 01-OCT-2000 (TREMURel. 15, Last annotation update;
DE Cloning factor VIII (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae;
CX NCBI_TaxID=9606;
RN [1]
RT SEQUENCE FROM N.A.
RA Shepard M., Saito M., Morichika S., Yoshida A.;
RT "Human clotting factor VIII gene: function, regions of the deletion of
RT exon 4 through 7."
PI Submitted (MAR 2000) to the EMBL/GenBank/CCRC databases.
DR EMBL; AB040872; BAA94312.1;
FT NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA, 866 MW, 1016.44AASBQKQ CR64,
Query Match 36.3%, Score 19, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EDG 3
DB 4 EDG 4
RESULT 4
C90265 PRELIMINARY; PRT; 4 AA.
ID C90265
DT 01-MAY-2000 (TREMURel. 13, Created;
DT 01-MAY-2000 (TREMURel. 13, Last sequence update;
DT 01-JUN-2002 (TREMURel. 21, Last annotation update;
DE 18 kDa cell growth factor (Fragment)
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus;
CX NCBI_TaxID=10116;
RN [1]
RT SEQUENCE
PX MEDLINE=92049971; PubMed=1656971;

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RA Milner P.G.;
RT "Simian sarcoma virus transformation of normal rat kidney fibroblasts
RT is associated with markedly increased basic fibroblast growth factor
RT expression."
RL Biochem. Biophys. Res. Commun. 180:423-430(1991).
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA, 807 MW, 3078.7AA0767JAPA CR64;
Query Match 46.2%, Score 17, DB 11, Length 8;
Best Local Similarity 100.0%, Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EDG 3
DB 5 EDG 7
RESULT 5
C90493 PRELIMINARY; PRT; 8 AA.
ID C90493
DT 01-NOV-1996 (TREMURel. 11, Created;
DT 01-NOV-1996 (TREMURel. 11, Last sequence update;
DT 01-NOV-1996 (TREMURel. 11, Last annotation update;
DE Myoglobin (fragment)
OS Eopsaltria australis (eastern yellow robin)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Petroicidae; Eopsaltria;
CX NCBI_TaxID=44319;
RN [1]
RT SEQUENCE FROM N.A.
RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
RX MEDLINE=9528047; PubMed=9548272;
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
RT assessed by temperature gradient Gel electrophoresis."
RL Electrophoresis 14:142-151(1993).
DR EMBL; J40495; AAC50362.1;
FT NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA, 921 MW, C6CA82DAF5R0450A CR64;
Query Match 34.0%, Score 16, DB 13, Length 8;
Best Local Similarity 50.0%, Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 4 QWQVVC 9
DB 2 Q1SXV 7
RESULT 6
C92452 PRELIMINARY; PRT; 9 AA.
ID C92452
DT 01-NOV-1996 (TREMURel. 11, Created;
DT 01-NOV-1996 (TREMURel. 11, Last sequence update;
DT 01-OCT-2002 (TREMURel. 22, Last annotation update;
DE Heat shock protein (fragment)
GN HSP26.7; OR HSP26.02;
OS Triticum aestivum (Wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spelmatoxyla; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Triticum;
CX NCBI_TaxID=4565;
RN [1]
RT SEQUENCE FROM N.A.
RA Coshi C.P., Kiew N., Nguyen H.T.;
RL Submitted (APR 1995) to the EMBL/GenBank/CCRC databases.
DR EMBL; L41804; AAC4972.1;
DR EMBL; L41803; AAC4971.1;

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KW Heat shock  
 FT NON-TER  
 SQ SEQUENCE 9 AA; 1084 MW; 46582122CAA04203 CRC64;  
 Query Match 34.3%; Score 15; DB 10; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 4 QWMDV 8  
 DB 2 KVIDV 6

RESULT 9  
 Q50812 Q9N6M5 PRELIMINARY; PRT; 4 AA;  
 ID Q50812  
 AC Q50812  
 DT 01-NOV-1996 (TRENBLER); 1; Created  
 DT 01-NOV-1996 (TRENBLER); 1; Last sequence update  
 DT 01-NOV-1996 (TRENBLER); 1; Last annotation update  
 DE Intergenic AT-rich DNA sequence (Fragment)  
 OS Methanococcus voltae  
 GC Archaea; Euryarchaeota; Methanococci; Methanococcoides;  
 NC Methanococcaceae; Methanococcus  
 NX NCBI\_TaxID:2184;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=85330552; PubMed=4006307;  
 RA Bollschweiler C., Kuehn P., Klein A.  
 PT "Non-repetitive AT-rich sequences are found in intergenic regions of  
 Methanococcus voltae DNA."  
 EVRC J. 4:1805-1810(1993)  
 EVOL XC2518; CAA26355.1;  
 FT NON-TER  
 SQ SEQUENCE 9 AA; 1087 MW; 95EDD0F0C40441FA CRC64;

Query Match 31.9%; Score 15; DB 10; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 6 MWDV 9  
 DB 1 MFIN 4

RESULT 9  
 P20149 Q9N6M5 PRELIMINARY; PRT; 4 AA;  
 ID P20149  
 AC P20149  
 DT 01-FEB-1997 (TRENBLER); 2; Created  
 DT 01-FEB-1997 (TRENBLER); 2; Last sequence update  
 DT 01-FEB-2001 (TRENBLER); 19; Last annotation update  
 DE Putative glucokinase (Fragment)  
 OS Glx  
 NC Pseudomonas aeruginosa  
 AC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonas  
 NX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN PAO1;  
 RX MEDLINE=96427144; PubMed=8830308;  
 RA Sage A.E., Proctor W.D., Phibbs P.V.  
 PT "A two-component response regulator, GltK, is required for glucose  
 transport activity in Pseudomonas aeruginosa PAO1."  
 RA J. Bacteriol. 178:6564-6566(1996)  
 EVMS; U50912; AA:44474.1;  
 FT NON-TER  
 SQ SEQUENCE 9 AA; 944 MW; C30710CAA20160 CRC64;

Query Match 32.9%; Score 15; DB 10; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 4 QWMDV 9  
 DB 3 QALDAE 8

RESULT 9  
 Q9N6M5 Q9N6M5 PRELIMINARY; PRT; 8 AA;  
 ID Q9N6M5  
 AC Q9N6M5  
 DT 01-OCT-2000 (TRENBLER); 15; Created  
 DT 01-OCT-2000 (TRENBLER); 15; Last sequence update  
 DT 01-OCT-2000 (TRENBLER); 15; Last annotation update  
 DE Dihydrofolate reductase (NADPH synthase (Fragment))  
 OS FOL1  
 NC Toxoplasma gondii  
 AC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimerida; Sarcocystidae;  
 OC Toxoplasma  
 NX NCBI\_TaxID:5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH; COUGAR T031034; SEA OTTER T082801; and BEVERLEY,  
 RA Lehmann C., Blackston C.R., Pamley S.F., Remington J.S., Dubey J.P.  
 PT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and  
 RT Housekeeping Genes."  
 RA J. Parasitol. 91: 012000;  
 DR EMBL; AF249695; AAF79153.1;  
 DR EMBL; AF249692; AAF79150.1;  
 DR EMBL; AF249693; AAF79151.1;  
 DR EMBL; AF249694; AAF79152.1;  
 FT NON-TER  
 SQ SEQUENCE 8 AA; 1015 MW; 33CAAAC5B131044 CRC64;

Query Match 39.9%; Score 14; DB 5; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 6.3e+05;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY 4 QWMDV 8  
 DB 1 PKEID 6

RESULT 10  
 Q42507 Q42507 PRELIMINARY; PRT; 8 AA;  
 ID Q42507  
 AC Q42507  
 DT 01-NOV-1996 (TRENBLER); 1; Created  
 DT 01-NOV-1996 (TRENBLER); 1; Last sequence update  
 DT 01-OCT-2002 (TRENBLER); 32; Last annotation update  
 DE Heat shock protein (Fragment)  
 NC HSP70 OR HSP72A OR HSP70S  
 OS Triticum aestivum (Wheat)  
 AC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
 OC Triticeae; Triticum  
 NX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV MUSTANG;  
 RX MEDLINE=96189275; PubMed=8605112;  
 RA Joshi C.P., Kumar S., Nguyen H.T.  
 PT "Application of modified differential display technique for cloning  
 RT and sequencing of the 3' region from three putative members of wheat  
 HSP70 gene family."  
 RA Plant Mol. Biol. 30:641-646(1996)  
 DR EMBL; L41507; AABR2333.1;  
 DR EMBL; L41505; AABR2331.1;  
 DR EMBL; L41506; AABR2332.1;  
 KW Heat shock  
 FT NON-TER  
 SQ SEQUENCE 8 AA; 840 MW; 71B2CB1B17512765 CRC64;

Query Match 29.8% Score 147 DB 10 Length 8;  
 Best Local Similarity 33.3% Pred. NO. 8.3e+05;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNDVD 9  
 DB 3 KFEVD 4

RESULT 13  
 Q9UB13 PRELIMINARY; PRT; 9 AA.  
 AC Q9UB13;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;  
 DT 01-NOV-1996 (TrEMBLrel. 06, Last annotation update;  
 DE Scfins (Fragment);  
 GN B13R/SPI-2;  
 OS Vaccinia virus  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus  
 CX NCBI TaxID:10245;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RX MEDLINE:9531144; PubMed:7431769;  
 FA Kettie S., Plake N.W., Law K.M., Smith G.D.;  
 FT "Vaccinia virus serpins B13r (SPI-2) and B13R (SPI-2) are 38-5  
 RT and 40K, intracellular polypeptides that do not affect virus virulence  
 RI in a guinea hiracass model";  
 RL Virology 256:147-147(1995);  
 RP EMBL: S75134; AA:50736.1; ;  
 FT NCN TER 9  
 SQ SEQUENCE 9 AA; 138 MW; 9594D00040905A CRR64;

Query Match 29.8% Score 147 DB 10 Length 8;  
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 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 NDV 4  
 DB 3 MDV 3

RESULT 14  
 Q91894 PRELIMINARY; PRT; 8 AA.  
 AC Q91894;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;  
 DE "ORF protein (Fragment);  
 OS Escherichia coli  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia  
 CX NCBI TaxID:562;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RX MEDLINE:8623322; PubMed:2423502;  
 FA Weber P.C., Palcaudhuri S.;  
 FT "Incompatibility repressor in a *Salmonella* like plasmid of the IncF;  
 RI Plasmid ColV2-K94";  
 RL J. Bacteriol. 166:1106-1112(1984);  
 RP EMBL: M13472; AA:23194.1; ;  
 FT NCN TER 1  
 SQ SEQUENCE 8 AA; 998 MW; 0F3705AA 44107 CRR64;

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 Best Local Similarity 40.0% Pred. NO. 8.3e+05;  
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QY 1 EDOO 4  
 DB 4 EDVQ 3

RESULT 15  
 Q51765

QY 4 QNDVD 8  
 DB 2 ORLDI 6

RESULT 13  
 Q9UB13 PRELIMINARY; PRT; 9 AA.  
 AC Q9UB13;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;  
 DE Calmodulin (Fragment);  
 OS Aibutaria hippolyti;  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Stgmuretrata; Clausilioides; Clausiliidae; Alopinae; Aibutaria;  
 CX NCBI TaxID:69418;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RA Schilthuisen M., Houkstra R.P., Gittenberger E.;  
 RT "Selective maintenance of a rare haplotype in a land snail hybrid  
 zone";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 266:218-2185(1999);  
 RP EMBL: AF132316; AA:34386.1; ;  
 FT NCN TER 1  
 SQ SEQUENCE 9 AA; 406 MW; F4ADAR30CH144056 CRR64;

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QY 5 VQVD 4  
 DB 2 INEVD 6

RESULT 14  
 Q94695 PRELIMINARY; PRT; 8 AA.  
 AC Q94695;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update;  
 DE Actin (Fragment);  
 GN ARDC  
 OS Physarum polycephalum (white mold);  
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
 OC Physarum  
 CX NCBI TaxID:5731;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RX MEDLINE:9618218; PubMed:8622700;  
 RA Renard M., Lagne C., Palicotta D., Pierron G.;  
 RT "Mapping of a replication origin within the promoter region of two  
 RI unlinked, abundantly transcribed actin genes of Physarum  
 polycephalum";  
 RL Mol. Cell. Biol. 15:968-976(1995);  
 RP EMBL: M73459; AA:3706.1; ;  
 FT NCN TER 8  
 SQ SEQUENCE 8 AA; 978 MW; F4C6C2CAAB197B16 CRR64;

Query Match 27.7% Score 137 DB 5 Length 8;  
 Best Local Similarity 75.0% Pred. NO. 8.3e+05;  
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QY 1 EDOO 4  
 DB 4 EDVQ 3

RESULT 15  
 Q51765

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ID C51765 PRELIMINARY; PRT; 9 AA
AC
CC 05-1996 (TREVBLREL_01, Created)
CC 01-NOV-1996 (TREVBLREL_01, Last sequence update)
CC 01-DEC-2001 (TREVBLREL_19, Last annotation update)
FE Unknown ORF (Fragment)
GI Pseudomonas fluorescens
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas
CX NCBI TaxID:2947
IL
PN
PF SEQUENCE FROM N.A.
PX MEDLINE:9013284, Pubmed:2515251.
RA Benen J.A., Van Berkel W.J., Van Dongen W.M., Miller P., De Rijk A.;
RI "Molecular cloning and sequence determination of the lpd gene encoding
RI lipamide dehydrogenase from Pseudomonas fluorescens";
RL J. Gen. Microbiol. 135:1787-1797(1989).
DR EVRI_128156; AAA9233.1;
RT NCN_188
SQ SEQUENCE 9 AA; 101 MW; 269EA7272743D07 CR084.

Query Match 27.7% Score 13; LG 2; Length 9.
Best local similarity 50.0%; Pred. NCN_913e-05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 5 VMDV 4
CG 4 LDDV 3

Search completed: November 5, 2003, 17:14:04
CPU time : 16 sec
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GenCore version 5.1.6  
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Query protein: protein search, using sw model

Run on: November 5, 2003, 17:34:52 : Search time 41 seconds  
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34 842 Million cell updates/sec

Title: US 09 324-088-1

Percent scores: 49

Sequences: 1 EFGGMDVD 9

Scoring table: EFGGMDVD

Gapop 10.0 , Gapext 0.5

Searched: 110783 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 176625

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	21	Immunoglobulin E
2	47	100.0	9	21	Immunoglobulin-2
3	47	100.0	9	22	Immunoglobulin-2
4	47	100.0	9	22	Immunoglobulin-2
5	47	100.0	9	23	Immunoglobulin-2
6	47	100.0	9	23	Immunoglobulin-2
7	47	100.0	9	24	Immunoglobulin-2
8	47	100.0	9	24	Immunoglobulin-2
9	47	100.0	9	24	Immunoglobulin-2

10	30	63.8	9	24	AAE35076	Human immunoglobulin
11	28	59.6	7	23	AAE14481	Oplophorus gracili
12	28	59.6	9	23	ABJ12821	Human 125P5C8 epit
13	26	55.3	9	24	AAE35101	Human immunoglobulin
14	25	53.2	9	23	ABG67564	Human ADP1 tryptic
15	25	53.2	9	24	AAE35082	Human immunoglobulin
16	23	48.9	8	17	AAE6589	Autoxin peptide
17	23	48.9	9	13	AAE29631	Adhesion inhibitor
18	23	48.9	9	13	AAE35433	Cell adhesion inhib
19	23	48.9	9	13	AAE28886	Cell adhesion inhib
20	22	46.6	6	20	AAE42592	Human IgF variant
21	22	46.6	7	21	AAE61729	Cadherin-8 cell ad
22	22	46.6	7	21	AAE61729	Cadherin-8 cell ad
23	22	46.6	8	21	AAE61785	Immunogenic peptid
24	22	46.6	9	20	AAE48666	Immunogenic peptid
25	22	46.6	9	20	AAE00372	Fragment of human
26	22	46.6	9	21	AAE61788	Cadherin-8 cell ad
27	22	46.6	9	23	ABJ13116	Human 125P5C8 epit
28	22	46.6	9	23	ABJ13116	Human 125P5C8 epit
29	22	46.6	9	24	ABJ20192	MHC binding peptid
30	21	44.7	7	19	AAE63724	C. histolyticum CH
31	21	44.7	8	23	AAE25317	Human LSI-01 cleav
32	21	44.7	9	18	AAE15176	Chlamydia trachoma
33	21	44.7	9	19	AAE0838	Cytotoxic Epstein-
34	21	44.7	9	20	AAE30292	Angiopoietin deriv
35	21	44.7	9	21	AAE3468	Human tyrosine-rel
36	21	44.7	9	22	ABJ53963	Human DNA derived
37	21	44.7	9	22	AAE11010	Tyrosinase melanoma
38	21	44.7	9	22	AAE11010	Glucuronoxylomanna
39	21	44.7	9	22	AAE43428	Peptide #7 used to
40	21	44.7	9	22	AAE24564	Human MHC class I
41	21	44.7	9	22	AAE24564	Human MHC class I
42	21	44.7	9	22	AAE24760	Human MHC class I
43	21	44.7	9	22	AAE24760	Human MHC class I
44	21	44.7	9	22	AAE24961	Human MHC class I
45	21	44.7	9	22	AAE25563	Human MHC class I

#### ALIGNMENTS

#### RESULT 1

AAE23867

ID AAE23867 standard; peptide; 9 AA.

XX AAE23867:

AC AC

DT 01-JAN-2001 (first entry)

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XX

Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.  
Immunoglobulin E: IgE, immunogenic; immunogen; Protein D, carrier;  
prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
malaria; cytostatic; anti-allergy; C; noctropic; neuroprotective;  
protozoicide; Alzheimer's disease; allergy.

OS Homo sapiens

PN WC2000050677-A1.

XX 31-AUG-2000.

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1R WPI: 2001-521967/57.  
 2X A linkage comprising an immunogenic conjugate useful treatment of IGE  
 3C mediated diseases.  
 4X  
 5X Example 4; Page 20; 49pp; English.  
 6X  
 7X The present invention relates to linkage methodology for use in the  
 8X conjugation of compounds (e.g. peptides) to carrier vehicles  
 9C (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 10C biological and immunological constructs. The invention provides a  
 11C method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 12C protein) for use in a pharmaceutical composition or a vaccine. The  
 13C invention describes peptides derived from or mimotopes of the  
 14C Cepsillon2, Cepsillon3 or Cepsillon4 regions of human immunoglobulin E  
 15C (IgE) which are used to produce conjugated compounds. The compounds or  
 16C conjugations of the invention are useful in the manufacture of a  
 17C medicament for the treatment of IGE-mediated diseases. The invention  
 18C allows for controlled conjugation of a peptide epitope designed to a  
 19C protein so as to form an immunogenic conjugate which may be able to  
 20C raise a protective antibody response in an animal or human patient.  
 21C AA016632-AAU6913 represent peptides derived from or mimotopes of  
 22C the Cepsillon2/Cepsillon3/Cepsillon4 region of human IgE.  
 23C  
 24C Sequence 9 AA:  
 25C  
 26C Query Match 100.0%; Score 47; DB 22; Length 9;  
 27C Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 28C Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 29C  
 30C QY 1 EDGQVMQVD 9  
 31C | | | | |  
 32C Db 1 EDGQVMQVD 9  
 33C  
 34C RESULT 4  
 35C AAE35091  
 36C ID AAE35091 standard; Peptide: 9 AA.  
 37C AC AAE35091  
 38C XX  
 39C XX IGE peptide #1.  
 40C XX Vaccine; immunoglobulin E; IgE; anti-allergy.  
 41C XX Mammalia  
 42C XX WC200204016 A2.  
 43C XX 14-DEC-2002.  
 44C XX 06-JUN-2000; 2002WO-EP05164.  
 45C XX 08-JUN-1999; 93JP-0013327.  
 46C XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 47C XX Pricels C;  
 48C XX WPI: 2001-031150/10.  
 49C XX New vaccine comprising allergy peptides linked by an inert carrier,  
 50C useful for boosting an anti-allergy immune response in an individual  
 51C susceptible to an allergic response.  
 52C  
 53C Claim 5; Page 20; 26pp; English.  
 54C  
 55C The present invention relates to a conjugation comprising allergy  
 56C peptides linked by an inert carrier. The allergy peptides are derived  
 57C from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 58C such peptide from IgE. The composition is useful as a vaccine or for

59C CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 60C In particular, for boosting an anti-allergy immune response in an  
 61C individual susceptible to an allergic response.  
 62C XX  
 63C SQ Sequence 9 AA:  
 64C  
 65C Query Match 100.0%; Score 47; DB 22; Length 9;  
 66C Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 67C Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 68C  
 69C QY 1 EDGQVMQVD 9  
 70C | | | | |  
 71C Db 1 EDGQVMQVD 9  
 72C  
 73C RESULT 5  
 74C ABJ00217  
 75C ID ABJ00217 standard; Peptide: 9 AA.  
 76C XX ABJ00217  
 77C XX C2-SEP-2002 (first entry)  
 78C XX Human IgE immunogenic peptide SEQ ID NO: 1.  
 79C XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 80C vaccine; anti-allergic.  
 81C XX Homo sapiens.  
 82C XX WC200216409 A2.  
 83C XX 28-FEB-2002.  
 84C XX 17-AUG-2001; 2001WO-EP09376.  
 85C XX 22-AUG-2000; 2000GB-0020117.  
 86C XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 87C XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 88C XX Friede M, Mason S, Turnell WG, Vinals Rassols YC;  
 89C WPI: 2002-489648/52.  
 90C XX Conjugate for use in vaccine for treatment of allergy, comprises  
 91C disulfide bridge cyclized peptide and immunogenic carrier.  
 92C  
 93C Claim 4; Page 9; 45pp; English.  
 94C  
 95C The present invention relates to conjugates suitable for use in vaccines,  
 96C where the conjugate comprises a disulphide bridge cyclized peptide and an  
 97C immunogenic carrier. The vaccines can be used in the treatment of  
 98C allergies. The present sequence is a peptide immunogen derived from human  
 99C immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 100C  
 101C SQ Sequence 9 AA:  
 102C  
 103C Query Match 100.0%; Score 47; DB 23; Length 9;  
 104C Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 105C Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 106C  
 107C QY 1 EDGQVMQVD 9  
 108C | | | | |  
 109C Db 1 EDGQVMQVD 9  
 110C  
 111C RESULT 6  
 112C AAE35091  
 113C ID AAE35091 standard; peptide: 9 AA.  
 114C XX AAE35091  
 115C AC AAE35091  
 116C XX

DT 28-MAY-2003 (first entry)  
XX Human immunoglobulin E (IgE) HLA A2 peptide motif #23.  
XX  
XX Cytotoxic T lymphocytes; CTLs; tumour; antigen presenting cells; allergy;  
XX lupus; autoimmune disease; rheumatoid arthritis; autoimmune hepatitis;  
XX psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
XX inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
XX transplant rejection; human; immunoglobulin E; IgE.  
XX  
XX Homo sapiens  
XX  
XX WO200232773 A2.  
XX  
XX 21-NOV-2002  
XX  
XX 13-MAY-2002; 2002WC US5341.  
XX  
XX 15 MAY 2001; 2001US-29130P.  
XX  
XX (ORF) : ORF1-MOVE11 PHARM INC.  
XX  
XX Cat Z, Jackson MR, Peterson PA, Shi W, Kono Y, Degraw G  
XX  
XX WPI; 2002 125671/11.  
XX  
XX Producing cytotoxic T lymphocytes for treating and autoimmune  
XX diseases, comprises culturing CD8+ T cells with antigen presenting  
XX cells to activate precursor CD8+ T cells specific for the cell  
XX epitopes  
XX  
XX Example 3; Column 48, 49pp; English.  
XX  
XX The invention relates to a method of producing cytotoxic T lymphocytes  
XX (CTLs) specific for one or more non-tumour self antigenic cell epitopes.  
XX The method involves loading antigen presenting cells (APCs) having class  
XX II major histocompatibility complex molecules with the T cell epitopes,  
XX and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
XX T cells specific for the T cell epitopes. The invention is useful for  
XX treating autoimmune disease including rheumatoid arthritis, psoriasis,  
XX lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
XX insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
XX graft versus host disease and transplant rejection and/or allergic  
XX disease such as food allergy, hay fever, allergic rhinitis, allergic  
XX asthma and venom allergy. The invention is also useful in cell therapy.  
XX The present sequence is human immunoglobulin E (IgE) HLA A2 peptide  
XX motif. This peptide is used in the exemplification of the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 66.0%; Score 11; DB 04; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : EDGQXX #  
DB 4 EDGQXX 4  
RESULT 7  
AA055923  
ID AAB05923 standard; Peptide: 7 AA.  
XX  
XX AAB05923;  
XX  
XX 05-JUN-2001 (first entry)  
XX  
XX P1 mimotope peptide P15s SEQ ID NO:17.  
XX  
XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
XX allergic disease; immunoprecipitation; immunotherapy; anti-allergic;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW

KW allergy; atopy.  
XX  
XX Homo sapiens.  
XX  
XX WO2002050460 A1.  
XX  
XX 31 AUG-2000.  
XX  
XX 22-FEB-2000; 2000WO-EP01455.  
XX  
XX 25-FEB-1999; 99GB-0004405.  
XX  
XX 23-MAR-1999; 99GB-0007151.  
XX  
XX 07-MAY-1999; 99GB-0010537.  
XX  
XX 07-MAY-1999; 99GB-0010538.  
XX  
XX 07-AUG-1999; 99GB-0018594.  
XX  
XX 07-AUG-1999; 99GB-0018603.  
XX  
XX 07-SEP-1999; 99GB-0021046.  
XX  
XX 07-SEP-1999; 99GB-0021047.  
XX  
XX 29-OCT-1999; 99GB-0025619.  
XX  
XX 23-NOV-1999; 99GB-0027698.  
XX  
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S,  
XX Randall F, Turnell MG, Van Mechelen MP, Vinals De Bassols YC;  
XX  
XX WPI; 2002-572073/53.  
XX  
XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E -  
XX  
XX Example 7; Page 35; 129pp; English.  
XX  
XX The present invention describes a peptide (I), comprising an isolated  
XX surface exposed group/epitope (S1) of C-epsilon-2 domain (D) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
XX immunogen (II) for treating allergy comprising (i); (2) a vaccine (III)  
XX for treating allergies comprising (ii); (3) a ligand (IV) capable of  
XX recognising E1; (4) a pharmaceutical composition (PC) comprising (i);  
XX (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
XX (IIa) comprising (Ia), and (7) producing (III) by producing (II) (7).  
XX CC can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (i), (ii) and (iii) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (iv) is useful for identifying mimotopes of E1.  
XX CC in medicine and also in manufacturing medicaments for treating  
XX allergies. (ii) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (iii), (iii), and (iv) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (iv) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.  
XX  
SQ Sequence 7 AA;  
Query Match 63.0%; Score 10; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 QVMDVC 9  
DB 1 QVMDVC 6  
RESULT 8  
AAU16648  
ID AAU16648 standard; Peptide: 7 AA.  
XX  
XX AAU16648;  
XX  
XX 07-NOV-2001 (first entry)  
XX



DE Peptide P115 derived as mimotope of Cepsilon2 region of human IgE.  
 XX  
 KW Human linkage technology; conjugated component; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 CS Homo sapiens  
 OS Synthetic.  
 XX  
 PN WO200145745 A2.  
 XX  
 PD 24 JUN-2001.  
 XX  
 PF 21-DEC-2000; 2001WO-GR04935.  
 XX  
 FR 21-FEB-1999; 93GB 0032233.  
 XX  
 FR 22 FEB-2000; 2000GB-0004098.  
 XX  
 FR 22 AUG-2000; 2000GB-0020707.  
 XX  
 FR 22 AUG-2000; 2000GB-0020708.  
 XX  
 PA ACAM-1 ACAM-BIOS RES LTD.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Elime N. Johnson T;  
 XX  
 DR WPI; 2001-521767/57.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases.  
 PT  
 PS Example 4; Page 21; 48pp; English.  
 PS  
 CC The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. CC AA016632 (AA01691) represents peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 63.8%; Score 30; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QVMDVD 9  
 DB 1 QVMDVD 6  
 RESULT 9  
 ABC0227  
 ID ABJ00227 standard; Peptide; 7 AA.  
 AC  
 XX ARJ00227;  
 XX  
 CC 02-SEP-2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 11  
 KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage; vaccine; anti-allergic.

XX Homo sapiens.  
 OS  
 PN WO200216409 A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EP09576.  
 XX  
 PR 22-AUG-2000; 2000GB-0020717.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (EPPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Friede M. Mason S. Turner; WG. Vinals Bassols YC;  
 XX  
 DR WPI; 2002-489648/51.  
 XX  
 CC Conjugate for use in vaccine for treatment of allergy, comprises disulfide bridge cyclized peptide and immunogenic carrier.  
 PT  
 PS Claim 4; Page 9; 48pp; English.  
 PS  
 CC The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulfide bridge cyclised peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 63.8%; Score 30; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QVMDVD 9  
 DB 1 QVMDVD 6  
 RESULT 10  
 AA035076  
 ID AA035076 standard; peptide; 9 AA.  
 AC  
 XX AA035076;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E (IgE) HLA-A2 peptide motif #14.  
 XX  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy; lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis; psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever; inflammatory bowel disease; insulin dependent diabetes; cell therapy; Crohn's disease; allergic rhinitis; graft versus host disease; asthma; transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200292773-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 13-MAY-2002; 2002WO-US15341.  
 XX  
 PR 15-MAY-2001; 2001US-291300P.  
 XX  
 PA (ORTH) ORTHO-McNEIL PHARM INC.  
 XX  
 PI Cai Z, Jackson MP, Peterson PA, Shi W, Korg Y, Degraw C;  
 XX  
 DR WPI; 2003-120673/11.  
 XX

PT Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T the cell  
 PT epitopes  
 PS Example 3: Column 47; 49pp; English.  
 XX The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumor self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune hepatitis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HcA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 63.8%; Score 10; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QYQVMD 9  
 PE 1 QYQVMD 6  
 RESULT 11  
 AAE1448:  
 ID AAE:4461 standard; Peptide; 7 AA  
 XX  
 AC AAE:4481:  
 DT 26-MAR-2002 (first entry;  
 XX  
 DE Cynophorus gracilirostris luciferase 35 kDa subunit peptide.  
 XX  
 KW luciferase; deep sea luminous shrimp; decapoda; reporter enzyme;  
 KW 35 kDa subunit; photoprotein.  
 XX  
 OS Cynophorus gracilirostris.  
 XX  
 PN EP115633 A2.  
 XX  
 PD 21 NOV-2001.  
 XX  
 PF 25-APR-2001; 2001EP-0109479.  
 XX  
 PP 26-APR-2000; 2000JP-0125053.  
 XX  
 PA (CHCC) CHISSO CORP.  
 XX  
 PI Inouye S.  
 XX  
 WPI; 2002 084118/12.  
 XX  
 XX Novel secretional luciferase derived from the deep sea luminous  
 PT shrimp Cynophorus gracilirostris consists of 19kDa and 35 kDa subunits  
 PT and is useful as a reporter enzyme.  
 XX  
 PS Example 4: Page 11; 35pp; English.  
 XX  
 XX The invention relates to polynucleotide encoding secretional luciferase  
 CC derived from deep sea luminous shrimp (Cynophorus gracilirostris). The  
 CC luciferase protein is composed of 19 and 35 kDa proteins and  
 CC is useful as a reporter enzyme. Antibodies against luciferase and  
 CC oligonucleotides derived from luciferase polynucleotides are useful for

CC identification of novel luciferase or photoproteins from related  
 CC species. The present sequence is a peptide from 35 kDa  
 CC subunit of Cynophorus gracilirostris luciferase.  
 XX  
 XX Sequence 7 AA:  
 SQ  
 Query Match 59.6%; Score 28; DB 23; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 QYQVMD 4  
 DB 1 QYQVMD 7  
 RESULT 12  
 ABJ1282:  
 ID ABJ1282 standard; Peptide; 9 AA.  
 XX  
 AC ABJ1282:  
 DT 10-DEC-2002 (first entry;  
 XX  
 DE Human 125P5C8 epitope #1447.  
 XX  
 KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
 KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200272785-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 13-MAR-2002; 2002WO-US07855.  
 XX  
 PP 14-MAR-2001; 2001US-CRC9635.  
 XX  
 PA (AGEN) AGENSYS INC.  
 XX  
 PI Faris M, Chailita eld PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
 PI Morrison RK, Morrison K, Jakobovits A;  
 XX  
 WPI; 2002-713510/77.  
 XX  
 XX New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8. Useful for  
 PT treating or preventing cancer that expresses or over expresses 125P5C8  
 PT .  
 XX  
 PS Disclosure; Page 163; 274pp; English.  
 XX  
 XX The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 59.6%; Score 28; DB 23; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ECGQVMD 9  
 DB 1 ECGVMD 9  
 RESULT 13

AAE5101  
 ID AAE5101 standard; peptide; 9 AA.  
 XX  
 KW AAE5101;  
 XX  
 XX 28-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E (IgE) HLA-A2 peptide motif #13.  
 XX  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 XX Lupus; autoimmune disease; rheumatoid arthritis; autoimmune hepatitis;  
 XX psoriasis; AIC; multiple sclerosis; autoimmune lymphoidosis; hay fever;  
 XX inflammatory bowel disease; insulin dependent diabetes mellitus; cell therapy;  
 XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 XX transplant rejection; human; immunoglobulin E; IgE  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2002029273 A2.  
 XX  
 PD 21-MAY-2002.  
 XX  
 PF 13-MAY-2002; 2002WC-US15341.  
 XX  
 PR 15 MAY 2002; 2002US-291300P.  
 XX  
 PA (ORTH) ORTHO MCNEIL PHARM INC.  
 XX  
 PI Gal Z, Jackson RR, Peterson PA, Shi W, Kong Y, Redraw J.  
 XX  
 DR WPI; 2003-120693/11.  
 XX  
 CC Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 CC diseases, comprises culturing CD8+ T cells with antigen presenting  
 CC cells to activate precursor CD8+ T cells specific for T cell  
 CC epitopes.  
 XX  
 PS Example 3; Column 45; 49pp; English.  
 CC The invention relates to a method of producing cytotoxic T lymphocytes  
 CC which are specific for one or more tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune hepatitis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection. Other autoimmune  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 55.1%; Score 24; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY : EQGVV 5  
 DB : EQGVV 9  
 DE AbG67564 standard; Peptide; 9 AA.  
 ID AbG67564  
 XX  
 KW AbG67564;  
 XX  
 XX 07-DEC-2002 (first entry)  
 XX  
 DE Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;

DE Human ADPI tryptic digest peptide #273.  
 XX  
 KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
 KW Alzheimer's disease-associated feature; neuroprotective;  
 KW Alzheimer's disease-associated protein isoform; nootropic;  
 KW ADPI tryptic digest peptide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246767-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 29-NOV-2001; 2001WA-GR05289.  
 XX  
 PR 08-DEC-2000; 2000WJ 25441F  
 XX  
 PA (OXFO) OXFORD GLYCONSCIENCES UK LTD.  
 XX  
 PI Herath HMAc, Parakk RB, Rohlf C;  
 XX  
 DR WPI; 2002-508575/54.  
 XX  
 CC Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 CC comprises detecting Alzheimer's disease-associated features or  
 CC Alzheimer's disease associated protein isoforms in brain tissue  
 CC from the subject.  
 XX  
 PS Claim 7; Page 55; 427pp; English.  
 CC The present invention relates to methods and compositions for the  
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in  
 CC a subject. The method comprises analysing a sample of brain tissue  
 CC from a subject by 2D electrophoresis to generate a 2D array of  
 CC Alzheimer's disease-associated features (ADFs), whose relative  
 CC abundance correlates with the presence, absence, stage or severity of  
 CC AD and comparing the abundance of each feature with the abundance of  
 CC that chosen feature in brain tissue from persons free from AD. The  
 CC invention also describes Alzheimer's disease associated protein  
 CC isoforms (ADPIs) detectable in brain tissue. The methods and  
 CC compositions of the invention are useful for the screening, diagnosis  
 CC or prognosis of AD in a subject, for determining the stage or severity  
 CC of AD in a subject, for identifying a subject at risk of developing AD,  
 CC or for monitoring the effect of therapy administered to a subject  
 CC having AD. Antibodies capable of binding to ADPIs are useful for  
 CC treating or preventing AD, and for determining the efficacy of a given  
 CC treatment regime. An agent that modulates the activity of ADPI is  
 CC useful in the manufacture of a medicament for the treatment or  
 CC prevention of AD in a subject. ABG67292-ABG68238 represent human ADPI  
 CC tryptic digest peptides.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 51.2%; Score 25; DB 23; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY : 3 GQVMDV 8  
 DB : 1 GQVMDV 6  
 DE AAE35082 standard; peptide; 9 AA.  
 ID AAE35082  
 XX  
 KW AAE35082;  
 XX  
 XX 28-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E (IgE) HLA-A2 peptide motif #20.  
 XX  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;



GenCore version 5.1.6  
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3M protein - protein search, using sw model

Run on: November 5, 2003, 13:14:14 / Search time: 29 seconds  
without alignment  
5,102 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDGQWMDV 9

Scoring table: BLOSUM62

Sapop 12.0, Gapext 0.5

Searched: 644070 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 1127

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA\*  
1: /sgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB pep.  
2: /sgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB pep.  
3: /sgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB pep.  
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17: /sgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB pep.  
18: /sgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB pep.

Prob. No. is the number of results produced by search. Prob. No. is the number of results greater than or equal to the score of the best hit printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	47	100.0	9	12	US-10-082-014-273
2	47	100.0	9	12	US-10-082-014-273
3	28	59.6	7	10	US-09-920-174-41
4	22	48.9	8	12	US-10-082-014-273
5	22	46.8	7	10	US-09-935-384-450
6	22	46.8	7	15	US-09-889-767A-110
7	22	46.8	8	15	US-10-082-014-273
8	22	46.8	9	12	US-10-082-014-273
9	22	46.8	9	15	US-09-920-174-41
10	22	46.8	9	15	US-10-082-014-273
11	21	44.7	9	11	US-09-935-384-450
12	21	44.7	9	10	US-09-935-384-450
13	21	44.7	9	10	US-09-935-384-450
14	21	44.7	9	10	US-09-935-384-450
15	21	44.7	9	10	US-09-935-384-450

16	21	44.7	9	10	US-09-780-053-454
17	21	44.7	9	10	US-09-780-053-454
18	21	44.7	9	10	US-09-920-174-41
19	21	44.7	9	12	US-09-920-174-41
20	20	42.6	6	11	US-09-935-384-450
21	20	42.6	6	12	US-09-935-384-450
22	20	42.6	6	12	US-09-935-384-450
23	20	42.6	6	12	US-09-935-384-450
24	20	42.6	6	12	US-09-935-384-450
25	20	42.6	6	12	US-09-935-384-450
26	20	42.6	6	12	US-09-935-384-450
27	20	42.6	6	12	US-09-935-384-450
28	20	42.6	6	12	US-09-935-384-450
29	19	40.4	6	12	US-09-935-384-450
30	19	40.4	6	12	US-09-935-384-450
31	19	40.4	6	12	US-09-935-384-450
32	19	40.4	6	12	US-09-935-384-450
33	19	40.4	6	12	US-09-935-384-450
34	19	40.4	6	12	US-09-935-384-450
35	19	40.4	6	12	US-09-935-384-450
36	19	40.4	6	12	US-09-935-384-450
37	19	40.4	6	12	US-09-935-384-450
38	19	40.4	6	12	US-09-935-384-450
39	19	40.4	6	12	US-09-935-384-450
40	19	40.4	6	12	US-09-935-384-450
41	19	40.4	6	12	US-09-935-384-450
42	19	40.4	6	12	US-09-935-384-450
43	19	40.4	6	12	US-09-935-384-450
44	19	40.4	6	12	US-09-935-384-450
45	19	40.4	6	12	US-09-935-384-450

ALIGNMENTS

RESULT 1  
US-10-082-014-273  
; Sequence 273, Application US10082014  
; Publication No. US200318588A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,315  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 273  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-273

Query Match 100.0% Score 47 DB 12 Length 9;  
Best Local Similarity 100.0% Prid. NO. 5.8e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
| | | | |  
DB 1 EDGQWMDV 9

RESULT 2  
US-10-372-076-127  
; Sequence 127, Application US10372076  
; Publication No. US2003198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,046  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,244  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 306  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 127  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10 102-07A-127

Query Match 100.0% Score 47 DB 147 Length 9  
Best Local Similarity 100.0% Pred No 5.8e+05  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQWMD 9  
DB 1 EQQWMD 9

RESULT 3  
US-09-842-164-12  
Sequence 12, Application US/09842154  
Publication No. US2002010587A1  
GENERAL INFORMATION:  
APPLICANT: INGOYE, Satoshi  
TITLE OF INVENTION: Luciferase and Photoprotein  
FILE REFERENCE: 206457US0  
CURRENT APPLICATION NUMBER: US/09/842,154  
CURRENT FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: JAPAN 2000-100053  
PRIOR FILING DATE: 2000-04-26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 12  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Opiliones graciliorstin  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: 111-171  
OTHER INFORMATION: PRT, 35 kDa protein, partial  
US 09 842 164-12

Query Match 59.8% Score 47 DB 147 Length 9  
Best Local Similarity 51.4% Pred No 5.8e+05  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQWMD 9  
DB 1 EQQWMD 9

RESULT 4  
US-10 147 40-47  
Sequence 47, Application US/10/47140  
Publication No. US2003015373A1  
GENERAL INFORMATION:  
APPLICANT: STRACKE, VARY  
APPLICANT: LIOTTA, LANCE  
APPLICANT: SCHIFFMAN, ELIJOTT  
APPLICANT: KRUTZ, HENRY  
APPLICANT: MURRAY, JON

TITLE OF INVENTION: MOTILITY STIMULATING AND BINDING AGENTS IN  
THERAPY FOR CANCER DIAGNOSIS AND THERAPY  
FILE REFERENCE: 2006 4149US4  
CURRENT APPLICATION NUMBER: US/10/147,140  
CURRENT FILING DATE: 2002-05-15  
PRIOR APPLICATION NUMBER: 07/822,044

PRIOR FILING DATE: 1992-01-17  
PRIOR APPLICATION NUMBER: 08/249,192  
PRIOR FILING DATE: 1994-05-25  
PRIOR APPLICATION NUMBER: 08/346,455  
PRIOR FILING DATE: 1994-11-28  
PRIOR APPLICATION NUMBER: 08/977,221  
PRIOR FILING DATE: 1997-11-24  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO: 47  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-10-147 140-47

Query Match 48.9% Score 23 DB 12 Length 8  
Best Local Similarity 80.0% Pred No 5.8e+05  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQWMD 7  
DB 3 GQWMD 7

RESULT 5  
US-09-884-767A-110  
Sequence 110, Application US/09884767A  
Publication No. US20020192799A1  
GENERAL INFORMATION:  
APPLICANT: DYAX Corp.  
APPLICANT: LANE, Christopher J.  
APPLICANT: LANE, Robert C.  
TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
CURRENT APPLICATION NUMBER: US/09/884,767A  
CURRENT FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 09/597,321  
PRIOR FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 110  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic enterokinase cleavage sequence  
US 09 884 767A-110

Query Match 48.8% Score 22 DB 10 Length 7  
Best Local Similarity 60.3% Pred No 5.8e+05  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQWMD 7  
DB 1 GQWMD 5

RESULT 6  
US-10-006-869-1617  
Sequence 1617, Application US/10006869  
Publication No. US20030082166A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W  
APPLICANT: SYNGENE, James Matthew  
APPLICANT: GOUR, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CACHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100066 407C7  
CURRENT APPLICATION NUMBER: US/10/006,869

? CURRENT FILING DATE: 2001-12-03  
 ? NUMBER OF SEQ ID NOS: 4052  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 1617

? LENGTH: 7  
 ? TYPE: PRT

? ORGANISM: Artificial Sequence  
 ? FEATURE:

? OTHER INFORMATION: Representative cyclic modulating agent based on  
 ? OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
 US-10-006 869-1623

Query Match: 46.8%; Score 22; DB 15; Length 7;

Best Local Similarity: 66.7%; Pred. No. 5.8e+55;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QINQVD 9

DB 1 1 1

2 QINQVD 7

RESULT 7

US-10-006 869-1623

? Sequence 1623, Application US/10006869

? Publication No. US20010052166A1

? GENERAL INFORMATION:

? APPLICANT: Blaschuk, Crest W.

? APPLICANT: Symonds, James Matthew

? APPLICANT: Gour, Barbara J.

? TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEUROLOGICAL

? TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

? FILE REFERENCE: 100066 407C7

? CURRENT APPLICATION NUMBER: US/10/006 869

? CURRENT FILING DATE: 2001-12-03

? NUMBER OF SEQ ID NOS: 4052

? SOFTWARE: Patent In Ver. 2.0

? SEQ ID NO 1623

? LENGTH: 8

? TYPE: PRT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Representative cyclic modulating agent based on

? OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence

US-10-006 869-1623

Query Match: 46.8%; Score 22; DB 15; Length 8;

Best Local Similarity: 66.7%; Pred. No. 5.8e+55;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QINQVD 9

DB 1 1 1

2 QINQVD 7

RESULT 8

US-10-160-162-263

? Sequence 263, Application US/10160162

? Publication No. US20030166541A1

? GENERAL INFORMATION:

? APPLICANT: Ruben et al.

? TITLE OF INVENTION: 83 Human Secreted Proteins

? FILE REFERENCE: P2012P2

? CURRENT APPLICATION NUMBER: US/10/160,162

? CURRENT FILING DATE: 2002-06-04

? PRIOR APPLICATION NUMBER: 60/295,558

? PRIOR FILING DATE: 2001-06-05

? PRIOR APPLICATION NUMBER: 09/236,557

? PRIOR FILING DATE: 1999-01-26

? PRIOR APPLICATION NUMBER: PCT/US99/15949

? PRIOR FILING DATE: 1998-07-29

? PRIOR APPLICATION NUMBER: 60/054,212

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,234

? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,234  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,218  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,214  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,236  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,215  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,211  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,217  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/054,113  
 ? PRIOR FILING DATE: 1997-07-30  
 ? PRIOR APPLICATION NUMBER: 60/055,968  
 ? PRIOR FILING DATE: 1997-08-18  
 ? PRIOR APPLICATION NUMBER: 60/055,969  
 ? PRIOR FILING DATE: 1997-08-18  
 ? PRIOR APPLICATION NUMBER: 60/055,972  
 ? PRIOR FILING DATE: 1997-08-18  
 ? PRIOR APPLICATION NUMBER: 60/056,561  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,534  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,729  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,543  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,727  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,554  
 ? PRIOR FILING DATE: 1997-08-19  
 ? PRIOR APPLICATION NUMBER: 60/056,730  
 ? PRIOR FILING DATE: 1997-08-19  
 ? NUMBER OF SEQ ID NOS: 353  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 263  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-10-160-162-263

Query Match: 46.8%; Score 22; DB 12; Length 9;

Best Local Similarity: 100.0%; Pred. No. 5.8e+55;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4

DB 5 EDGQ 8

RESULT 9

US-03-820-649-263

? Sequence 263, Application US/09820649

? Publication No. US20030199683A1

? GENERAL INFORMATION:

? APPLICANT: Ruben et al.

? TITLE OF INVENTION: 83 Human Secreted Proteins

? FILE REFERENCE: P2012P1

? CURRENT APPLICATION NUMBER: US/09/820,649

? CURRENT FILING DATE: 2001-03-30

? PRIOR APPLICATION NUMBER: US/09/236,557

? PRIOR FILING DATE: 1999-01-26

? PRIOR APPLICATION NUMBER: PCT/US98/15949

? PRIOR FILING DATE: 1998-07-29

? PRIOR APPLICATION NUMBER: 60/054,212

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,209

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,234

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1 PRIOR FILING DATE: 1997-07-30
2 PRIOR APPLICATION NUMBER: 60/054,218
3 PRIOR FILING DATE: 1997-07-30
4 PRIOR APPLICATION NUMBER: 60/054,219
5 PRIOR FILING DATE: 1997-07-30
6 PRIOR APPLICATION NUMBER: 60/054,219
7 PRIOR FILING DATE: 1997-07-30
8 PRIOR APPLICATION NUMBER: 60/054,219
9 PRIOR FILING DATE: 1997-07-30
10 PRIOR APPLICATION NUMBER: 60/054,219
11 PRIOR FILING DATE: 1997-07-30
12 PRIOR APPLICATION NUMBER: 60/054,219
13 REMAINING PRIOR APPLICATION DATA REMOVED See File Wrapper on PAM
14 NUMBER OF SEQ ID NOS: 353
15 SOFTWARE: Patent in Ver. 2.0
16 SEQ ID NO: 263
17 LENGTH: 9
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-09-914-088-1

```

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Query Match 46.8% Score 21 DB 12 Length 9
Best Local Similarity 100.0% Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY : EGG 4
DB : 5 EGG 8

```

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RESULT 10
US-09-914-088-1
Sequence 1626, Application US/1002866
Publication No. US20020082166A1
GENERAL INFORMATION:
APPLICANT: Symonds, Orest W.
APPLICANT: Gehr, Barbara C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELLULAR
FILE REFERENCE: 100286.407C7
CURRENT APPLICATION NUMBER: US/100286.863
PRIOR FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO: 1626
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative of a family of related sequences
US-09-914-088-1

```

```

Query Match 46.8% Score 21 DB 12 Length 9
Best Local Similarity 100.0% Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY : 4 GQVVD 9
DB : 4 GQVVD 9

```

```

RESULT 11
US-09-914-088-1
Sequence 28, Application US/09993180
Publication No. US20030054445A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN PERTIN SECRETED FROM LIVER
FILE REFERENCE: C22S, LSI-11
CURRENT APPLICATION NUMBER: US/099931.11
PRIOR FILING DATE: 2001-11-14

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1 PRIOR APPLICATION NUMBER: US 60/248,434
2 PRIOR FILING DATE: 2000-11-24
3 PRIOR APPLICATION NUMBER: US 60/257,610
4 PRIOR FILING DATE: 2000-12-21
5 PRIOR APPLICATION NUMBER: US 60/282,745
6 PRIOR FILING DATE: 2001-04-10
7 NUMBER OF SEQ ID NOS: 46
8 SOFTWARE: Patent in version 3.0
9 SEQ ID NO: 28
10 LENGTH: 8
11 TYPE: PRT
12 ORGANISM: Homo sapiens
13 US-09-914-088-1

```

```

Query Match 44.7% Score 21 DB 11 Length 8
Best Local Similarity 50.0% Pred. No. 5.8e-05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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```

QY : 3 GQVVD 8
DB : 2 GQVVD 2

```

```

RESULT 12
US-09-780-053-57
Sequence 57, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Bid
APPLICANT: Mary Faris
APPLICANT: Eliana Levin
APPLICANT: Steve Chappel Mitchell
APPLICANT: Aya Laskovics
TITLE OF INVENTION: 81P5G4: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.505J1
CURRENT APPLICATION NUMBER: US/09780.053
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,261
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 57
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-57

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```

Query Match 44.7% Score 21 DB 10 Length 9
Best Local Similarity 100.0% Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY : 2 DQGV 5
DB : 3 DQGV 6

```

```

RESULT 13
US-09-780-053-142
Sequence 142, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Bid
APPLICANT: Mary Faris
APPLICANT: Eliana Levin
APPLICANT: Steve Chappel Mitchell
APPLICANT: Aya Laskovics
TITLE OF INVENTION: 81P5G4: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.505J1
CURRENT APPLICATION NUMBER: US/09780.053

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FILE REFERENCE: 129.5USU1  
 CURRENT APPLICATION NUMBER: US/09/780,053  
 CURRENT FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/181,261  
 PRIOR FILING DATE: 2000-02-09  
 NUMBER OF SEQ ID NOS: 716  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 142  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 US-09-914-088-1-434

Query Match 44.7%; Score 21; PR 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 DGGV 5  
 DE 6 DGGV 9

## RESULT 14

US-09-914-088-1-253  
 Sequence 253, Application US/09780053  
 Patent No. US2002102640A1  
 GENERAL INFORMATION:  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Paros  
 APPLICANT: Elana Levin  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN  
 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 FILE REFERENCE: 129.5USU1  
 CURRENT APPLICATION NUMBER: US/09/780,053  
 CURRENT FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/181,261  
 PRIOR FILING DATE: 2000-02-09  
 NUMBER OF SEQ ID NOS: 716  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 253  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 US-09-914-088-1-253

Query Match 44.7%; Score 21; PR 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 DGGV 5  
 DE 3 DGGV 6

## RESULT 15

US-09-914-088-1-434  
 Sequence 434, Application US/09780053  
 Patent No. US2002102640A1  
 GENERAL INFORMATION:  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Paros  
 APPLICANT: Elana Levin  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN  
 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 FILE REFERENCE: 129.5USU1

CURRENT APPLICATION NUMBER: US/09/780,053  
 CURRENT FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/181,261  
 PRIOR FILING DATE: 2000-02-09  
 NUMBER OF SEQ ID NOS: 716  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 434  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 US-09-914-088-1-434

Query Match 44.7%; Score 21; PR 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 DGGV 5  
 DE 1 DGGV 4

Search completed: November 5, 2003, 17:19:16  
 Job time : 30 secs



```

1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: WordPerfect 5.1
3 CURRENT APPLICATION NUMBER: US/09/346,455B
4 FILING DATE: 28 NOV-1994
5 CLASSIFICATION: 530
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: PCT/US95/756e13
8 FILING DATE: 24 MAY-1995
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/249,182
11 FILING DATE: 25 MAY-1994
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 07/822,043
14 FILING DATE: 17 JAN-1992
15 NAME: DOROTHY R. AUTH
16 REGISTRATION NUMBER: 36,434
17 REFERENCE/DOCKET NUMBER: 2026 4149PCT
18 TELEPHONE: 1212 758-4800
19 TELEFAX: 1212 758-6849
20 INFORMATION FOR SEQ ID NO: 47:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 8
23 TYPE: amino acids
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: peptide
27 DESCRIPTION: Peptide
28 HYPOTHETICAL: NO
29 FEATURES:
30 NAME/KEY: ATX 206
31 LOCATION:
32 IDENTIFICATION METHOD:
33 OTHER INFORMATION:
34 US 08-146-455B-47
35
36 Query Match 48.9% Score 23; DB 1; Length 8;
37 Best Local Similarity 80.0%; Pred. No. 2.5e+09;
38 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
39
40 QY 3 QQVMD 7
41 I I I
42
43 Db 3 QQLMD 7
44
45 RESULT 1
46 US 09-914-088-1
47 Sequence 47, Application US/09/346,455B
48 Patent No. 6417318
49 GENERAL INFORMATION:
50 APPLICANT: STRACK, VARY
51 APPLICANT: LIOTTA, DANCE
52 APPLICANT: SCHEFFMANN, ELLIOTT
53 APPLICANT: KRUTZ, HENRY
54 APPLICANT: MURATA, JUN
55 TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
56 TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
57 FILE REFERENCE: 2026 4149US4
58 CURRENT APPLICATION NUMBER: US/09/463,831-B
59 PRIOR FILING DATE: 2000-01-17
60 PRIOR APPLICATION NUMBER: 07/822,043
61 PRIOR FILING DATE: 1992-01-17
62 PRIOR APPLICATION NUMBER: 08/249,182
63 PRIOR FILING DATE: 1994-05-25
64 PRIOR APPLICATION NUMBER: 08/346,455
65 PRIOR FILING DATE: 1994-11-28
66 PRIOR APPLICATION NUMBER: 08/977,221
67 PRIOR FILING DATE: 1997-11-24
68 NUMBER OF SEQ ID NOS: 70
69 SOFTWARE: Patent In Ver. 2.1
70 SEQ ID NO 47
71 LENGTH: 8
72 TYPE: PR
73 ORGANISM: Artificial Sequence
74 FEATURE:
75 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

```

1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/346,455
4 FILING DATE: 28 NOV-1994
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/249,182
7 FILING DATE: 25 MAY-1994
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 07/822,043
10 FILING DATE: 17 JAN-1992
11 ATTORNEY/AGENT INFORMATION:
12 NAME: DOROTHY R. AUTH
13 REGISTRATION NUMBER: 36,434
14 REFERENCE/DOCKET NUMBER: 2026-4149US3
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 1212 758-4800
17 TELEFAX: 1212 758-6849
18 INFORMATION FOR SEQ ID NO: 47:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8
21 TYPE: amino acids
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 DESCRIPTION: Peptide
26 HYPOTHETICAL: NO
27 FEATURES:
28 NAME/KEY: ATX 216
29 LOCATION:
30 IDENTIFICATION METHOD:
31 OTHER INFORMATION:
32 US-08-977-221-47
33
34 Query Match 48.9% Score 23; DB 3; Length 8;
35 Best Local Similarity 80.0%; Pred. No. 2.5e+09;
36 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
37
38 QY 3 QQVMD 7
39 I I I
40
41 Db 3 QQLMD 7
42
43 RESULT 4
44 US 09-463 831B-47
45 Sequence 47, Application US/09463831-B
46 Patent No. 6417318
47 GENERAL INFORMATION:
48 APPLICANT: STRACK, VARY
49 APPLICANT: LIOTTA, DANCE
50 APPLICANT: SCHEFFMANN, ELLIOTT
51 APPLICANT: KRUTZ, HENRY
52 APPLICANT: MURATA, JUN
53 TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
54 TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
55 FILE REFERENCE: 2026 4149US4
56 CURRENT APPLICATION NUMBER: US/09/463,831-B
57 PRIOR FILING DATE: 2000-01-17
58 PRIOR APPLICATION NUMBER: 07/822,043
59 PRIOR FILING DATE: 1992-01-17
60 PRIOR APPLICATION NUMBER: 08/249,182
61 PRIOR FILING DATE: 1994-05-25
62 PRIOR APPLICATION NUMBER: 08/346,455
63 PRIOR FILING DATE: 1994-11-28
64 PRIOR APPLICATION NUMBER: 08/977,221
65 PRIOR FILING DATE: 1997-11-24
66 NUMBER OF SEQ ID NOS: 70
67 SOFTWARE: Patent In Ver. 2.1
68 SEQ ID NO 47
69 LENGTH: 8
70 TYPE: PR
71 ORGANISM: Artificial Sequence
72 FEATURE:
73 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

## OTHER INFORMATION: Peptide

US-09-914-088-1

Query Match 49.98; Score 23; DB 4; Length 4;  
Best Local Similarity 80.08; Pred. NC. 2.5e-05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMD 7  
I I I I  
Db 3 GQLMD 7

## RESULT 5

US-09-914-088-1-47  
Sequence 47, Application PC/US9506613  
GENERAL INFORMATION:  
APPLICANT: STRACKS, VARY, LIOTTA, LENSE,  
APPLICANT: SCHIFFMANN, ELICOTT, KRUTSCH,  
APPLICANT: HENRY, MURATA, JUN  
TITLE OF INVENTION: MOTILITY STIMULATING  
TITLE OF INVENTION: PROTEIN USED IN CANCER DIAGNOSIS AND  
TITLE OF INVENTION: THERAPY  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PC/US9506613  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,455  
FILING DATE: 26-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,182  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/822,041  
FILING DATE: 17-JAN-1992

ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY P. JUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026-4-1-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: peptide  
HYPOTHETICAL: No  
FEATURE:  
NAME/KEY: ATX-216  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PT US95-06613-47

Query Match 49.98; Score 23; DB 4; Length 4;  
Best Local Similarity 80.08; Pred. NC. 2.5e-05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMD 7  
I I I I  
Db 3 GQLMD 7

## RESULT 6

US-08-447-010-26  
Sequence 26, Application US/06447010  
Patent No. 5703718  
GENERAL INFORMATION:  
APPLICANT: MORFATT, BARBARA  
TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 330 University Avenue, Suite 701  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,010  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/230,695  
FILING DATE: 21-APR-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/888,132  
FILING DATE: 26-MAY-1992  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: STEWART, MICHAEL I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1811 181 XIS-V9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
TELEX: 065-24567 SIMBAS  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-447-010-26

Query Match 45.88; Score 22; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. NC. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
I I I I  
Db 1 EDGQ 4

## RESULT 7

US-08-421-155-8  
Sequence 8, Application US/28421155  
Patent No. 5703057  
GENERAL INFORMATION:  
APPLICANT: Barry, Michael A.  
APPLICANT: Lal, Wayne C.  
APPLICANT: Johnston, Stephen A.

TITLE OF INVENTION: Expression Library Immunization  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421-155  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: JTXD-411-KIT  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 418-3000  
TELEX: 79 0944  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US 08 421-155 8

Query Match 46.8% Score 22: DB 1: Length 6;  
Best Local Similarity 60.0% Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0;

CY 3 EGGQ 7  
DB 2 EGGQ 6

RESULT 9  
US-08-232-539D-26  
Sequence 26, Application US/08/232539D  
Patent No. 5965769  
GENERAL INFORMATION:  
APPLICANT: Pressa, Leonard G.  
ADDRESSEE: Cardillo, Paula M.  
TITLE OF INVENTION: Igs Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178563  
FILING DATE: 07-JAN-1994  
PRICE APPLICATION DATA:

APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: PC7-8P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1469  
TELEFAX: 650/295-5988  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-26  
Query Match 46.8% Score 22: DB 2: Length 6;  
Best Local Similarity 100.0% Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

CY 1 EGGQ 4  
DB 3 EGGQ 6

RESULT 9  
US-09-001-157-8  
Sequence 8, Application US/09001157  
Patent No. 5989553  
GENERAL INFORMATION:  
APPLICANT: Johnston, Stephen A.  
APPLICANT: Barry, Michael A.  
APPLICANT: Lai, Wayne C.  
TITLE OF INVENTION: EXPRESSION LIBRARY IMMUNIZATION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/001,157  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/421,155  
FILING DATE: 07-APR 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: JTXD-529  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474 7577  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-001-157-8

Query Match 46.8% Score 22: DB 2: Length 6;  
Best Local Similarity 60.0% Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0;

QY 3 QGVND 7  
1111  
DB 2 QGILD 6

RESULT 10  
US-09-147-859-1617  
Sequence 1617, Application US/09187869A  
Patent No. 6159320  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Crest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING N-GLYCOSYLATION  
FILE REFERENCE: 13086-40701  
CURRENT APPLICATION NUMBER: US/09/147-859A  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 4552  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1617  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Representative cyclic modulation agent based on  
OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-147-859-1617

Query Match 46.8%, Score 22, DB 4, Length 7  
Best Local Similarity 66.7%, Pref No 2.5e+05  
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0

QY 4 QGVND 9  
1111  
DB 2 QGVND 7

RESULT 11  
US-09-147-859-1617  
Sequence 1617, Application US/09187869A  
Patent No. 6159320  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Crest W.  
APPLICANT: Symonds, James Matthew  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING N-GLYCOSYLATION  
FILE REFERENCE: 13086-40701  
CURRENT APPLICATION NUMBER: US/09/147-859A  
CURRENT FILING DATE: 2001-04-20  
NUMBER OF SEQ ID NOS: 4552  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1617  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Representative cyclic modulation agent based on  
OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-147-859-1617

Query Match 46.8%, Score 22, DB 4, Length 7  
Best Local Similarity 66.7%, Pref No 2.5e+05  
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0

QY 4 QGVND 9  
1111  
DB 2 QGVND 7

RESULT 12  
US-09-421-155-6  
Sequence 6, Application US/09421155

Patent No. 5763257  
GENERAL INFORMATION:  
APPLICANT: Barry, Michael A.  
APPLICANT: Lai, Wayne C.  
APPLICANT: Johnston, Stephen A.  
TITLE OF INVENTION: Expression Library Immunization  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/421,155  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSD:411/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 489-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-421-155-6

Query Match 46.8%, Score 22, DB 1, Length 8;  
Best Local Similarity 60.0%, Pref No 2.5e+05;  
Matches 3, Conservative 2, Mismatches 0, Indels 0, Gaps 0;

QY 3 QGVND 7  
1111  
DB 2 QGILD 6

RESULT 13  
US-08-571-485-24  
Sequence 20, Application US/08571485  
Patent No. 5783557  
GENERAL INFORMATION:  
APPLICANT: Burstein, Vigal  
APPLICANT: Traiman, Nathan  
APPLICANT: Rykus, Avigail  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
TITLE OF INVENTION: Compositions Comprising Them  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 40500 No. 5753557 Western Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/571,985  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth J.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2163 0049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 910 539-5050  
TELEFAX: 910 539-5055  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09 371-995 20

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+55;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
DB 2 EDGQ 5

RESULT 14  
US-09-487-860 60  
Sequence 60, Application US/08487560  
Patent No. 5792456  
GENERAL INFORMATION:  
APPLICANT: Yellon, Dale  
APPLICANT: Glaser, Scott  
APPLICANT: Huse, William  
APPLICANT: Kosak, Mae J.  
TITLE OF INVENTION: No. 5792456-2 Mutant ER96 Antibodies and  
Functional Equivalents Reactive With Human Carcinomas  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 11150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025 1975  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,860  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30456 14791  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310 445-1140  
TELEFAX: 310 445-9031  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-487-860-60 14

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 42.9%; Pred. No. 2.5e+55;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQWD 7  
DB 2 QCGDITD 5

RESULT 15  
US-09 116-766-20  
Sequence 20, Application US/59116766  
Patent No. 5968898  
GENERAL INFORMATION:  
APPLICANT: Burstein, Yigal  
APPLICANT: Trautman, Nathan  
APPLICANT: Ryckman, Avigail  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
Compositions Comprising Them  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5968898thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/116,766  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 2163 00050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 439 5055  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09 116-766-20

Query Match 46.8%; Score 22; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
DB 2 EDGQ 5

Search completed: November 5, 2003, 17:15:10  
Job time : 22 secs

GenCore version 5.1.15  
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(X) protein - protein search, using sw model

Run on: November 5, 2003, 15:19:51 / Search time 8 04:15 seconds  
(without alignment)  
47 141 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EGVMDVD 9

Scoring table: BLOSUM62

Gap: 10.0, Gapext 2.5

Searched: 318711 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 18711

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: /sgn2\_6/ptodata/1/aa/5A\_COMB pep.
- 2: /sgn2\_6/ptodata/1/aa/5B\_COMB pep.
- 3: /sgn2\_6/ptodata/1/aa/5A\_COMB pep.
- 4: /sgn2\_6/ptodata/1/aa/5B\_COMB pep.
- 5: /sgn2\_6/ptodata/1/aa/5A\_COMB pep.
- 6: /sgn2\_6/ptodata/1/aa/5B\_COMB pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	70.2	462	US-09-914-088-1	Sequence 7128, Ap
2	33	70.2	468	US-09-914-088-1	Sequence 17208, A
3	33	70.2	948	US-09-914-088-1	Sequence 6123, Ap
4	33	70.2	1119	US-09-914-088-1	Sequence 1, Appl
5	32	68.1	273	US-09-914-088-1	Sequence 121, Appl
6	32	68.1	293	US-09-914-088-1	Sequence 2215, A
7	32	68.1	394	US-09-914-088-1	Sequence 21, Appl
8	32	68.1	422	US-09-914-088-1	Sequence 3, Appl
9	32	68.1	426	US-09-914-088-1	Sequence 7, Appl
10	32	68.1	478	US-09-914-088-1	Sequence 9, Appl
11	32	68.1	508	US-09-914-088-1	Sequence 1, Appl
12	32	68.1	508	US-09-914-088-1	Sequence 1, Appl
13	32	68.1	1357	US-09-914-088-1	Sequence 21306, A
14	31.5	67.0	90	US-09-914-088-1	Sequence 615, App
15	31.5	67.0	232	US-09-914-088-1	Sequence 1, Appl
16	31.5	67.0	232	US-09-914-088-1	Sequence 1, Appl
17	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
18	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
19	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
20	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
21	31	66.0	247	US-09-914-088-1	Sequence 44, Appl
22	31	66.0	294	US-09-914-088-1	Sequence 22068, A
23	31	66.0	294	US-09-914-088-1	Sequence 168, Ap
24	31	66.0	303	US-09-914-088-1	Sequence 6113, Ap
25	31	66.0	332	US-09-914-088-1	Sequence 1193, Ap
26	31	66.0	410	US-09-914-088-1	Sequence 22140, A
27	31	66.0	411	US-09-914-088-1	Sequence 2, Appl

28	31	66.0	411	US-09-914-088-1	Sequence 2, Appl
29	31	66.0	411	US-09-914-088-1	Sequence 2, Appl
30	31	66.0	414	US-09-914-088-1	Sequence 7057, Ap
31	31	66.0	517	US-09-914-088-1	Sequence 31115, A
32	31	66.0	520	US-09-914-088-1	Sequence 2, Appl
33	31	66.0	520	US-09-914-088-1	Sequence 2, Appl
34	31	66.0	604	US-09-914-088-1	Sequence 6437, Ap
35	31	66.0	735	US-09-914-088-1	Sequence 3440, Ap
36	30	63.8	29	US-09-914-088-1	Sequence 6, Appl
37	30	63.8	115	US-09-914-088-1	Sequence 6466, Ap
38	30	63.8	236	US-09-914-088-1	Sequence 5486, Ap
39	30	63.8	233	US-09-914-088-1	Sequence 36, Appl
40	30	63.8	237	US-09-914-088-1	Sequence 12496, A
41	30	63.8	240	US-09-914-088-1	Sequence 10, Appl
42	30	63.8	247	US-09-914-088-1	Sequence 46, Appl
43	30	63.8	252	US-09-914-088-1	Sequence 14, Appl
44	30	63.8	280	US-09-914-088-1	Sequence 323, App
45	30	63.8	283	US-09-914-088-1	Sequence 6278, Ap

ALIGNMENTS

RESULT 1  
US-09-914-088-1  
; Sequence 7128, Application US/09128352  
; Patent No. 6562959  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09128352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7128  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-914-088-1

Query Match: 70.2%, Score 33; DB 4; Length 462;  
Best Local Similarity: 65.7%; Pred. No: 1.2e+02;  
Matches: 6; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 3 GQVMDVD  
Db: 188 GQVMDVD

RESULT 2  
US-09-914-088-1  
; Sequence 17208, Application US/09128352  
; Patent No. 6561795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenstein et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09128352  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/374,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/394,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17208  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-914-088-1

Query Match: 70.2%, Score 33; DB 4; Length 468;



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Best Local Similarity 85.78; Score 30; DB 4; Length 119;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 3
US-09-396-6518 6123
; Sequence 6123, Application US/09396518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G099-03PA
; CURRENT APPLICATION NUMBER: US/09/094,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 50.0%; Pred. No. 1e-02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 4
US-09-396-6518 6123
; Sequence 6123, Application US/09396518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G099-03PA
; CURRENT APPLICATION NUMBER: US/09/094,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 50.0%; Pred. No. 1e-02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 5
US-09-427-7001 12
; Sequence 427, Application US/09427700
; Patent No. 6372489
; GENERAL INFORMATION:
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: METHOD AND MODEL FOR HAIR PIGMENTATION
; FILE REFERENCE: 31276-20017 C3
; CURRENT APPLICATION NUMBER: US/09/427,700
; CURRENT FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 60/105,725
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reduced amino acid sequence of SEQ ID NO:11
US-09-427-7001 12

Query Match 68.1%; Score 32; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 112 DGGQVMD 112

RESULT 6
US-09-252-991A-22215
; Sequence 22215, Application US/99252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Ruberfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 101361136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22215
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22215

Query Match 68.1%; Score 32; DB 4; Length 293;
Best Local Similarity 66.7%; Pred. No. 1e-02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGQVMD 9
DB 233 FIAEVALVD 241

RESULT 7
US-08-705-771-21
; Sequence 21, Application US/08705771
; Patent No. 6554289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, RAIN, GILFILLAN,
```

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Best Local Similarity 85.78; Score 30; DB 4; Length 119;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 3
US-09-396-6518 6123
; Sequence 6123, Application US/09396518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G099-03PA
; CURRENT APPLICATION NUMBER: US/09/094,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 50.0%; Pred. No. 1e-02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 4
US-09-396-6518 6123
; Sequence 6123, Application US/09396518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G099-03PA
; CURRENT APPLICATION NUMBER: US/09/094,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 50.0%; Pred. No. 1e-02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 194 GQLMVD 200

RESULT 5
US-09-427-7001 12
; Sequence 427, Application US/09427700
; Patent No. 6372489
; GENERAL INFORMATION:
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: METHOD AND MODEL FOR HAIR PIGMENTATION
; FILE REFERENCE: 31276-20017 C3
; CURRENT APPLICATION NUMBER: US/09/427,700
; CURRENT FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 60/105,725
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reduced amino acid sequence of SEQ ID NO:11
US-09-427-7001 12

Query Match 68.1%; Score 32; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQVMD 9
DB 112 DGGQVMD 112

RESULT 6
US-09-252-991A-22215
; Sequence 22215, Application US/99252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Ruberfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 101361136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22215
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22215

Query Match 68.1%; Score 32; DB 4; Length 293;
Best Local Similarity 66.7%; Pred. No. 1e-02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGQVMD 9
DB 233 FIAEVALVD 241

RESULT 7
US-08-705-771-21
; Sequence 21, Application US/08705771
; Patent No. 6554289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, RAIN, GILFILLAN,
```

ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/756,671  
 FILING DATE: August 30, 1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J.G.  
 REGISTRATION NUMBER: 33,073  
 REFERENCE/DOCKET NUMBER: 32581-344 (HF136)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 973-994-1720  
 TELEFAX: 973-994-1744  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 394 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09 705-771-21

Query Match 68.1%; Score 32; DB 1; Length 394;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDQGVMD 9  
 |||||  
 US 9 EDQGVMD 17

RESULT 8  
 US-08-152-483B-3  
 Sequence 3, Application US/08152483B  
 Patent No. 5529909  
 GENERAL INFORMATION:  
 APPLICANT: Della Cioppa, Guy  
 APPLICANT: Kumagai, Monte  
 TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
 TITLE OF INVENTION: PROTEIN FUSION ENZYME  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Perrine & Edmonds  
 STREET: 2730 Sand Hill Road  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/152,483B  
 FILING DATE: No. 5529909eember 12, 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 7/857,602  
 FILING DATE: March 30, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 923,692  
 FILING DATE: July 31, 1992  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 600,244  
 FILING DATE: October 22, 1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 641,617  
 FILING DATE: January 16, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 737,899  
 FILING DATE: July 26, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hattis, Albert P.  
 REGISTRATION NUMBER: 25,227  
 REFERENCE/DOCKET NUMBER: BIOG-20240/8129 040  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-854-3660  
 TELEFAX: 415-854-3694  
 TELEFAX: 6614; PENN: E  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 422  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: SOURCE:  
 ORGANISM:  
 IMMEDIATE SOURCE:  
 CLONE:  
 FEATURE:  
 US-08-152-483B-3

Query Match 68.1%; Score 32; DB 1; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGVMD 7  
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 DB 112 DGVMD 117

RESULT 9  
 US-08-152-483B-7  
 Sequence 7, Application US/08152483B  
 Patent No. 5529909  
 GENERAL INFORMATION:  
 APPLICANT: Della Cioppa, Guy  
 APPLICANT: Kumagai, Monte  
 TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
 TITLE OF INVENTION: PROTEIN FUSION ENZYME  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Perrine & Edmonds  
 STREET: 2730 Sand Hill Road  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/152,483B  
 FILING DATE: No. 5529909eember 12, 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 7/857,602  
 FILING DATE: March 30, 1992  
 PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: 923,692  
 2 FILING DATE: July 31, 1992  
 3 PRIOR APPLICATION DATA:  
 4 APPLICATION NUMBER: 600,244  
 5 FILING DATE: October 22, 1990  
 6 PRIOR APPLICATION DATA:  
 7 APPLICATION NUMBER: 641,617  
 8 FILING DATE: January 16, 1991  
 9 PRIOR APPLICATION DATA:  
 10 APPLICATION NUMBER: 737,899  
 11 FILING DATE: July 26, 1991  
 12 ATTORNEY/AGENT INFORMATION:  
 13 NAME: Halling, Albert P.  
 14 REGISTRATION NUMBER: 25,227  
 15 TELECOMMUNICATION INFORMATION:  
 16 TELEPHONE: (415) 854-3660  
 17 TELEFAX: (415) 854-3694  
 18 INFORMATION FOR SEQ ID NO: 1:  
 19 SEQUENCE CHARACTERISTICS:  
 20 LENGTH: 426  
 21 TYPE: amino acid  
 22 STRANDEDNESS:  
 23 TOPOLOGY: circular  
 24 MOLECULE TYPE:  
 25 DESCRIPTION: protein  
 26 HYPOTHEetical: NO  
 27 ANTI-SENSE: NO  
 28 ORIGINAL SOURCE:  
 29 ORGANISM:  
 30 IMMEDIATE SOURCE:  
 31 CLONE:  
 32 FEATURE:  
 33 US-09-152-483B-9

Query Match: 68.14, Score 12, DB 1, Length 478  
 Best Local Similarity: 100.0%, Prod. No.: 9e+22,  
 Matches: 6, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 2 DQVMD 7  
 DB 264 DQVMD 269

RESULT 1:  
 US-09-152-483B-9  
 1 Sequence 1, Application: US/914-088-1  
 2 Patent No. 584,089  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Schlegel, C. Richard  
 5 APPLICANT: Jensen, A. Bennett  
 6 TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
 7 TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
 8 NUMBER OF SEQUENCES: 2  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 11 STREET: P.O. Box 1404  
 12 CITY: Alexandria  
 13 STATE: Virginia  
 14 COUNTRY: United States  
 15 ZIP: 22313-1404  
 16 COMPUTER READABLE FORM:  
 17 MEDIUM TYPE: Floppy disk  
 18 OPERATING SYSTEM: PC-DOS/MS-DOS  
 19 SOFTWARE: Patent in Release #1.0,  
 20 VERSION: Version #1.25  
 21 CURRENT APPLICATION DATA:  
 22 APPLICATION NUMBER: US/08/152-483B  
 23 FILING DATE: Nov 6, 1993  
 24 PRIORITY DATA:  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: 923,692  
 27 FILING DATE: July 31, 1992  
 28 PRIOR APPLICATION DATA:  
 29 APPLICATION NUMBER: 600,244  
 30 FILING DATE: October 22, 1990  
 31 PRIOR APPLICATION DATA:  
 32 APPLICATION NUMBER: 641,617  
 33 FILING DATE: January 16, 1991  
 34 PRIOR APPLICATION DATA:  
 35 APPLICATION NUMBER: 737,899  
 36 FILING DATE: July 26, 1991  
 37 ATTORNEY/AGENT INFORMATION:  
 38 NAME: Halling, Albert P.  
 39 REGISTRATION NUMBER: 25,227  
 40 TELECOMMUNICATION INFORMATION:  
 41 TELEPHONE: (415) 854-3660  
 42 TELEFAX: (415) 854-3694  
 43 INFORMATION FOR SEQ ID NO: 1:  
 44 SEQUENCE CHARACTERISTICS:  
 45 LENGTH: 426  
 46 TYPE: amino acid  
 47 STRANDEDNESS:  
 48 TOPOLOGY: circular  
 49 MOLECULE TYPE:  
 50 DESCRIPTION: protein  
 51 HYPOTHEtical: NO  
 52 ANTI-SENSE: NO  
 53 ORIGINAL SOURCE:  
 54 ORGANISM:  
 55 IMMEDIATE SOURCE:  
 56 CLONE:  
 57 FEATURE:  
 58 US-09-152-483B-9

1 APPLICATION NUMBER: 7/857,602  
 2 FILING DATE: March 30, 1992  
 3 PRIOR APPLICATION DATA:  
 4 APPLICATION NUMBER: 923,692  
 5 FILING DATE: July 31, 1992  
 6 PRIOR APPLICATION DATA:  
 7 APPLICATION NUMBER: 600,244  
 8 FILING DATE: October 22, 1990  
 9 PRIOR APPLICATION DATA:  
 10 APPLICATION NUMBER: 641,617  
 11 FILING DATE: January 16, 1991  
 12 PRIOR APPLICATION DATA:  
 13 APPLICATION NUMBER: 737,899  
 14 FILING DATE: July 26, 1991  
 15 ATTORNEY/AGENT INFORMATION:  
 16 NAME: Halling, Albert P.  
 17 REGISTRATION NUMBER: 25,227  
 18 REFERENCE/DOCKET NUMBER: BIOG-20240/8123-040  
 19 TELECOMMUNICATION INFORMATION:  
 20 TELEPHONE: (415) 854-3660  
 21 TELEFAX: (415) 854-3694  
 22 TELEX: 66-41 PENNIE  
 23 INFORMATION FOR SEQ ID NO: 1:  
 24 SEQUENCE CHARACTERISTICS:  
 25 LENGTH: 478  
 26 TYPE: amino acid  
 27 STRANDEDNESS: single  
 28 TOPOLOGY: linear  
 29 MOLECULE TYPE:  
 30 DESCRIPTION: DNA  
 31 HYPOTHEtical: NO  
 32 ANTI-SENSE: NO  
 33 ORIGINAL SOURCE:  
 34 ORGANISM:  
 35 IMMEDIATE SOURCE:  
 36 CLONE:  
 37 FEATURE:  
 38 US-08-152-483B-9

Query Match: 69.14, Score 12, DB 1, Length 478  
 Best Local Similarity: 100.0%, Prod. No.: 9e+22,  
 Matches: 6, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 2 DQVMD 7  
 DB 316 DQVMD 301

RESULT 1:  
 US-08-152-483B-9  
 1 Sequence 1, Application: US/914-088-1  
 2 Patent No. 584,089  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Schlegel, C. Richard  
 5 APPLICANT: Jensen, A. Bennett  
 6 TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
 7 TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
 8 NUMBER OF SEQUENCES: 2  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 11 STREET: P.O. Box 1404  
 12 CITY: Alexandria  
 13 STATE: Virginia  
 14 COUNTRY: United States  
 15 ZIP: 22313-1404  
 16 COMPUTER READABLE FORM:  
 17 MEDIUM TYPE: Floppy disk  
 18 OPERATING SYSTEM: PC-DOS/MS-DOS  
 19 SOFTWARE: Patent in Release #1.0,  
 20 VERSION: Version #1.25  
 21 CURRENT APPLICATION DATA:  
 22 APPLICATION NUMBER: US/08/152-483B  
 23 FILING DATE: Nov 6, 1993  
 24 PRIORITY DATA:  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: 923,692  
 27 FILING DATE: July 31, 1992  
 28 PRIOR APPLICATION DATA:  
 29 APPLICATION NUMBER: 600,244  
 30 FILING DATE: October 22, 1990  
 31 PRIOR APPLICATION DATA:  
 32 APPLICATION NUMBER: 641,617  
 33 FILING DATE: January 16, 1991  
 34 PRIOR APPLICATION DATA:  
 35 APPLICATION NUMBER: 737,899  
 36 FILING DATE: July 26, 1991  
 37 ATTORNEY/AGENT INFORMATION:  
 38 NAME: Halling, Albert P.  
 39 REGISTRATION NUMBER: 25,227  
 40 TELECOMMUNICATION INFORMATION:  
 41 TELEPHONE: (415) 854-3660  
 42 TELEFAX: (415) 854-3694  
 43 INFORMATION FOR SEQ ID NO: 1:  
 44 SEQUENCE CHARACTERISTICS:  
 45 LENGTH: 478  
 46 TYPE: amino acid  
 47 STRANDEDNESS: single  
 48 TOPOLOGY: linear  
 49 MOLECULE TYPE:  
 50 DESCRIPTION: DNA  
 51 HYPOTHEtical: NO  
 52 ANTI-SENSE: NO  
 53 ORIGINAL SOURCE:  
 54 ORGANISM:  
 55 IMMEDIATE SOURCE:  
 56 CLONE:  
 57 FEATURE:  
 58 US-08-152-483B-9

```

CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 60/004,691
  FILING DATE: 02-OCT-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Teskin, Robin L.
  REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: C10091-015
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703) 836-6620
  TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 508 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-09-914-088-1

Query Match 68.1%; Score 32; DB 2; Length 508;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMQV 8
DB 200 EDSMDMDI 207

RESULT 13
US-09-252-991A-21308
; Sequence 21308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubinfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 21308
; LENGTH: 1357
; TYPE: PPT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21308

Query Match 68.1%; Score 32; DB 4; Length 1357;
Best Local Similarity 85.7%; Pred. No. 6.1e+2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMDVD 9
DB 603 GQVMDVD 609

RESULT 14
US-09-227-157-635
; Sequence 635, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P201291
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,503
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08

```



GenCore version 5.1.6  
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OM protein - protein search, using sw moduli

Run on: November 5, 2003, 15:18:11 / Search time 2.14375 seconds  
(without alignments)  
121.147 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 223308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 28134

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR061\*

1: Pir1\*

2: Pir2\*

3: Pir3\*

4: Pir4\*

Prod No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	426	2	Ig epsilon chain -
2	47	100.0	426	2	Ig epsilon chain -
3	38	80.0	118	2	probable transcrip
4	36	76.6	480	2	hypothetical prote
5	36	76.6	655	2	probable transcrip
6	35	74.5	198	2	hypothetical prote
7	35	74.5	265	2	hypothetical prote
8	35	74.5	846	2	hypothetical prote
9	35	74.5	1275	2	hypothetical prote
10	35	74.5	13555	2	hypothetical prote
11	34	72.3	203	2	probable transcrip
12	34	72.3	210	2	hypothetical prote
13	34	72.3	264	2	hypothetical prote
14	34	72.3	286	2	hypothetical prote
15	34	72.3	561	2	DNA ligase (import
16	34	72.3	677	2	sensory transduct
17	34	72.3	841	2	proprotein transla
18	34	72.3	1379	2	YTA7 protein - yea
19	33	70.2	189	2	hnaf protein - Syn
20	33	70.2	287	2	hnaf protein - Syn
21	33	70.2	314	2	hypothetical prote
22	33	70.2	347	2	actanylyseranyl di
23	33	70.2	448	2	beta-alanine-pyruv
24	33	70.2	503	2	ribulose ABC trans
25	33	70.2	634	2	hypothetical prote
26	33	70.2	725	2	probable kinase/ph
27	33	70.2	860	2	hypothetical prote
28	33	70.2	1155	2	probable protein k
29	33	70.2	1491	2	hypothetical prote

ALIGNMENTS

RESULT: 1

136948

Ig epsilon chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000

C:Accession: I36948

R:Sakoyama, Y.; Hong, K.

Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987

A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangut

A:Reference number: I36948; MUID:87147196; PMID:3103123

A:Accession: I36948

A:Status: preliminary; translated from GB/EMBL/DBE\*

A:Molecule type: DNA

A:Residues: 1-426 <RES>

A:Cross-references: GR:M13398; NID:G176797; PIRN:AAA35416.1; PID:G176798

C:Genetics:

A:Introns: 103/1; 209/1; 317/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:336-405/Domain: immunoglobulin homology <IMM>

Query Match:

Best Local Similarity 100.0%; Score 47; DB 2; Length 426;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 EDGQVMDVD 9

DB 149 EDGQVMDVD 157

RESULT 2

EHHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence\_revision 13-Jun-1983 #text\_change 16-Jul-1999

C:Accession: A22771; A21195; PH12.4; A93491; A90824; A94418; B93933; SC2438; A53116; C4

R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region ger

A:Reference number: A22771; MUID:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: GB:J00022; GB:V00555; NID:G185035

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hatajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo

A:Reference number: A23195; MUID:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <JEU>

A:Cross-references: GB:J00022; NID:G184755

R:Zhang, K.; Saxon, A.; Max, E.E.

A:Experimental source: B cell myeloma J-266  
A:Note: sequence extracted from NCBI backbone (NCBI:P125299)  
A:Accession: A46536  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 401-428 <HE>  
A:Cross-references: DB:Q63162; PID: AAB24855.1; PID: Q63165  
A:Experimental source: B cell myeloma J-266  
A:Note: sequence extracted from NCBI backbone (NCBI:P123483)  
C:Genetics:  
A:Gene: GRI1GR  
A:Cross-references: GDB:119135; OMIM:147180  
A:Map position: 14q32.31-14q32.33  
A:Introns: 1/1; 104/1; 111/1; 119/1  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a chain disulfide bonds. C region: immunoglobulin homology  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin; immunoglobulin homology <IM>  
F:128-195/Domain: immunoglobulin homology <IM>  
F:232-301/Domain: immunoglobulin homology <IM>  
F:339-407/Domain: immunoglobulin homology <IM>  
F:4/Disulfide bonds: interchain (to light chain); #status predicted  
F:5-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted  
F:21-49,99-146,252,275/binding site: carboxydrate (Asn) (covalent) #status experimental  
F:21,209/Disulfide bonds: interchain (to heavy chain) #status predicted  
Query Match 100.0%; Score 47; DB 1; Length 428;  
Best Local Similarity 100.0%; Pred No. 0.26; 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : EGGQWMDVC 9  
|||  
DB 151 EGGQWMDVC 159  
RESULT 3  
GB4322  
50S ribosomal protein L24P (imported); - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: GB4322  
R:Ng, M.V.; Kennedy, S.P.; Maritzas, G.G.; Perquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leithausner, B.; Kellert, K.; Cruz, R.; Datscan, M.; Hough, D.W.; Maddocks, D.G.; Jachung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hsu, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebnhardt, B.; Lowe, T.M.; Jachung, K.H.; Alam, M.; Freitas, T.  
A:Title: Genomic sequence of Halobacterium species NRC-1.  
A:Reference number: 99460; PMID:20534483; PMID:11016950  
A:Accession: GB4322  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-118 <HE>  
A:Cross-references: GB:AE004437; NID:gl0561170; PID:NAG19947.1; GSPDB:GK00138  
C:Genetics:  
A:Gene: rpl24P  
C:Superfamily: 30S ribosomal protein L26  
Query Match 90.9%; Score 18; DB 2; Length 118;  
Best Local Similarity 77.8%; Pred No. 3.7;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EGGQWMDVC 9  
|||  
DB 59 EGGQWMDVC 67  
RESULT 4  
T46047  
Hypothetical protein T46047.160 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46047







AtGenetic code: SGC3

Query Match 72.3% Score 347 DB 2 Length 264;  
Best Local Similarity 44.4% Pred. No. 49;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDCQWVD 9

DB 96 EDCQWVD 104

58SUD 14

D69272

Hypothetical protein AF0180 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence\_revision: 05 Dec 1997 #text\_change: 12 Dec 1999

C:Accession: D69272

R:Klesch, H.P.; Clayton, R.A.; Torb, J.P.; White, G.; Nelson, R.F.; Fletcher, K.A.; Dodson

; Fleischnann, P.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.; Gill, S.; Kirkness, E.F.

; Glodex, A.; Zhou, L.; Overbeek, R.; Goodwin, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-369, 1997

At:Authors: Utterback, T.; Cotton, M.D.; Springs, T.; Ariuchi, P.; Paine, B.P.; Sykes, S.

Smith, R.O.; Keese, C.R.; Venter, C.C.

At:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

At:Reference number: AW252; WJID:9804933; PX:03380475

At:Accession: D69272

At>Status: preliminary, nucleic acid sequence not shown; translation not shown

At:Molecule type: DNA

At:Residues: 1-286 <KLE>

At:Cross-references: GB:AE001093; GB:AE000782; NCBI:265946; PDB:1AAR/1050.1; PDB:265046

Query Match

Best Local Similarity 85.7% Pred. No. 54

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDCQWVD 7

DB 7 EDCQWVD 13

RESULT 15

GB4244

DNA ligase (imported) - Halobacterium sp. NRC 1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence\_revision: 02-Feb-2001 #text\_change: 16-Feb-2001

C:Accession: GB4244

R:Nij, M.V.; Kennedy, S.P.; Mahairas, S.J.; Holquist, B.; Pao, W.; Shukla, R.D.; Lasky, S.

; Leibhauser, B.; Miller, K.; Cruz, R.; Banton, M.J.; Berman, N.; Madsen, D.G.; Jablo

ung, K.H.; Alam, X.; Fierman, T.

Proc. Natl. Acad. Sci. USA 97, 1225-1229, 2000

At:Authors: Hol, S.; Fuhls, G.; Demis, P.; Pao, W.; Shukla, R.D.; Lasky, S.

At:Title: Genome sequence of Halobacterium sp. NRC-1

At:Reference number: A4460; NCBI:2650443; PM161116

At:Accession: GB4244

At>Status: preliminary

At:Molecule type: DNA

At:Residues: 1-561 <STH>

At:Cross-references: GB:AE004437; NCBI:2680446; PDB:1AAR/1421.1; GSPUB:GNC0138

C:Genetics:

At:Gene: lig

C:Superfamily: DNA ligase

Query Match

Best Local Similarity 55.6% Pred. No. 124-02

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDCQWVD 9

DB 497 EDCQWVD 505

Search completed: November 5, 2003, 15:56:12

Job time: 8:14:35 sels

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Computer Aid.

QM protein protein search, using sw model

Run on: November 5, 2003, 15:44:15 Search time 3.6420 seconds  
without alignment  
115,748 Million cell by 3.45/sec

Title: US 09 914 088 1

Perfect score: 47

Sequence: EDSYKQWD 9

Scoring table: SCDSUM62

Searched: 127463 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Testing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	47	100.0	428	EPC_HUMAN
2	37	78.7	980	Q8XJ74 homo sapien
3	36	78.6	655	Q95X88 cat. bacter
4	36	78.6	677	Q95X76 homydx mori
5	34	72.3	561	Q95X35 bacteri
6	34	72.3	841	Q95X66 bacillus su
7	34	72.3	1379	Q95X40 saccharo
8	33	70.2	287	Q95X26 spherococ
9	33	70.2	634	Q95X79 moluscu
10	33	70.2	860	Q95X33 spherococ
11	33	70.2	877	Q95X39 bacilla
12	33	70.2	1119	Q95X37 thermu
13	32	68.1	95	Q95X21 bacille
14	32	68.1	97	Q95X21 methanoc
15	32	68.1	121	Q95X21 methanoc
16	32	68.1	211	Q95X21 pyrobacul
17	32	68.1	235	Q95X21 populus
18	32	68.1	240	Q95X21 saccharo
19	32	68.1	272	Q95X21 streptomy
20	32	68.1	367	Q95X21 mycobact
21	32	68.1	398	Q95X21 trypocema
22	32	68.1	501	Q95X21 vascinia
23	32	68.1	508	Q95X21 vascinia
24	32	68.1	513	Q95X21 vascinia
25	32	68.1	556	Q95X21 vascinia
26	32	68.1	602	Q95X21 vascinia
27	32	68.1	631	Q95X21 vascinia
28	32	68.1	631	Q95X21 vascinia
29	32	68.1	631	Q95X21 vascinia
30	32	68.1	631	Q95X21 vascinia
31	32	68.1	631	Q95X21 vascinia
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33	32	68.1	631	Q95X21 vascinia
34	32	68.1	631	Q95X21 vascinia
35	32	68.1	631	Q95X21 vascinia
36	32	68.1	631	Q95X21 vascinia
37	32	68.1	631	Q95X21 vascinia
38	32	68.1	631	Q95X21 vascinia
39	32	68.1	631	Q95X21 vascinia
40	32	68.1	631	Q95X21 vascinia
41	32	68.1	631	Q95X21 vascinia
42	32	68.1	631	Q95X21 vascinia
43	32	68.1	631	Q95X21 vascinia
44	32	68.1	631	Q95X21 vascinia
45	32	68.1	631	Q95X21 vascinia

34	31.5	67.0	218	1	NIPL_MOUSE
35	31.5	67.0	219	1	NIPL_HUMAN
36	31	66.0	119	1	RJ24_HALWA
37	31	66.0	145	1	RJ13_HALWA
38	31	66.0	171	1	CRIO_MOUSE
39	31	66.0	180	1	ROC2_AGRRH
40	31	66.0	217	1	P55_METJA
41	31	66.0	222	1	YAGY_ECOLI
42	31	66.0	251	1	GJFR_PSEAF
43	31	66.0	258	1	AFGB_SALTY
44	31	66.0	282	1	PDHD_STRCO
45	31	66.0	290	1	CMFK_SCH2C

## ALIGNMENTS

RESULT 1	
EPC_HUMAN	
ID_EPC_HUMAN	STANDARD; PRT: 428 AA.
AC	PC1854;
DT	21-JUL-1986 (Rel. 0; Created)
DT	21-JUL-1986 (Rel. 0; Last sequence update)
DT	15-SEP-2003 (Rel. 42; Last annotation update)
DE	Ig epsilon chain C region.
GN	IGHF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=81168997; PubMed=6300763;
RA	Seno M., Kurokawa T., Ogo Y., Onda H., Sasada R., Igarashi K.,
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.,
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin
RT	epsilon chain cDNA";
RL	Nucleic Acids Res. 11:9 726(1983).
RN	[2]
RP	SEQUENCE FROM N.A. AND VARIANT IED-359.
RX	MEDLINE=83001945; PubMed=6288268;
RA	Max E.B., Rattey J., Ney R., Kirsch I.R., Leder P.,
RT	"Duplication and deletion in the human immunoglobulin epsilon genes";
RL	Cell 29:691-699(1982).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=84236029; PubMed=6234164;
RA	Flanagan J.G., Rabbitts T.H.,
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant
RT	region gene, and evidence for three non allelic genes.";
RL	EMBO J. 1:655-660(1982).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=84207910; PubMed=6142726;
RA	Jeda S., Naka S., Nishida Y., Hisajima H., Honjo T.,
RT	"Long terminal repeat-like elements flank a human immunoglobulin
RT	epsilon pseudogene that lacks introns.";
RL	EMBO J. 1:1539-1544(1982).
RN	[5]
RP	PRELIMINARY SEQUENCE 'MYELOMA PROTEIN ND'.
RA	Bernick H.H., Johansson S.G.O., von Baer-Lindstrom H.,
RT	(in) Bach M.K. (eds.);
RL	Immediate hypersensitivity: modern concepts and developments, pp. 1-36,
RL	Marcel Dekker, New York (1978).
RN	[6]
RP	SEQUENCE OF 1,423, 68-114 AND 427-428 FROM N.A.
RX	MEDLINE=8306233; PubMed=6815656;
RA	Kentel S.H., Molgaard H.V., Houghron M., Derbyshire R.B., Viney J.,
RA	Beck J.G., Gould H.J.,
RT	"Cloning and sequence determination of the gene for the human
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN	[7]



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EMBL: AF464765; AAJ69963.1;  
 InterPro: IPR007031; LRR\_RNinh.  
 InterPro: IPR007111; NACHT\_NTPase.  
 InterPro: IPR004023; PAAD\_DAPIN\_dom.  
 Pfam: PF02758; PAAD\_DAPIN; 1.  
 ProSITE: PS00624; DAPIN; 1.  
 ProSITE: PS00637; NACHT; 1.  
 ATP binding; Leucine-rich repeat, Repeat  
 Domain 1 93 DAPIN.  
 FT DOMAIN 172 491 NACHT.  
 FT REPEAT 614 638 LRR 1.  
 FT REPEAT 674 697 LRR 2.  
 FT REPEAT 760 784 LRR 3.  
 FT REPEAT 798 810 LRR 4.  
 FT REPEAT 817 840 LRR 5.  
 FT REPEAT 845 868 LRR 6.  
 FT REPEAT 874 897 LRR 7.  
 FT REPEAT 902 928 LRR 8.  
 FT REPEAT 933 957 LRR 9.  
 FT REPEAT 178 185 ATP POTENTIAL.  
 SQ SEQUENCE 380 AA; 111866 MW; 42462F0439D0D CRC64;

Query Match 78.7%; Score 37; DB 1; Length 388;  
 Best Local Similarity 66.7%; Pred. NC. 32;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EQGVQVVD 9  
 |||||  
 DB 93 EQGVQVGEID 101

RESULT 1  
 SYT CAUCR STANDARD; PRI: 655 AA  
 AC Q9AAX8;  
 DT 28-FEB-2003 (Rel. 4); Created;  
 DT 28-FEB-2003 (Rel. 4); Last sequence update;  
 DT 28-FEB-2003 (Rel. 4); Last annotation update;  
 DE Threonyl-tRNA synthetase (EC 6.1.1.1) (Threonyl-tRNA ligase (threonyl-))  
 GN THRS CA Q9AAX8;  
 GS Caulobacter crescentus  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteraceae  
 CC Caulobacteraceae; Caulobacter  
 CC NCBI TaxID:155497;  
 PN 1;  
 RP SEQUENCE FROM N.A.  
 RX STRAIN:ATCC 19299 / CB15;  
 RX MEDLINE:21173698; PubMed:11259647;  
 RA Kierman W.C., Feldblyum T.V., Cobb M.T., Paulsen O., Nelson K.E., Eisen J., Heidelberg J.F., Alvey M.R., Ohta N., Maddock J.R., Patoka J., Nelson W.C., Newton A., Stephens C., Plazek R.L., Sly B., Daboy R.J., Dodson R.J., Durkin A.S., Gwinn M.H., Haft D.H., Kolonay J.F., Sait J., Graven M.B., Khouri H., Shetty A., Berry K., Ueberback T., Tran K., Wolf A., Vamathevan M., White O., Salzberg S.L., Venter J.C., Shapiro B., Fraser C.V.  
 RA "Complete genome sequence of Caulobacter crescentus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA-Thr + AMP + diphosphate + L-threonyl-tRNA<sup>Thr</sup>.  
 CC -1- COPACTOR: Binds 1 zinc ion per subunit by similarity.  
 CC -1- SUBUNIT: Homodimer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to class-II aminocyl-tRNA synthetase family.  
 CC This SWISS-PROT entry is copyrighted. It is included through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

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EMBL: AE005719; AA22451.1;  
 PIR: G87306; G87306.  
 HSSP: P03955; LEVH.  
 TIGR: CC9464;  
 DR HAMAP: MF\_00184;  
 DR InterPro: IPR004154; HCTP\_anticodon.  
 DR InterPro: IPR004095; TGS\_dom.  
 DR InterPro: IPR002114; tRNA\_synth\_2n.  
 DR InterPro: IPR002123; tRNA\_synth\_thr.  
 DR Pfam: PF03129; HGT9\_anticodon; 1.  
 Dr Pfam: PF02824; TGS;  
 Dr Pfam: PF00587; tRNA-synth\_2b; 1.  
 DR PRINTS: PR01347; TENASYNTHRA.  
 DR TIGRFAMs: TIGR00418; tlys; 1.  
 DR PROSITE: PS0862; AA\_tRNA\_LIGASE\_11; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Metal-binding; Zinc; Complete proteome  
 FT DOMAIN 248 540 CATALYTIC  
 FT METAL 340 340 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 517 517 ZINC (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 655 AA; 73719 MW; BB75D312CC887799 CRC64;

Query Match 76.6%; Score 36; DB 1; Length 655;  
 Best Local Similarity 75.0%; Pred. NC. 33;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQVVDV 9  
 |||||  
 DB 41 DGQVLDL 48

RESULT 4  
 SAGS BOMYC STANDARD; PRI: 677 AA.  
 AC Q9BLT6;  
 DT 28-FEB-2003 (Rel. 4); Created;  
 DT 28-FEB-2003 (Rel. 4); Last sequence update;  
 DT 28-FEB-2003 (Rel. 4); Last annotation update;  
 DE BAG domain-containing protein Samd1.  
 GN SAMU1.  
 GS Rorbyx maki (Silk moth).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 CC Rorbyxidae; Bombyx.  
 CC NCBI TaxID:70917;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RX STRAIN:N4; TISSUE:Egg;  
 RX MEDLINE:21115830; PubMed:11422373;  
 RA Moribe Y., Nimi T., Yasuhika C., Yaginuma T.;  
 RA "Samu1, a novel cold-inducible gene, encoding a protein with a BAG domain similar to silencer of death domains (SODD/BAG-4), isolated from Rorbyx diapause eggs."  
 RA Eur. J. Biochem. 268:332-342 (2001).  
 CC -1- FUNCTION: May play a role in transmitting a signal which both protects nondiapause eggs from cold injury and terminates diapause in diapause eggs.  
 CC -1- SUBUNIT: Binds to HSP70.  
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in chilled diapause eggs and to a lesser extent in chilled nondiapause eggs.  
 CC -1- DEVELOPMENTAL STAGE: In diapause eggs, expressed after chilling at 5 degrees Celsius for 5-6 days, persists for 30 days and then decreases.  
 CC -1- INDUCTION: By cold.  
 CC -1- MISCELLANEOUS: 'Samu1' means 'cold' in Japanese.  
 CC -1- SIMILARITY: Contains 1 BAG domain.

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ENBL: AB032717; BAB19763.1;  
 SP: G00030444; E-Hsp70 protein binding activity; HA.  
 InterPro: IPR003103; BAG.  
 Pfam: PF02179; BAG; 1.  
 SMART: SM00264; BAG; 1.  
 Craperone: Developmental protein.  
 POLY QIU.  
 DOMAIN 22 25  
 DOMAIN 103 141 GLN-RICH  
 DOMAIN 233 380 GLN/RG-RICH  
 DOMAIN 607 643 LYS-RICH  
 DOMAIN 380 457 BAG  
 SQ SEQUENCE 677 AA; 75979 MW; 308174CAF064EB43 CRC64;

Query Match 76.6%; Score 46; DB 1; Length 677;  
 Best Local Similarity 87.5%; Prol No. 34;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EDGQWQVD 9  
 Db 665 DSQWQVD 672

RESULT 5  
 DND1 HALMI  
 ID DND1 HALMI STANDARD; PRT: 661 AA;  
 AC C9835;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28 FEB 2003 (Rel. 41, Last annotation update)  
 DE DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP])  
 GN 136 OR VNC04410  
 OS Halobacterium sp. (strain NRC 1 / ATCC 70622 / JCV 11541)  
 CC Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Halobacterium.  
 CC Halobacteriaceae; Halobacterium.  
 CC NCBI TaxID:64091;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2050448; PubMed=1116950;  
 RA NG W.V., Kennedy S.P., Mahaitas G.J., Bergquist K., Hsu M.,  
 RA Shukla H.D., Busby S.R., Hallica M., Technosmith J., Hsu M.,  
 RA Swartzel S., Wolf D., Hall J., Hsu M., Mahaitas G.J., Hsu M.,  
 RA DeRudder P., Feller K., Cruz P., Hsu M., Mahaitas G.J., Hsu M.,  
 RA Maddocks D.G., Mahonski P.E., Kiebs V., Mahaitas G.J., Hsu M.,  
 RA Isenbarger T.A., Beck R.F., Pohlschneider M., Feller K., Hsu M.,  
 RA Adam M., Freitas T., Hou S., Daniels T.J., Feller K., Hsu M.,  
 RA Ethardt H., Lowe T.M., Liang P., Feller K., Hsu M., Feller K.,  
 RA "Genome sequence of Halobacterium species NRC 1".  
 RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).  
 CC ! FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION. DNA  
 CC RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA BY  
 CC SIMILARITY.  
 CC ! CATALYTIC ACTIVITY: ATP + [deoxyribonucleotide] N  
 CC [deoxyribonucleotide] (X) = AMP + diphosphate +  
 CC [deoxyribonucleotide] (N-M).  
 CC ! SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY

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ENBL: AE005027; AAG19323.1;  
 SP: G00030444; E-Hsp70 protein binding activity; HA.  
 InterPro: IPR003103; BAG.  
 Pfam: PF02179; BAG; 1.  
 SMART: SM00264; BAG; 1.  
 Craperone: Developmental protein.  
 POLY QIU.  
 DOMAIN 22 25  
 DOMAIN 103 141 GLN-RICH  
 DOMAIN 233 380 GLN/RG-RICH  
 DOMAIN 607 643 LYS-RICH  
 DOMAIN 380 457 BAG  
 SQ SEQUENCE 677 AA; 75979 MW; 308174CAF064EB43 CRC64;

PIR: G84244; G94244.  
 HAVAP: MF 00407; 1.  
 InterPro: IPR003977; DNA\_Ligase.  
 Pfam: PF01068; DNA\_Ligase; 1.  
 Pfam: PF04679; DNA\_Ligase\_A\_C; 1.  
 Pfam: PF04675; DNA\_Ligase\_A\_N; 1.  
 TIGRfam: TIGR00574; dn1; 1.  
 PROSITE: PS00697; DNA\_LIGASE\_A1; 1.  
 PROSITE: PS01331; DNA\_LIGASE\_A2; 1.  
 PROSITE: PS01601; DNA\_LIGASE\_A3; 1.  
 KW DNA repair; DNA replication; DNA recombination; Cell division; Ligase;  
 KW ATP-binding; Comp-ute proteome.  
 FT BINDING 255 255 AMP (BY SIMILARITY)  
 SQ SEQUENCE 561 AA; 59619 MW; 5B530D3C1D106D2E CRC64;

Query Match 72.3%; Score 34; DB 1; Length 561;  
 Best Local Similarity 55.6%; Prol No. 66;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWQVD 9  
 Db 497 EDGQWQVD 505

RESULT 6  
 SECA\_BACSU  
 ID SECA\_BACSU STANDARD; PRT: 841 AA;  
 AC P28366;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Preprotein translocase secA subunit.  
 GN SECA OR DIV.  
 OS Bacillus subtilis  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI TaxID:1423;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / Marburg;  
 RX MEDLINE=91192600; PubMed=1901557;  
 RA Sadale Y., Takamatsu H., Nakamura K., Yamae K.,  
 RT "Sequencing reveals similarity of the wild-type div- gene of Bacillus  
 RL subtilis to the Escherichia coli secA gene".  
 RL Gene 98:101-105 (1991).  
 RN 2;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA Soldo B., Lazarevic V., Mauer C., Karamata D.,  
 RT "Sequence of the Bacillus subtilis 168 chromosomal region from 105  
 RT to 307 degree".  
 RL Submitted (JAN 1979) to the EMBL/GenBank/CDR databases.  
 RN 3;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9394377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Bortiss R., Boursier L., Brans A., Braun M., Bignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Deniset F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Enlihan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fura S., Galizzi A., Galleron N.,  
 RA Ghim S.V., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
 RA Guiseppe G., Guy R.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Karamata Y., Klier-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Leveire A., Liu H., Masuda S., Maue C., Medigic C.,  
 RA Medhara N., Mellado R.F., Mizuno M., Mestl D., Nakai S., Noback M.,  
 RA Noone E., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Potwolk D., Prescott A.M.,



FT CONFLICT 1153 1153 K -> E (IN REF. 21)  
FT CONFLICT 1276 1276 I -> R (IN REF. 21)  
FT CONFLICT 1283 1283 O -> P (IN REF. 21)  
SQ SEQUENCE 1379 AA; 157406 MW; 3102156F87E62E04F CRC64;

Query Match 72.3%; Score 34; DB 1; Length 1379;  
Best Local Similarity 77.8%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9  
DB 57 EDGQVMVLD 65

## RESULT 8

DNAB SYN7 STANDARD; PRT; 287 AA.  
ID DNAB SYN7 STANDARD; PRT; 287 AA.  
AC PS0026;  
DT 31 OCT-1996 (Rel. 34, Created;  
DT 15-DEC-1999 (Rel. 37, Last sequence update;  
DT 16 OCT-2001 (Rel. 40, Last annotation update;  
DE Chapterone protein dnab.  
GN DNAB  
OS Synchococcus sp. strain PCC 7942 (Ancestris nidulans 821.  
CC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
CX NCBI\_TaxID=1140;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:97382457; PubMed:924046;  
RA Ouchii K., Nimura K., Yoshikawa H., Takahashi H.,  
RT "Sequence and analysis of a dnab homologue gene in cyanobacterium"  
RL Synchococcus sp. PCC7942."  
RL Biochem. Biophys. Res. Commun. 236:461-466(1997).  
RN [1]  
RP SEQUENCE OF 159 FROM N.A.  
RX MEDLINE:94271241; PubMed=8003021;  
RA Nimura K., Yoshikawa H., Takahashi H.,  
RT "Sequence analysis of the third dnab homolog gene in Synchococcus"  
RL Sp. PCC7942."  
RL Biochem. Biophys. Res. Commun. 201:848-854(1994).  
RN [1]  
RP ERRATUM  
RX MEDLINE:95110350; PubMed=7811295;  
RA Nimura K., Yoshikawa H., Takahashi H.,  
RL Biochem. Biophys. Res. Commun. 201:848-854(1994).  
CC FUNCTION: ANALYSIS AS A CHAPTERONE SUBUNITED. ONLY WITH USE.  
CC THE ATPASE ACTIVITY OF DNAB IS SIMILARITY.  
CC SUBCELLULAR LOCATION: CYTOPLASM; BY SIMILARITY.  
CC 1. SIMILARITY: BELONGS TO THE DNAB FAMILY.  
CC 2. SIMILARITY: CONTAINS 1 J domain.

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EMBL: AB03529; BA421679.1;  
DR EXPI: D29968; BAAC8235.1;  
DR PIR: J05950; J05550.  
DR PIR: PC2306; PC2306.  
DR HSSP: P23685; 18DJ.  
DR InterPro: IPR003339; DnaJ\_C.  
DR InterPro: IPR01623; DnaJ\_N.  
DR Pfam: PF02226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C\_1.  
DR PRINTS: F00625; DNAB-PROTEIN.  
DR SMART: SV00315; DnaJ\_1.  
DR PROSITE: PS00618; DnaJ\_1;  
DR PROSITE: PS55076; DnaJ\_2; 1.

KW Chapterone; DNA replication; Heat shock.  
FT DOMAIN 4 73 J-DOMAIN.  
SQ SEQUENCE 287 AA; 131980 MW; 2927A2692E6C546 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 287;  
Best Local Similarity 55.6%; Pred. No. 52;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9  
DB 51 EDGQVMVLD 159

## RESULT 9

NTPI MCV1 STANDARD; PRT; 634 AA.  
ID NTPI MCV1 STANDARD; PRT; 634 AA.  
AC Q98267;  
DT 30-MAY-2003 (Rel. 35, Created;  
DT 30-MAY-2003 (Rel. 35, Last sequence update;  
DT 30-MAY-2003 (Rel. 35, Last annotation update;  
DE Nucleoside triphosphatase 1 (NTP 3.6.1.15) (Nucleoside triphosphate  
DE phosphohydrolase 1) (NTP 1) (MCL00R).  
GN MCL00L.  
OS Moluscum contagiosum virus subtype 1 (MCV1).  
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
CC Moluscipoxvirus.  
CX NCBI\_TaxID=10280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:96325459; PubMed=8670425;  
RA Senkevich T.G., Sugert J.C., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RT "Genome sequence of a human tumorigenic poxvirus: prediction of  
RT specific host response-evasion genes."  
RL Science 273:813-816(1996).  
CC FUNCTION: SERVES TWO ROLES IN TRANSCRIPTION: IT ACTS IN CONCERT  
CC WITH VIRAL TERMINATION FACTOR/CAPPING ENZYME TO CATALYZE RELEASE  
CC OF JUNCTION-CONTAINING NASCENT RNA FROM THE ELONGATION COMPLEX, AND  
CC IT ACTS BY ITSELF AS A POLYMERASE ELONGATION FACTOR TO FACILITATE  
CC REATROUGH OF INTRINSIC PAUSE SITES (BY SIMILARITY).  
CC 1. CATALYTIC ACTIVITY: NTP + H2O -> NDP + phosphate.  
CC 2. SIMILARITY: BELONGS TO THE NPH I SUBFAMILY OF HELICASES.

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EMBL: U60315; AAC55228.1;  
DR PIR: T30702; T30702.  
DR InterPro: IPR001410; DEAD.  
DR InterPro: IPR001550; Helicase\_C.  
DR InterPro: IPR000330; SNF2\_N.  
DR Pfam: PF00271; Helicase\_C\_1.  
DR Pfam: PF00176; SNF2\_N\_1.  
DR SMART: SM00487; DEXDC\_1.  
DR SMART: SM00490; HELIC\_C\_1.  
KW Helicase; ATP binding; Transcription.  
FT DOMAIN 33 311 SNF2\_N.  
FT DOMAIN 394 490 HELICASE\_C.  
FT NP BIND 54 61 ATP (BY SIMILARITY).  
FT SITE 140 143 DEXH BOX.  
SQ SEQUENCE 634 AA; 72102 MW; B786EFA17E12F56 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 634;  
Best Local Similarity 65.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9  
DB 51





DE RNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase  
 CE beta chain) (RNA polymerase beta subunit).  
 GN BRCB.  
 GS Thermus aquaticus.  
 CC Bacteria; Deinococcus-Thermus; Proteobacteria; Thermus; Thermotoga;  
 CC Thermus.  
 CX NCBI\_TaxID=2217.  
 RN 1.  
 RP SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).  
 RX XREFLINE:99428144; PubMed:10499796.  
 RA Zhang G., Campbell E.A., Minakhin G., Richter C., Severinov E.,  
 RA Dairat S.A.  
 RT Crystal structure of Thermus aquaticus RNA polymerase at 3.5 A  
 RT resolution.  
 RL Cell 18:811-824 (1999).  
 CC 1. FUNCTION: DNA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOTIDE TRIPHOSPHATES AS  
 CC SUBSTRATES.  
 CC 2. CATALYTIC ACTIVITY: N nucleoside triphosphate + N dinucleotide +  
 CC (RNA)n -> (RNA)n+1.  
 CC 3. SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE  
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1  
 CC BETA' CHAIN.  
 CC 4. SIMILARITY: Belongs to the RNA polymerase beta chain family.  
 CC  
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 CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 CC  
 DR EMBL: Y19223; GenBank: U04546.2; .  
 DR PDB: 1HQM; 67 FEB-01.  
 DR PIR: 1192; 31-MAY-92.  
 DR InterPro: IPR001572; RNA\_pol\_B.  
 DR Pfam: PF04563; RNA\_pol\_RPB2\_1.  
 DR Pfam: PF04563; RNA\_pol\_RPB2\_2.  
 DR Pfam: PF04565; RNA\_pol\_RPB2\_3.  
 DR Pfam: PF04565; RNA\_pol\_RPB2\_4.  
 DR Pfam: PF04567; RNA\_pol\_RPB2\_5.  
 DR Pfam: PF04567; RNA\_pol\_RPB2\_6.  
 DR Pfam: PF04567; RNA\_pol\_RPB2\_7.  
 DR PROSITE: PS0166; RNA\_POL\_BETA.  
 KW 3'-phosphatase; transcription; DNA directed RNA polymerase.  
 KW AC structure.  
 SC SEQUENCE 1119 AA; 124757 MW; 13846200 Da; 13846200 Da.  
 Query Match 70.3%; Score 32; DB 1; Length 95;  
 Best Local Similarity 66.3%; Pred. No. 26;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EDGQVNVVD 607  
 FE 599 EDGQVNVVD 607  
 RESULT 14  
 CH10 BUREP  
 ID CH10 BUREP STANDARD; PRT; 60 AA  
 AC F45227  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 29 FEB 2003 (Rel. 41, Last annotation update)  
 DE 10 kDa Chaperonin (Protein Cpn10) (GroES protein)  
 GN GROES OR GROPS OR CPN10.  
 OS Bordetella pertussis.  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Bordetella  
 CC Alcaligenaceae; Bordetella  
 CX NCBI\_TaxID=520;  
 RN 1.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN Tohama / RP119;  
 RX MEDLINE:95329719; PubMed:7789805;

RA Fernandez R.C., Weiss A.A.  
 RT Cloning and sequencing of the Bordetella pertussis cpn10/cpn60  
 RT (groES) homolog.  
 RL Gene 158:151-152 (1995).  
 CC 1. FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses  
 CC the ATPase activity of the latter.  
 CC 2. SUBUNIT: Heptamer of 7 subunits arranged in a ring (By  
 CC similarity).  
 CC 3. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 4. SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.  
 CC  
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 CC  
 DR EMBL: U12277; AAA74966.1;  
 DR PIR: I4C330; I4C330.  
 DR HSSP: P05360; TACN.  
 DR HAMAP: MF\_00580; 1.  
 DR InterPro: IPR001476; Chaperonin\_Cpn10.  
 DR Pfam: PF00166; cpn10.1.  
 DR PRINTS: PR03297; CHAPERONIN10.  
 DR PRODOM: PDOC566; Chaperonin\_Cpn10.1.  
 DR PROSITE: PS03681; CHAPERONIN\_CPN10.1.  
 KW Chaperone. 95 AA; 10272 MW; 21CA938AF6780D38 CRC64;  
 SC SEQUENCE 95 AA; 10272 MW; 21CA938AF6780D38 CRC64;  
 Query Match 69.1%; Score 32; DB 1; Length 95;  
 Best Local Similarity 55.6%; Pred. No. 26;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EDGQVNVVD 9  
 DB 50 EDGKIDPVD 58  
 RESULT 14  
 RE21 MEIMA  
 ID RE21 MEIMA STANDARD; PRT; 97 AA  
 AC Q8P021  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 29 FEB 2003 (Rel. 41, Last annotation update)  
 DE GroES ribosome binding site  
 GN GroES OR ME2016  
 OS Methanocaldococcus jassonii  
 CC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 CC Methanococcales; Methanococcaceae; Methanococcaceae.  
 CX NCBI\_TaxID=2209;  
 RN 1.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gcel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE:2120827; PubMed:12128924;  
 RA Depkenmeier U., Johann A., Hartsch T., Yeckl R., Schmitz R.A.,  
 RA Vattinen-Akias P., Heine A., Wietzer A., Baermer S., Jacobl S.,  
 RA Bruggemann H., Lienhard T., Christmann A., Boencke M., Steckel S.,  
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,  
 RA Fritz H. C., Gottschalk G.  
 RT The genome of Methanocaldococcus jassonii: evidence for lateral gene  
 RT transfer between Bacteria and Archaea.  
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).  
 CC 1. SIMILARITY: BELONGS TO THE G2E FAMILY OF RIBOSOMAL PROTEINS.  
 CC  
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Search completed: November 5, 2003, 15:47:55  
Job time : 4.65625 secs

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE013498; AAK32232.1; --
DR HAVAP; NF_05169; -- 1.
DR InterPro; IP020147; Ribosomal_L21e.
DR Pfam; PF01157; Ribosomal_L21e; 1.
DR PROSITE; PS0171; RIBOSOMAL_L21E; FALSE NEG.
KW Ribosome; Proteins; Complete proteome.
SQ SEQUENCE 97 AA; 11090 MW; 2824EEFC06A13E58 CRC64;

Query Match 68.1%; Score 12; E: 1; Length 97.
Best Local Similarity 55.5%; Pref. No: 26;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 1 EDQGMVVD 9
|||
DB 15 EDQGMVHD 43

RESULT 15
Y408 METUA
ID Y408 METUA STANDARD; PRT: 121 AA.
AC Q57851;
DT 02-NOV-1997 (Rel: 35, Last sequence update)
DT 02-NOV-1997 (Rel: 35, Last sequence update)
DT 16 Oct 2001 (Rel: 40, Last annotation update)
DE Hypothetical protein MJ0408.
GN M50409.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococaceae; Methanocaldococcus.
CX NCBI_TaxID=2193;
RN 1;
RP SEQUENCE FROM N.A.
RC SPRAIN JALIN / USV 2661 / ATCC 43047;
RX MBLN196331993; PubMed8688087;
RA Smith G.J., White G., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake C.A., FitzGerald J.M., Clayton R.A., Gocayne J.D.,
RA Krollavag A.R., Dougherty B.A., Tomb J.F., Adams M.D., Belin G.P.,
RA Overbook R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glock A.,
RA Scott J.L., George N.S.M., Weidman J.F., Ehrlich J.L., Nguyen D.,
RA Ulfreback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.G.,
RA Clifton M.D., Roberts K.M., Hurst V.A., Kaine B.P., Borodovsky M.,
RA Zank H.P., Fraser C.M., Smith H.C., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RI jannaschii."
PL Science 273:1058-1073(1996);
CC
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CC
CC EMBL; U67491; AAK99398.1;
DR P13; H64350; H64350.
DR TIGR; M20408; --
DR Pfam; PF04036; DUF172; 1.
DR Pfam; PF04039; DUF181; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 121 AA; 14181 MW; 281669A6B1616F3 CRC64;
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Query Match 68.1%; Score 12; E: 1; Length 121.
Best Local Similarity 62.5%; Pref. No: 31;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 2 DGMVVD 9
|||
DB 32 DGMVVD 59
```

GenCore version 3.1.6  
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CM protein - protein search, using sw model:  
Run on: November 5, 2003, 15:37:41 Search time 19.466 seconds  
(without alignments)  
119,679 million cells updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: ECGYQWQVD 9

Scoring table: BLOSUM62  
Gap: 10.0, Gapext 0.5

Searched: 910526 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 10525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SPTRXAL\_23:  
1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.mhc:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.podent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:  
15: sp.virus:  
16: sp.bacteriap:  
17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	80.9	118	17 Q9HPC3	Q9HPC3 Halobacterium
2	37	78.7	144	10 Q92R01	Q92R01 Arabidopsis
3	37	78.7	747	9 Q8SP42	Q8SP42 pseudomonas
4	37	78.7	1250	5 Q9NS95	Q9NS95 caenorhabdi
5	36	76.6	448	10 Q8LFR1	Q8LFR1 Arabidopsis
6	36	76.6	459	16 Q8NQ21	Q8NQ21 corynebacte
7	36	76.6	480	10 Q9M2X7	Q9M2X7 Arabidopsis
8	36	76.6	487	10 Q8W426	Q8W426 oryza sativ
9	36	76.6	569	10 Q8LQZ1	Q8LQZ1 oryza sativ
10	36	76.6	977	5 P91775	P91775 bacillus
11	35	74.5	198	16 Q9P141	Q9P141 campylobact
12	35	74.5	265	17 Q26562	Q26562 methanobact
13	35	74.5	358	1 Q9P914	Q9P914 Halococcus
14	35	74.5	574	16 Q856P9	Q856P9 leptospira
15	35	74.5	846	16 Q87RFA	Q87RFA arabidopsis
16	35	74.5	1016	16 Q8XJH4	Q8XJH4 caenorhabdi

17	35	74.5	1222	5 Q81BL4	Q81BL4 plasmodium
18	35	74.5	1275	3 Q9P6A4	Q9P6A4 neurospora
19	35	74.5	12268	5 Q8M008	Q8M008 caenorhabdi
20	35	74.5	13100	5 Q91F65	Q91F65 caenorhabdi
21	34	72.3	94	16 Q8XKC4	Q8XKC4 clostridium
22	34	72.3	178	5 Q8M2R8	Q8M2R8 acanthochei
23	34	72.3	203	16 Q92WL6	Q92WL6 rhizobium m
24	34	72.3	210	10 Q9XB4	Q9XB4 arabidopsis
25	34	72.3	264	16 Q98R24	Q98R24 mycoplasma
26	34	72.3	286	17 Q30057	Q30057 archaeoglob
27	34	72.3	342	16 Q8ENJ2	Q8ENJ2 oceanobacill
28	34	72.3	531	10 Q94HDE	Q94HDE oryza sativ
29	34	72.3	546	2 Q9KVZ8	Q9KVZ8 xanthomoras
30	34	72.3	557	3 Q9Y7B0	Q9Y7B0 yarrowia li
31	34	72.3	571	2 Q8V754	Q8V754 xanthomoras
32	34	72.3	584	16 Q88RK6	Q88RK6 thermocanaer
33	34	72.3	677	17 Q26913	Q26913 methanobact
34	33	70.2	173	5 Q81GK9	Q81GK9 drosophila
35	33	70.2	231	16 Q8XJH7	Q8XJH7 raietonia s
36	33	70.2	249	5 Q9VPM9	Q9VPM9 drosophila
37	33	70.2	267	16 Q8EGL2	Q8EGL2 shewanella
38	33	70.2	314	9 Q9ZXD5	Q9ZXD5 bacterioph
39	33	70.2	335	5 Q866K5	Q866K5 caenorhabdi
40	33	70.2	347	17 Q9HCL3	Q9HCL3 halobacteri
41	33	70.2	413	10 Q9LIL1	Q9LIL1 arabidopsis
42	33	70.2	448	16 Q917G3	Q917G3 pseudomonas
43	33	70.2	455	5 Q23644	Q23644 caenorhabdi
44	33	70.2	503	16 Q92VT6	Q92VT6 rhizobium m
45	33	70.2	516	17 Q9HJH4	Q9HJH4 thermoplasm

## ALIGNMENTS

RESULT :

ID	Q9HPC3	PRELIMINARY:	PRT:	118 AA.
AC	Q9HPC3			
DT	C1-MAR-2001 (TrEMBL:rel_16, Created)			
DT	C1-MAR-2001 (TrEMBL:rel_16, Last sequence update)			
DT	C1-MAR-2001 (TrEMBL:rel_23, Last annotation update)			
DE	5CS_ribosomal protein:24P.			
GN	RP24P OR VNG1723.			
OS	Halobacterium sp. (strain NRC-1).			
OC	Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;			
OC	Halobacteriaceae; Halobacterium.			
OX	NCBI:taxid:54091.			
RN	11			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:2053483; PubMed:1016950;			
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,			
RA	Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna C.,			
RA	Swartzel S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,			
RA	Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,			
RA	Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,			
RA	Isenberger T.A., Peck R.F., Kohlshroder M., Spudich J.L., Jung K.-H.,			
RA	Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,			
RA	Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasGupta S.,			
RT	"Genome sequence of Halobacterium species NRC-1".			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).			
DR	EMBL: AE05077; AAG1947.1;			
DR	InterPro: IPR005824; K0M.			
DR	InterPro: IPR006646; K0M_sub.			
DR	InterPro: IPR005825; Ribosomal_L24_26.			
DR	Pfam: PFC0467; K0M.			
DR	SMART: SM00739; K0M.			
DR	PROSITE: PS01108; RIBOSOMA_L24; 1.			
KW	Ribosomal protein; Complete proteome.			
SQ	SEQUENCE 118 AA; 13369 MW; 90C2FIC4577190A8 CRC64;			

Query Match 80.9%; Score 3d: DB 17; Length 118;  
Best Local Similarity 77.8%; Pred. No: 12;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



BT "Full length cDNA from Arabidopsis sequencing project";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DP EMBL; AY094597; AY061258.1; -;  
 DR InterPro: IPR003613; Znf\_modRING.  
 DR SMART: SM0504; Ubox; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 448 AA; 43011 MW; 4A06975D554F563 CRC64;

Query Match: 76.6%; Score 36; DB 10; Length 448;  
 Best Local Similarity: 75.0%; Pred. No. 12x2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGVMDVC 9  
 |||||  
 DB 20 DGGVLDLD 27

## RESULT 6

Q8N021 PRELIMINARY; PRT: 450 AA  
 AC Q8N021  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Uncharacterized AtPase related to the helicase subunit of the Heliday  
 DE function resolvase.  
 GN GUS1633.  
 OS Arabidopsis thaliana (Brassicaceae).  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.  
 CC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 CC NCBI\_TaxID:1718.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN ATCC 13030 / DSM 20190 / NCIE 100257  
 RA Nakagawa S.  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13030";  
 DR EMBL: AB004299; BAB99026.1; -;  
 DR InterPro: IPR003959; AAA\_Atpase\_cent1.  
 DR SMART: SM000862; RECDomain.  
 DR Pfam: PF00004; AAA; 1.  
 KW Helicase; Complete proteome.  
 SQ SEQUENCE 459 AA; 49478 MW; 8A58PFFA755405 CRC64;

Query Match: 76.6%; Score 36; DB 10; Length 448;  
 Best Local Similarity: 66.7%; Pred. No. 12x2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGGVMDVC 9  
 |||||  
 DB 245 DGGVLDLD 253

## RESULT 7

Q9MXX7 PRELIMINARY; PRT: 460 AA  
 AC Q9MXX7  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 55.6 kDa protein.  
 GN T16K5.160.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudots; Euroids;  
 CC euroids 11; Brassicales; Brassicaceae; Arabidopsis  
 CC NCBI\_TaxID:1072.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Plesner M., Gabel C., Mueller-Auer S., Schneider M., Vitz M.,  
 RA Weiss H.W., Gerke K., Mayer K.F.X., Gantner F., Bialas J. et al.  
 FL Submitted (NOV 1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DP EMBL; AL132965; CAB6619.1; -;  
 DR InterPro: IPR003613; Znf\_modRING.  
 DR SMART: SM0504; Ubox; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 52645 MW; CC4E011E9306FBA CRC64;

Query Match: 76.6%; Score 36; DB 10; Length 480;  
 Best Local Similarity: 75.0%; Pred. No. 13x02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGVMDVC 9  
 |||||  
 DB 20 DGGVLDLD 27

## RESULT 8

Q8W426 PRELIMINARY; PRT: 487 AA  
 AC Q8W426  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE 21D7.  
 GN OS21D7.  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Ehrhartoideae; Oryzaceae; Oryza.  
 CC NCBI\_TaxID:4510.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN cv. Nipponbare;  
 RA Yanagawa Y., Hasezawa S., Kuragaki E., Fujimuro M., Yokosawa H.,  
 RA Tanaka K., Komamine A., Hashimoto S., Sato T., Nakagawa H.;  
 RT "Clonalization of protease subunits and plant specific  
 RT microbubbles, preprotease bands and phragoplast, during cell cycle";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB011299; BAB92474.1; -;  
 DR Gramene: G8W426; -;  
 DR InterPro: IPR003917; PCT.  
 DR Pfam: PF01399; PCT; 1.  
 DR SMART: SM00088; PNT; 1.  
 SQ SEQUENCE 487 AA; 54980 MW; 5B91593A4812AC1 CRC64;

Query Match: 76.6%; Score 36; DB 10; Length 487;  
 Best Local Similarity: 75.0%; Pred. No. 13x02;  
 Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGVMDVC 9  
 |||||  
 DB 91 DGGSEMDVC 99

## RESULT 9

Q8LQGI PRELIMINARY; PRT: 569 AA  
 AC Q8LQGI  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Vacuolar sorting receptor-like protein.  
 GN P004012.8.  
 OS Oryza sativa (Japanese cultivar-group).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Ehrhartoideae; Oryzaceae; Oryza.  
 CC NCBI\_TaxID:39547.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN cv. Nipponbare.

RA Sasaki T., Matsutani T., Yamamoto K.  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
 RT clone: P004012."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBE databases.  
 DR EMBL: AP004943; BAB2664.1; ;  
 DR Gramsel; O8LQ01; ;  
 DR InterPro; IPR001337; PA;  
 DR InterPro; IPR006639; PSN;  
 DR Pfam; PF04258; DUF435; 1;  
 DR Pfam; PF02225; PA; 1;  
 DR SMART; SM00730; PSN; 1;  
 DR PROSITE; PS00943; PA; 1;  
 KW Receptor;  
 SQ SEQUENCE 569 AA; 61340 MW; 560788444401E R044;  
 Query Match 76.6%; Score 45; DB 16; Length 198;  
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDCQVMDV 9  
 DB 148 EDCQVMDV 156

## RESULT 10

CD P11775 PRELIMINARY; PST; 977 AA  
 AC P11775;  
 DT 01 MAY 1999 (TREMBLrel\_01, Created;  
 DT 01 MAY 1999 (TREMBLrel\_01, Last sequence update;  
 DT 01 DEC 2001 (TREMBLrel\_19, Last annotation update;  
 DE Pacifastin, a novel 155-kDa heterodimeric proteinase inhibitor  
 DE containing a unique transerferin chain;  
 OS Pacificastus leniscus (Signal crayfish);  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Piloceyemata; Astacidea;  
 CC Astacidea; Astacidae; Pacifastacus;  
 OX NCBI\_TaxID:6729;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9138078; PubMed-9192625;  
 RA Liang Z., Sottrup-Jensen L., Asnab A., Hall M., Soderlund K.,  
 RT "Pacifastin, a novel 155-kDa heterodimeric proteinase inhibitor  
 RT containing a unique transerferin chain";  
 SC Proc. Natl. Acad. Sci. U.S.A. 94:6692-6697 (1997);  
 DR EMBL: U8424; AAC84660.1;  
 DR HSP; P58410; ZMW;  
 DR InterPro; IPR001150; Transerferin  
 DR Pfam; PF04258; Transerferin\_2;  
 DR PAINS; P00424; TRANSFERRIN;  
 DR SMART; SM00744; TRFER; 1;  
 DR PROSITE; PS1206; TRANSFERRIN\_2; 1  
 KW SIGNAL;  
 FT SIGNAL 1 22 POTENTIAL;  
 FT CHAIN 23 977 PACIFASTIN HEAVY CHAIN;  
 SQ SEQUENCE 977 AA; 106866 MW; 581001191197E R044;

Query Match 76.6%; Score 45; DB 16; Length 198;  
 Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDCQVMDV 9

DB 155 EDCQVMDV 163

## RESULT 11

CD Q0142 PRELIMINARY; PST; 126 AA  
 AC Q0142;  
 DT 01 OCT 2000 (TREMBLrel\_15, Created;  
 DT 01 OCT 2000 (TREMBLrel\_15, Last sequence update;  
 DT 01 DEC 2001 (TREMBLrel\_19, Last annotation update;  
 DE Putative transcriptional regulator;

GN Q00465.  
 OS Campylobacter jejuni;  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter;  
 OX NCBI\_TaxID:197;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:NC011169;  
 RX MEDLINE-2015912; PubMed-1068204;  
 RA Parkhill J., Wren B.W., Murgall K., Ketley C.M., Clutter C.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
 RA Cagelli K., Kariyasek A.V., Maud S., Pallen M.J., Penn C.W.,  
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.V.,  
 RA Whitehead S., Barratt B.G.;  
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 RT reveals hypervariable sequences";  
 RL Nature 403:665-668 (2000);  
 DR EMBL; AL190075; CAB75154.1; ;  
 DR InterPro; IPR000595; CNMP binding;  
 DR Pfam; PF00027; CNMP binding; 1;  
 DR SMART; SM00100; CNMP; 1;  
 DR PROSITE; PS00342; CNMP\_BINDING\_3; 1;  
 KW Complete proteome;  
 SQ SEQUENCE 195 AA; 21221 MW; 785932863910A030 CRC64;

Query Match 74.5%; Score 45; DB 16; Length 198;  
 Best Local Similarity 44.4%; Pred. No. 77;  
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDCQVMDV 9

DB 83 EDCQVMDV 91

## RESULT 12

O26562 PRELIMINARY; PST; 265 AA  
 ID O26562;  
 AC O26562;  
 DT 01 JAN 1998 (TREMBLrel\_05, Created;  
 DT 01 JAN 1998 (TREMBLrel\_05, Last sequence update;  
 DT 01 JUN 2002 (TREMBLrel\_21, Last annotation update)  
 DE Hypothetical protein MTH462;  
 GN MTH462;  
 OS Methanobacterium thermoautotrophicum;  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanotherobacter;  
 OX NCBI\_TaxID:18420;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:Doita 1;  
 RX MEDLINE-98139514; PubMed-9171463;  
 RA Smith D.R., Decotte Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
 RA Aldredge T., Rashirzadeh R., Blakey D., Cook R., Gilbert K.,  
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
 RA McDougall S., Scher G., Goyal A., Pietrowski S., Church G.M.,  
 RA Daniels C., Mao C., Rice P., Noelling J., Reeve J.N.;  
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
 RT delahat: functional analysis and comparative genomics";  
 RL J. Bacteriol. 179:7135-7155 (1997);  
 DR EMBL; AE005810; AAB84968.1; ;  
 KW Hypothetical protein; Complete proteome;

Query Match 74.5%; Score 35; DB 17; Length 265;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDCQVMDV 9

DB 155 EDCQVMDV 163

## RESULT 13

Q99914 PRELIMINARY; PRT: 158 AA.  
 ID Q99914  
 AC Q99914  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Nitrate reductase subunit 2 (EC 1.6.99.4)  
 GN NARH  
 OS Halococcus marismortui (Halobacterium marismortui), Act  
 OS Halococcus marismortui subsp. marismortui  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales  
 OC Halobacteriaceae; Halobacteri  
 CC NCBI\_TaxID=2238, 122093;  
 RN 1;  
 RF SEQUENCE FROM N.A.  
 RC SPECIES: marismortui  
 RA Yoshinaka K., Iwasaki T., Fujiwara T.,  
 RT "Sequence and Electron Paramagnetic Resonance Analyses of the Archaeal  
 RT Nitrate Reductase NARH from the Denitrifying Halophilic Euryarchaeote  
 RT Halococcus marismortui";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RC SPECIES: marismortui subsp. marismortui  
 RA Yoshinaka K., Yamamoto A., Fujiwara T.,  
 RT "Sequence analysis of the dissimilatory nitrate reductase from a  
 RT denitrifying halophilic archaeon, Halococcus marismortui";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A322007; CAB22070.1;  
 DR EMBL: A322007; CAB22070.1;  
 DR InterPro: IPR001450; 4FeS\_Ferredoxin.  
 DR Pfam: PF00337; fer4.1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 358 AA; 41122 MW; 380A308740516105 CP564;

Query Match 74.5%; Score 35; DB 15; Length 154;  
 Best Local Similarity 55.8%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9

DB 292 EGQTVMD 100

## RESULT 14

Q99914 PRELIMINARY; PRT: 158 AA.  
 ID Q99914  
 AC Q99914  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 23, Last sequence update)  
 DE Hypothetical protein.  
 GN LAL389  
 OS Leptospira interrogans.  
 CC Bacteria; Spirochaetes; Spirochaetiales; Leptospiraceae; Leptospira.  
 CC NCBI\_TaxID 173;  
 RN 1;  
 RF SEQUENCE FROM N.A.  
 RC STRAIN: S6601 / Serogroup Icterohaemorrhagiae / Serovar 1a;  
 RA Ren S.;  
 RT Submitted (MAR 2002) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AE011118; AAM48588.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 574 AA; 65826 MW; 1F5E251C81B310E0 CP764;

Query Match 74.5%; Score 35; DB 15; Length 154;  
 Best Local Similarity 75.0%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGVMDVD 9

DB 292 EGQTVMD 100

DB 497 DGGVMDVD 504

## RESULT 15

Q99914 PRELIMINARY; PRT: 846 AA.  
 ID Q99914  
 AC Q99914  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Primosomal protein N.  
 GN AL4248.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 CC NCBI\_TaxID=101690;  
 RN 1;  
 RF SEQUENCE FROM N.A.  
 RC MEDLINE=21595265; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Higuchi M., Ishikawa A., Kawashima K., Kikura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shingo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tacata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120";  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL: AP003595; BAB75947.1;  
 DR InterPro: IPR001410; DEAC.  
 DR InterPro: IPR001650; Helicase C.  
 DR InterPro: IPR005259; PflA.  
 DR Pfam: PF03271; Helicase C; 1.  
 DR SMART: SM00487; DEXOC; 1.  
 DR SMART: SM00490; HELICC; 1.  
 DR TIGRFAMs: TIGR00595; pflA; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 846 AA; 94775 MW; 7352DF49D40A6726 CP664;

Query Match 74.5%; Score 35; DB 16; Length 846;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EDGQVMDVD 9

DB 280 EGQVMDVD 288

Search completed: November 5, 2003, 15:53:53  
 Job time: 20.4777 sec









DT 05 JAN 2001 (first entry)  
 XX  
 DE P1 mimotope peptide P1st SEQ ID NO:211  
 XX  
 KW Epitope: mimotope; human; immunoglobulin E; IgE; Cepsilon2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW Allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20020460 A1  
 XX  
 PC 31 AUG 2002  
 XX  
 PF 22-FEB-2002; 2002WO-EPC1455.  
 XX  
 PR 24-FEB-1999; 99GB-0004405.  
 PR 29-MAR-1999; 99GB-0007151.  
 PR 07-MAY-1999; 99GB-0010537.  
 PR 03-MAY-1999; 99GB-0010538.  
 PR 07 AUG 1999; 99GB 0018594.  
 PR 07 AUG 1999; 99GB-0018603.  
 PR 07 SEP-1999; 99GB-0021546.  
 PR 07 SEP-1999; 99GB-0021547.  
 PR 24-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027658.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (INVENTOR) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dwyer M., Flade M., Greenwood J., Hewitt E., Larned A., Mason S.,  
 Randall R., Turnbull W.G., Van Neehelen X.P., Vinals De Bascols Y.  
 XX  
 DE WPI: 2000-520767/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Disclosure, Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E) of C epsilon2 domain (2) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are (II) an  
 CC immunogen (III) for treating allergy comprising (I), a vaccine (III)  
 CC for treating allergies comprising (II), (III) and (IV) capable of  
 CC recognising (II), (III) and (IV) and (V) comprising (IV),  
 CC (6) a peptide (II) capable of being recognised by (I), (II) and (III), (II)  
 CC (III) comprising (Ia) and (Ib) producing (II) (Ib) and (III) are  
 CC as a vaccine and histamine release-inhibitor (II), (Ib) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of (I),  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (V) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (I), (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. Amino acid sequences of the present  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA:  
 XX  
 Query Match 100.0%; Score 47; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. Gaps: 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 EDGQWMDVD 9  
 |||||  
 2 EDGQWMDVD 10  
 RESULT 8  
 ABJ00228  
 ID ABJ00228 standard; Peptide; 10 AA.  
 XX  
 AC ABJ00228.

RESULT 7  
 AAU16654  
 ID AAU16654 standard; Peptide; 10 AA.  
 XX  
 AC AAU16654;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Peptide P1st derived as mimotope of Cepsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200145745-A2.  
 XX  
 PC 28-JUN-2001.  
 XX  
 PF 21-DEC-2000; 2000WO GB04935.  
 XX  
 PR 21-DEC-1999; 99GB 0030233.  
 PR 22-FEB-2000; 2000GB 0034096.  
 PR 22-AUG-2000; 2000GB-0020707.  
 PR 22-AUG-2000; 2000GB-0020708.  
 XX  
 PA (ACAM) ACAMBI'S RES LTD  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Flinn N., Johnson T.  
 XX  
 DE WPI: 2001-521367/53.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 XX  
 PS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16654-ABJ1693 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 10 AA:  
 XX  
 Query Match 100.0%; Score 47; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. Gaps: 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 EDGQWMDVD 9  
 |||||  
 2 EDGQWMDVD 10  
 RESULT 8  
 ABJ00228  
 ID ABJ00228 standard; Peptide; 10 AA.  
 XX  
 AC ABJ00228.



PR 07-AUG-1999; 99GB-0018603.  
 PR 07-SEP-1999; 99GB-0021046.  
 PR 07-SEP-1999; 99GB-0021047.  
 PR 29-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Fliede M, Greenwood J, Hewitt E, Lamont A, Mason S,  
 PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassois YC.  
 XX  
 DR WPI: 2000-572073/51.  
 XX  
 PS Claim 14; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 CC immunogen (III) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (IIa) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (IIa); and (7) producing (III) by producing (II); (1)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (i), (ii) and (iii) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (iv) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (ii) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (ii), (iii) and (iv) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (iv) is also useful in diagnosing atopy. AAB25917 : AAB25917 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%; Score 47; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EDSQWMDVD 9  
 ||| |||  
 DB 3 EDSQWMDVD 11  
 RESULT 12  
 AAB25917  
 ID AAB25917 standard; Peptide; 13 AA  
 XX  
 AC AAB25917;  
 XX  
 DT 05 JAN 2001 (first entry)  
 XX  
 DE P1 mimotope peptide P15p SEQ ID NO:11.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.  
 XX  
 PR WO20005040-A1  
 PR 31 AUG 2000.  
 PR 20 FEB 2001; EDSQWMDVD-EP01455.

XX 25-FEB-1999; 99GB-0004403.  
 PR 29-MAR-1999; 99GB-0007151.  
 PR 07-MAY-1999; 99GB-0010537.  
 PR 07-MAY-1999; 99GB-0010538.  
 PR 07-AUG-1999; 99GB-0018594.  
 PR 07-AUG-1999; 99GB-0018603.  
 PR 07-SEP-1999; 99GB-0021046.  
 PR 07-SEP-1999; 99GB-0021047.  
 PR 29-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Fliede M, Greenwood J, Hewitt E, Lamont A, Mason S,  
 PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassois YC.  
 XX  
 DR WPI: 2000-572073/51.  
 XX  
 PS Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Disclosure; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 CC immunogen (III) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (IIa) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (IIa); and (7) producing (III) by producing (II); (1)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (i), (ii) and (iii) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (iv) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (ii) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (ii), (iii) and (iv) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (iv) is also useful in diagnosing atopy. AAB25917 : AAB25917 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%; Score 47; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EDSQWMDVD 9  
 ||| |||  
 DB 3 EDSQWMDVD 11  
 RESULT 12  
 AAB25917  
 ID AAB25917 standard; Peptide; 13 AA  
 XX  
 AC AAB25917;  
 XX  
 DT 05 JAN 2001 (first entry)  
 XX  
 DE P1 mimotope peptide P15p SEQ ID NO:11.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.



```

OS Synthetic
XX WO200145745-A2.
XX
XX 26 JUN 2001.
XX
XX 21-DEC-2000; 2006WO-GB04935.
XX
XX 21-DEC-1999; 99GB-C030233.
XX
XX 22-FEB-2000; 2000GB-C004596.
XX
XX 22-AUG-2000; 2000GB-0026757.
XX
XX 22-AUG-2000; 2000GB-0026768.
XX
XX (ACAM) ACAMHS RES LTD.
XX (SMK) SVITHKLINE BEECHAM BIOLOGICALS.
XX
XX Flinn N. Johnson T.
XX
XX WPI; 2001-521967/57.
XX
XX A linkage comprising an immunogenic conjugate useful treatment of Ige
XX mediated diseases
XX
XX Example 4; Page 21; 48pp; English.
XX
XX The present invention relates to linkage methodology for use in the
XX conjugation of compounds (e.g. peptides) to carrier vehicles
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX biological and immunological constructs. The invention provides a
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX protein) for use in a pharmaceutical composition or a vaccine. The
XX invention describes peptides derived from or mimotopes of the
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E
XX (IgE) which are used to produce conjugated compounds. The compounds or
XX compositions of the invention are useful in the manufacture of a
XX medicament for the treatment of Ige-mediated diseases. The invention
XX allows for controlled conjugation of a peptide epitope (antigen) to a
XX protein so as to form an immunogenic conjugate which may be able to
XX raise a protective antibody response in an animal or human patient.
XX AAU1632-AAU1693 represent peptides derived from or mimotopes of
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
XX
XX Sequence 13 AA.
XX
XX Query Match 100.0% Score 47; DB 25; Length 13;
XX Best Local Similarity 100.0%; Pos. Num. 0:0:4;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX QY 1 EDGQWMD 9
XX Db 3 EDGQWMD 11
XX
XX Search completed November 6, 2003, 15:46:37
XX Job time: 24.65 secs

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XX 21-DEC-2000; 2006WO-GB04935.
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XX 21-DEC-1999; 99GB-C030233.
XX
XX 22-FEB-2000; 2000GB-C004096.
XX
XX 22-AUG-2000; 2000GB-0026757.
XX
XX 22-AUG-2000; 2000GB-0026768.
XX
XX (ACAM) ACAMHS RES LTD.
XX (SMK) SVITHKLINE BEECHAM BIOLOGICALS.
XX
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XX WPI; 2001-521967/57.
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XX
XX The present invention relates to linkage methodology for use in the
XX conjugation of compounds (e.g. peptides) to carrier vehicles
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX biological and immunological constructs. The invention provides a
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX protein) for use in a pharmaceutical composition or a vaccine. The
XX invention describes peptides derived from or mimotopes of the
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E
XX (IgE) which are used to produce conjugated compounds. The compounds or
XX compositions of the invention are useful in the manufacture of a
XX medicament for the treatment of Ige-mediated diseases. The invention
XX allows for controlled conjugation of a peptide epitope (antigen) to a
XX protein so as to form an immunogenic conjugate which may be able to
XX raise a protective antibody response in an animal or human patient.
XX AAU1632-AAU1693 represent peptides derived from or mimotopes of
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
XX
XX Sequence 13 AA.
XX
XX Query Match 100.0% Score 47; DB 25; Length 13;
XX Best Local Similarity 100.0%; Pos. Num. 0:0:4;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX QY 1 EDGQWMD 9
XX Db 3 EDGQWMD 11
XX
XX Search completed November 6, 2003, 15:46:37
XX Job time: 24.65 secs

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RESULT 5
AAC16642
ID AAC16642 standard; Peptide, 13 AA.
XX
XX AC AAU16642;
XX
XX 09-NOV-2001 (first entry)
XX
XX Peptide P15q derived as mimotope of conjugated to form of human IgE.
XX
XX Human linkage technology; conjugated to form of human IgE.
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; Cepsilon5; Cepsilon6.
XX Ige mediated disease; antibody response.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200145745 A2.
XX
XX 26 JUN 2001.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX Protein: protein search, using sw model

Run on: November 5, 2003, 15:54:16 / Search time 15.4937 Seconds  
Pairwise alignment  
98.494 Million Cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: EDGQWMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Seam-thed: 644079 segs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 2  
Maximum DB seq length: 200000000  
Post processing: Minimum Match 38  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications, AA\*  
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2: /cgn2\_6/prodata/2/pub/paa/US06\_PUBCOMB.pat.  
3: /cgn2\_6/prodata/2/pub/paa/US06\_PUBCOMB.pat.  
4: /cgn2\_6/prodata/2/pub/paa/US06\_PUBCOMB.pat.  
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16: /cgn2\_6/prodata/2/pub/paa/US09\_PUBCOMB.pat.  
17: /cgn2\_6/prodata/2/pub/paa/US09\_PUBCOMB.pat.  
18: /cgn2\_6/prodata/2/pub/paa/US09\_PUBCOMB.pat.  
19: /cgn2\_6/prodata/2/pub/paa/US09\_PUBCOMB.pat.

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	47	100.0	9	12	US-10-082-014-273
2	47	100.0	9	12	US-10-372-076-127
3	47	100.0	10	12	US-10-082-014-282
4	47	100.0	10	12	US-10-372-076-136
5	47	100.0	128	15	US-10-152-190-11
6	47	100.0	236	15	US-10-152-190-9
7	47	100.0	320	11	US-09-847-208-6
8	47	100.0	323	10	US-09-949-375A-2
9	47	100.0	323	10	US-09-949-375A-4
10	47	100.0	323	10	US-09-949-375A-6
11	47	100.0	330	10	US-09-949-375A-10
12	47	100.0	331	9	US-09-401-636-1
13	47	100.0	331	15	US-10-176-664-1
14	47	100.0	331	15	US-10-207-655-313
15	47	100.0	336	10	US-09-949-375A-8

16	47	100.0	346	15	US-10-152-190-10
17	47	100.0	346	15	US-10-152-190-14
18	47	100.0	347	15	US-10-152-190-12
19	47	100.0	347	15	US-10-152-190-13
20	47	100.0	348	15	US-10-152-190-11
21	47	100.0	426	15	US-10-214-524-26
22	47	100.0	427	11	US-09-847-208-5
23	47	100.0	428	10	US-09-916-230-1
24	47	100.0	428	10	US-09-949-375A-1
25	47	100.0	428	14	US-10-047-542-60
26	47	100.0	441	10	US-09-949-375A-7
27	47	100.0	549	11	US-09-847-208-7
28	47	100.0	574	12	US-10-050-898-176
29	47	100.0	574	12	US-10-050-902-176
30	47	100.0	574	14	US-10-047-542-45
31	47	100.0	574	15	US-10-214-524-37
32	47	100.0	592	15	US-10-207-655-334
33	41	87.2	110	12	US-10-144-188-55
34	38	80.9	249	15	US-10-156-761-14113
35	37	78.7	821	9	US-09-848-035-2
36	37	78.7	821	10	US-09-986-224-2
37	37	78.7	980	9	US-09-848-035-13
38	37	78.7	980	10	US-09-986-224-13
39	37	78.7	1249	12	US-10-239-663-42
40	37	78.7	1178	14	US-10-041-856-9
41	36	76.6	383	15	US-10-078-770-170
42	36	76.6	459	10	US-09-738-626-5333
43	35	74.5	328	15	US-10-128-714-3134
44	35	74.5	330	15	US-10-128-714-8134
45	33	70.2	139	9	US-09-815-242-10722

ALIGNMENTS

RESULT 1  
US-10-082-014-273  
; Sequence 273, Application US-10-082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: 100-130,045,647/85,524  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/940,915  
; PRIOR FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 273  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-273

Query Match	100.0%	Score 47:	DB 12:	Length 9:
Best Local Similarity	100.0%	Pred. No. 5.9e+05:		
Matches	9:	Conservative 0:	Mismatches 0:	Indels 0:
Gaps	0:			
QY	1	EDGQWMDVD 9		
DB	1	EDGQWMDVD 9		
RESULT 2				
US-10-372-076-127				
; Sequence 127, Application US/10372076				
; Publication No. US20030198645A1				
; GENERAL INFORMATION:				
; APPLICANT: Fiedler, Martin				
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR				
; CHRONIC HEPATITIS				

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 127  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-136

Query Match 100.0% Score 47; DB 15; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
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DB : EDGQWMDV 9

## RESULT 3

US-10-082-014-282  
Sequence 282, Application US/10082014  
Publication No. US2003018588A1  
GENERAL INFORMATION:  
APPLICANT: Biogen, Ashley J.

TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CYSTEINE  
FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 282  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-082-014-282

Query Match 100.0% Score 47; DB 15; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 10

## RESULT 4

US-10-372-076-136  
Sequence 136, Application US/10/372076  
Publication No. US20030198645A1  
GENERAL INFORMATION:  
APPLICANT: Biogen, Mark

TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR CHRONIC HEPATITIS  
FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 136  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-136

Query Match 100.0% Score 47; DB 15; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 78

## RESULT 7

US-09-947-238-6  
Sequence 6, Application US/09947238  
Publication No. US20030082190A1  
GENERAL INFORMATION:  
APPLICANT: Saxon, Andrew

Query Match 100.0% Score 47; DB 15; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 78

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-136

Query Match 100.0% Score 47; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 10

## RESULT 5

US-10-152-190-7  
Sequence 7, Application US/10/152190  
Publication No. US20030096369A1  
GENERAL INFORMATION:  
APPLICANT: Morsey, Mohammad A.

TITLE OF INVENTION: NO US20030096369A1 anaphylactogenic IgE vaccines  
FILE REFERENCE: PC11011A  
CURRENT APPLICATION NUMBER: US/10/152,190  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 7  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Modified Human CH2 domain  
US-10-152-190-7

Query Match 100.0% Score 47; DB 15; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 78

## RESULT 6

US-10-152-190-9  
Sequence 9, Application US/10/152190  
Publication No. US20030096369A1  
GENERAL INFORMATION:  
APPLICANT: Morsey, Mohammad A.

TITLE OF INVENTION: NO US20030096369A1 anaphylactogenic IgE vaccines  
FILE REFERENCE: PC11011A  
CURRENT APPLICATION NUMBER: US/10/152,190  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 9  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Modified Human CH2 CH4 carrier protein  
US-10-152-190-9

Query Match 100.0% Score 47; DB 15; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9  
||| |||  
DB : EDGQWMDV 78

```

; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: U097-002A
; CURRENT APPLICATION NUMBER: US/09/847,228
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-228-6

Query Match      100.0%; Score 47; DB 11; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9
DB 43 EDGQWMDV 51

RESULT 8
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: 111-311
; OTHER INFORMATION: Human Ige heavy chain C2 domain
; NAME/KEY: DOMAIN
; LOCATION: 312-311
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: 1216-1317
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1104-1111
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1212-1215
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1100-1114
; OTHER INFORMATION: Epitope including C2/C3 linker
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1210-1218
; OTHER INFORMATION: Epitope including C3/C4 linker
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1130-1145
; OTHER INFORMATION: Epitope in AC loop
; FEATURES:

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; NAME/KEY: MISC FEATURE
; LOCATION: 1167-1175
; OTHER INFORMATION: Epitope in DE loop
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: 1195-1226
; OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2

Query Match      100.0%; Score 47; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9
DB 46 EDGQWMDV 54

RESULT 9
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.
US-09-949-375A-4

Query Match      100.0%; Score 47; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9
DB 46 EDGQWMDV 54

RESULT 10
US-09-949-375A-6
; Sequence 6, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.
US-09-949-375A-6

Query Match      100.0%; Score 47; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDV 9
DB 46 EDGQWMDV 54

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Db 46 EDGQWMDVD 54

## RESULT 11

US-09-949-375A-10  
Sequence 10, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE  
FILE REFERENCE: 3631-011P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 10  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO 9.  
US-09-949-375A-10

Query Match 100.0% Score 47; DB 15; Length 330;

Best Local Similarity 100.0%; Pred. No. 0.58; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQWMDVD 9

Db 46 EDGQWMDVD 54

## RESULT 12

US-09-421-616-1  
Sequence 10, Application US/09421616F  
Patent No. US20010618943A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/056001  
CURRENT APPLICATION NUMBER: US/09/401,616  
CURRENT FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-09-401-616-1

Query Match 100.0% Score 47; DB 9; Length 331;

Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQWMDVD 9

Db 54 EDGQWMDVD 62

## RESULT 13

US-10-176-664-1  
Sequence 1, Application US/10176664  
Publication No. US2003031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10033/006001  
CURRENT APPLICATION NUMBER: US/10/176,664  
CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/09/401,636  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-10-176-664-1

Query Match 100.0% Score 47; DB 15; Length 331;

Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQWMDVD 9

Db 54 EDGQWMDVD 62

## RESULT 14

US-10-207-655-329  
Sequence 129, Application US/10207655  
Publication No. US20030118592A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Hayden-Ledbetter, Martha S.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390049.401C  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 329  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion polypeptide  
US-10-207-655-329

Query Match 100.0% Score 47; DB 15; Length 331;

Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQWMDVD 9

Db 50 EDGQWMDVD 56

## RESULT 15

US-09-949-375A-8  
Sequence 8, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE  
FILE REFERENCE: 3631-011P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 8  
LENGTH: 336  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: 17-105  
OTHER INFORMATION: ICE heavy chain 12 domain



GenCore version 5.1.6  
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QX Protein - protein search, using sw model

Run on: November 5, 2003, 17:18:39 ; Search time 13.5 Seconds  
(without alignments)  
56,989 Million cell updates/sec

Title: US-09-914 088 2

Perfect score: 39

Sequence: 1 STR-JEGL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 36168692 residues

Total number of hits satisfying chosen parameters: 604

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	41.0	8	D61512	variant surface gl
2	15	40.5	6	JH0784	neuropeptide TE-6
3	15	33.3	5	JT0520	gamma chain V I
4	13	43.3	7	PT0581	T-cell receptor be
5	13	33.3	8	C39690	hemat cell adhesi
6	12	30.8	4	I40697	biofilm A - Citrob
7	12	30.8	5	PT0684	T-cell receptor be
8	12	30.8	6	S29637	jacalin beta-II ch
9	12	30.8	6	A20186	fatty-acid synthas
10	12	30.8	6	PT0662	T-cell receptor be
11	12	30.8	6	PT0648	T-cell receptor be
12	12	30.8	7	E61491	seed protein ws-5
13	12	30.8	7	PT0529	T-cell receptor be
14	12	30.8	7	PT0667	T-cell receptor be
15	12	30.8	8	S37141	tpsa protein - Brw
16	12	30.8	8	S63493	dissimilatory sulf
17	12	30.8	8	PT0595	T-cell receptor be
18	12	30.8	8	PT0653	T-cell receptor be
19	11	28.2	4	PT0677	T-cell receptor be
20	11	28.2	4	A26209	protein-glutamine
21	11	28.2	5	B45525	actin 1 - malaria
22	11	28.2	5	PT0543	T-cell receptor be
23	11	28.2	6	A61419	serine dehydrog
24	11	28.2	6	I51317	hmlh transcription
25	11	28.2	6	PT0516	T-cell receptor be
26	11	28.2	6	PT0657	T-cell receptor be
27	11	28.2	6	PT0726	T-cell receptor be
28	11	28.2	7	S16364	opacity protein P
29	11	28.2	7	S16365	opacity protein P

30	11	28.2	7	2	A44428	platelet aggregati
31	11	28.2	7	2	H33098	180K exoantigen -
32	11	28.2	7	2	PC1316	large granule L3 c
33	11	28.2	7	2	PT0526	T-cell receptor be
34	11	28.2	7	2	PT0676	T-cell receptor be
35	11	28.2	7	2	S58797	serine/threonine-s
36	11	28.2	7	4	I55382	hypothetical pepti
37	11	28.2	8	2	S20162	leghemoglobin II
38	11	28.2	8	2	S43971	tumor-associated a
39	11	28.2	8	2	S43972	tumor-associated a
40	11	28.2	8	2	S13661	polygalacturonase
41	11	28.2	8	2	S71919	alcohol dehydrogen
42	11	28.2	8	2	I48934	apolipoprotein A-I
43	11	28.2	8	2	PT0613	T-cell receptor be
44	11	28.2	8	2	PT0554	T-cell receptor be
45	11	28.2	8	2	PT0691	T-cell receptor be

## ALIGNMENTS

RESULT 1  
D61512  
variant surface glycoprotein X1Tat 1.6 - Trypanosoma brucei (fragment)  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1994 #sequence\_revision: 28-Oct-1994 #text\_change 07-May-1999  
C:Accession: D61512  
R:Holder, A.A.; Cross, G.A.M.  
Mol. Biochem. Parasitol. 2, 135-150, 1981  
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-term  
A:Reference number: A61512; MJD:8:172836; PMID:6163983  
A:Accession: D61512  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <HCL>  
C:Keywords: glycoprotein  
  
Query Match 41.0%; Score 16; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
DB 2 EGE 4

RESULT 2  
JH0784  
neuropeptide TE-6 pig roundworm (fragment)  
C:Species: Ascaris suum (pig roundworm)  
C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 28-Apr-1995  
C:Accession: JH0784  
R:Smart, D.; Shaw, C.; Curry, W.J.; Conston, C.F.; Thim, L.; Halton, D.W.; Buchanan, K  
Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992  
A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris  
A:Reference number: JH0784; MJD:93038603; PMID:1417808  
A:Accession: JH0784  
A:Molecule type: protein  
A:Residues: 1-6 <SMA>  
A:Experimental source: gonoduct  
C:Keywords: neuropeptide  
  
Query Match 38.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. NO. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGE 7  
DB 1 TQGELE 6

RESULT 3  
JT0520

19 kappa chain V H1 region (SD1) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 16-Aug-1996  
 C:Accession: J05220  
 R:Anker, R.; Conley, M.E.; Follok, B.A.  
 J. Exp. Med. 169, 2109-2119, 1989  
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia  
 A:Reference number: J05220; MUID:89279157; PMID:2786447  
 A:Accession: J05220  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <ANK>  
 A:Note: the sequence shown here is one of eight promutative V-D-J mu chain rearrangements  
 A:Note: a stop codon terminates the sequence in the V region  
 C:Keywords: heterodimer; immunoglobulin  
 F:1-5/Domain: V kappa region <VRE>

Query Match 33.3% Score 13; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 1 TQEG 4

RESULT 4  
 P0684  
 T-cell receptor: beta chain V-D-J region (159 AA) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: P0684  
 R:Petrey, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T-cell receptor beta chains have few N regions.  
 A:Reference number: P0684; MUID:91277601; PMID:1711558  
 A:Accession: P0684  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <PEE>  
 A:Experimental source: day 15 fetal thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 33.3% Score 13; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 2 SSEG 7

RESULT 5  
 P0684  
 neutral cell adhesion molecule, cardiac splice form (159 AA) - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 24-Jan-1997 #sequence\_revision 24-Jan-1997 #text\_change 16-Jul-1997  
 C:Accession: C19690  
 R:Reyes, A.A.; S-wall, S.J.; Akerson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A:Title: At least 22 alternatively spliced forms of the neutral cell adhesion molecule mRNA  
 A:Reference number: A39690; MUID:91415161; PMID:1996115  
 A:Accession: C19690  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <PEE>  
 A:Cross references: GI:861970  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 33.3% Score 13; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 2 SSEG 7

Db 4 QGE 6

RESULT 6  
 I40697  
 bactin A - Citrobacter freundii (fragment)  
 C:Species: Citrobacter freundii  
 C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C:Accession: I40697  
 R:Shuan, C.; Campbell, A.  
 Gene 67, 203-211, 1985  
 A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter  
 A:Reference number: I40697; MUID:89006280; PMID:2971595  
 A:Accession: I40697  
 A>Status: preliminary; translated from GE/EMBL/DCBU  
 A:Molecule type: DNA  
 A:Residues: 1-4 <RES>  
 A:Cross references: GB:M2:922; NID:gl44434

Query Match 30.8% Score 12; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQEG 5  
 DB 1 TQEG 4

RESULT 7  
 P0684  
 T-cell receptor: beta chain V-D-J region (140-18X) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: P0684  
 R:Petrey, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T-cell receptor beta chains have few N regions.  
 A:Reference number: P0684; MUID:91277601; PMID:1711558  
 A:Accession: P0684  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PEE>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 30.8% Score 12; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 2 SSEG 5

RESULT 8  
 S29637  
 jacalin beta-II chain - Artocarpus champedac (fragment)  
 C:Species: Artocarpus champedac  
 C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C:Accession: S29637  
 R:Ngoc, L.; Brillard, M.; Hoebeke, J.  
 Biochim. Biophys. Acta 1156, 219-222, 1993  
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-k  
 A:Reference number: S29635; MUID:91152601; PMID:8427879  
 A:Accession: S29637  
 A:Molecule type: protein  
 A:Residues: 1-6 <NGO>  
 A:Experimental source: seed  
 C:Complex: heterotetramer; two alpha and two beta chains  
 C:Function  
 A:Description: seed storage protein  
 A:Note: lectin for L-galactosyl-beta-1,3-N-acetylgalactosamine

C;Keywords: heterotetramer; lectin; seed; storage protein

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSGE 7  
|||  
Db 3 QSGK 6

RESULT 9

A20186

fatty-acid synthase (FC 2.3.1.185) - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 05-May-2000

C;Accession: A20186

R;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.

FEBS Lett. 160, 296-303, 1983

A;Title: Amino acid sequence around the active serine in the acyl transferase domain of

A;Reference number: A20186; MUID:83287768; PMID:6554204

A;Accession: A20186

A;Molecule type: Protein

A;Residues: 1-6 <P>

C;Keywords: acyl-transferase; coenzyme A

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GEL 8  
|||  
Db 3 GEV 5

RESULT 10

PT0662

T-cell receptor beta chain V-D-J region (121-38A) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0662

R;Feeney, A.C.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0662

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <P>

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQGE 7  
|||  
Db 2 SRTGE 6

RESULT 11

PT0649

T-cell receptor beta chain V-D-J region (121-38X) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0649

R;Feeney, A.C.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0649

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <P>

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
|||  
Db 2 SSEG 5

RESULT 12

E61491

seed protein ws-5 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C;Accession: E61491

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-d

A;Reference number: A61491; MUID:89351806; PMID:2765119

A;Accession: E61491

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <P>

C;Keywords: glycoprotein; seed

Query Match 30.8%; Score 12; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 STQEG 6  
|||  
Db 1 STVPGG 6

RESULT 13

PT0529

T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0529

R;Feeney, A.C.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0529

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <P>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
|||  
Db 2 SSEG 5

RESULT 14

PT0667

T-cell receptor beta chain V-D-J region (121-21) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0667

R;Feeney, A.C.

J. Exp. Med. 174, 115-124, 1991



A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0667  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-7 <PE>  
A:Experimental source: day 4 postnatal thymus, strain HA.B/c  
C:Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.9e-05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCEG 6  
DB 2 SSEG 5

## RESULT 15

S37141  
Ipsa protein - Erwinia chrysanthemi  
C:Species: Erwinia chrysanthemi  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Oct 1999  
C:Accession: S37141  
R:Docillie, A.; Toussaint, A.; Faelen, M.  
submitted to the EMBL Data Library, August 1993  
A:Description: Identification of the integration host factor genes of E. chrysanthemi.  
A:Reference number: S37139  
A:Accession: S37141  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-8 <DCU>  
A:Cross-references: EMBL:X74750; NID:g393669, PIDN:CAA52769.1; PDB:g581138

Query Match 30.8%; Score 12; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.9e-05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
DB 6 KGE 5

Search completed: November 5, 2003, 17:22:55  
Job time: 14.5 secs

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OM protein - protein search, using sw mode:

Run on: November 5, 2003, 17:15:14 / Search time 9.5 seconds  
(without alignments)  
35.60 / Million cell updates/sec

Title: US-09-914-088-2

Perfect score: 39

Sequence: 1 STRGEGEL 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 6

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Swissprot\_41.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	41	0	7 1 UF03_MOUSE	P80488
2	16	41	0	8 1 CLP_THICU	P80488
3	13	33	3	7 1 UN11_RAT	P80488
4	13	33	3	8 1 LMT1_MOUSE	P80488
5	12	30	5	1 BICA_CITR	P80488
6	12	30	5	7 1 PPR2_TYCS	P80488
7	12	30	5	8 1 RSI_EPMCH	P80488
8	11	28	2	8 1 UPAA_HUMAN	P80488
9	11	28	2	8 1 WPI_PEBAT	P80488
10	10	25	6	5 1 PSK_DASCA	P80488
11	10	25	6	7 1 E105_LITRU	P80488
12	10	25	6	7 1 UC24_MAIZE	P80488
13	10	25	6	7 1 UN06_PINPS	P80488
14	10	25	6	8 1 ORMY_ORCL	P80488
15	10	25	6	8 1 UN09_RAT	P80488
16	9	23	1	4 1 RM01_YEAST	P80488
17	9	23	1	6 1 UN06_CLOFA	P80488
18	9	23	1	7 1 BRHP_CONIX	P80488
19	9	23	1	7 1 GFRP_MOUSE	P80488
20	9	23	1	7 1 MNPI_LERPE	P80488
21	9	23	1	8 1 AKHG_GRYBI	P80488
22	9	23	1	8 1 GCLR_HUMAN	P80488
23	8	20	5	4 1 GCP1_CCTNY	P80488
24	8	20	5	5 1 UKA4_CHEJTR	P80488
25	8	20	5	7 1 PARI_HSCG	P80488
26	8	20	5	7 1 IGAC_DACLE	P80488
27	8	20	5	8 1 ACI_THAL	P80488
28	8	20	5	8 1 AL12_CARVA	P80488
29	8	20	5	8 1 PARI_PENK	P80488
30	8	20	5	8 1 LCK3_LEUNA	P80488
31	8	20	5	8 1 RS7_MYCT	P80488
32	8	20	5	8 1 UF06_MOUSE	P80488
33	7	17	9	5 1 TRM3_EGGL	P80488

34	7	17.9	7	1	PARS_HIRME	P42564
35	7	17.9	7	1	LANC_CARUT	P36960
36	7	17.9	7	1	WMA1_ACHFU	P35919
37	7	17.9	7	1	WMA1_ACHFU	P35921
38	7	17.9	8	1	AKH_TABAT	P14595
39	7	17.9	8	1	LPK_LEUNA	P13049
40	7	17.9	8	1	RT34_BOVIN	P82929
41	7	17.9	8	1	UPAA_HUMAN	P30096
42	7	17.9	8	1	VGIG_HSV2B	P81780
43	6	15.4	3	1	GRWM_HUMAN	P01157
44	6	15.4	4	1	ACH1_ACHFU	P35904
45	6	15.4	4	1	DCML_PSECH	P19916

## ALIGNMENTS

RESULT 1  
ID UF03\_MOUSE STANDARD: PRT: 7 AA.  
AC P38641:  
DT 01-OCT-1994 (Rel. 30, Created:  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RC TSSUS=Fibroblast;  
RX MEDLINE=95009507; PubMed=7521108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Sellkirk C.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis";  
RL Electrophoresis 15:735-745(1994);  
CC -!- MUSCELLANEUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.  
FT NON TER 7  
SQ SEQUENCE 7 AA: 842 MW: 6AA72B10DB1B180 CRC64:

Query Match 41.0% Score 16; DB ID: Length 7;  
Best Local Similarity 60.0%; Pred. NC: 1.3e-05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8  
DB 2 EEAEI 6

RESULT 2  
ID CLP\_THICU STANDARD: PRT: 6 AA.  
AC P80488:  
DT 01-OCT-1996 (Rel. 34, Created:  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Chemolithotrophic specific protein (fragment).  
OS Thiobacillus cuprinus.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Thiomonas.  
OX NCBI\_TaxID=36860;  
RN [1]  
RP SEQUENCE  
RC STRAIN=DSM 5494;  
RA Martin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
RT Submitted (SEP-1995) to the SWISS-PROT data bank.  
CC -!- MUSCELLANEUS: FOUND SPECIFICALLY IN CELLS CULTURED  
CC CHEMOLITHOTROPHICALLY.  
FT NON TER 6  
SQ SEQUENCE 6 AA: 485 MW: 91487B05DC2076D CRC64:

Query Match 41.0%; Score 16; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QEG 6  
 DB 5 QEG 7

RESULT 3  
 ID UNIL RAT STANDARD; PRT; 7 AA  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created);  
 DT 15-DEC-1998 (Rel. 37, Last sequence update);  
 DT 15-DEC-1998 (Rel. 37, Last annotation update);  
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE:  
 CC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pfeissner K.-P., Scheller C., Regitz-Zagadeck V., Salikov J.,  
 RA Jurgbitt P.R.;  
 RA Submitted P.R.;  
 CC -1- MUSCLE-LANEOS; ON THE 2D-GEL THE DETERMINED P: OF THIS UNKNOWN  
 CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.  
 CC UNSURE 2 2 OR A.  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 775 MW; 6866PDC4DQSA6B0 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STCEG 6  
 DB 2 SAREQG 7

RESULT 4  
 ID LMT2\_LCCMI STANDARD; PRT; 8 AA  
 AC P22156;  
 DT 01-AUG-1991 (Rel. 19, Created);  
 DT 01-AUG-1991 (Rel. 19, Last sequence update);  
 DT 01-AUG-1991 (Rel. 19, Last annotation update);  
 DE Locustamytropin 2 (LOM-MT-2).  
 OS Locusta migratoria (migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pretygella;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoimorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 CC NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE:  
 CC TISSUE=Corpora cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.D., de Loof A.;  
 RA "Isolation, identification and synthesis of locustamytropin 2, an  
 RT additional neuropeptide of Locusta migratoria. Member of the  
 RT cephalomyotropic peptide family."  
 RA Insect Biochem. 20:479-484 (1990).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 9 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA875 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
 DB 1 EGD 3

RESULT 5  
 ID BIOA\_CITFR STANDARD; PRT; 5 AA  
 AC P13071;  
 DT 01-JAN-1990 (Rel. 13, Created);  
 DT 01-JAN-1990 (Rel. 13, Last sequence update);  
 DT 16-OCT-2001 (Rel. 40, Last annotation update);  
 DE Adenosylmethionine 8-amino-7-oxonanoate aminotransferase  
 DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA  
 DE aminotransferase) (Fragment).  
 GN BIOA.  
 OS Citrobacter freundii.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Citrobacter.  
 CC NCBI\_TaxID=546;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89006280; PubMed=2971595;  
 RA Shivan D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli.  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons."  
 RL Gene 67:203-211 (1988).  
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-  
 CC oxonanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-  
 CC diaminonanoate.  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Biotin biosynthesis.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to class III of pyridoxal-phosphate-dependent  
 CC aminotransferases.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL: M21922; -1- NOT\_ANNOTATED\_CDS.  
 DR PIR: I40697; I40697.  
 DR InterPro: IPR005814; Aminotrans\_3.  
 DR PROSITE: PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
 KW Biotin biosynthesis; Transferase; Aminotransferase;  
 KW Pyridoxal phosphate.  
 FT NON TER 5 5  
 SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TIOE 5  
 DB 2 TDD 5

RESULT 6  
 ID PPH2\_LYCES STANDARD; PRT; 7 AA  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created);  
 DT 28-FEB-2003 (Rel. 41, Last sequence update);  
 DT 28-FEB-2003 (Rel. 41, Last annotation update);  
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).

OS Lycopersicon esculentum (Tomato).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 CC Asteridae; families; Solanales; Solanaceae; Solanum.  
 CC NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STRAIN=cv. MoneyMaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.S., Raghothama K.G., Pixton W.C.,  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures."  
 RL Eur. J. Biochem. 269:6278-6286(2002)  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H<sub>2</sub>O → an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Glycosylated.  
 CC -!- M-SCCELLANEGUS: In L. esculentum there are at least two isozymes of  
 CC purple acid phosphatase.  
 CC Hydrolyase; Glycoprotein.  
 KW NON\_TER 1  
 FT NON\_TER 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA662C9C729A0 CRC64;  
 Query Match 30.8%; Score 12; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QEGEL 8  
 DB 5 GDS 7  
 RESULT 7  
 RS\_LERWCH STANDARD; PRT; 9 AA.  
 AC P37985;  
 DT 01-OCT-1994 (Rel. 10, Created).  
 DT 01-OCT-1994 (Rel. 32, Last sequence update).  
 DT 01-NOV-1995 (Rel. 32, Last annotation update).  
 DE 30S ribosomal protein S1 (fragment).  
 GN RPSA.  
 CS Escherichia chrysanthemi.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Pectobacterium.  
 CC NCBI\_TaxID=556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3937;  
 RA Douville A., Toussaint A., Faelen M.,  
 RL Submitted (Aug-1993) to the EMBL/GenBank/DBS databases.  
 CC -!- FUNCTION: BINDS MRNA, THIS FACILITATES RECOGNITION OF THE  
 CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT  
 CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC or send an email to [license@1st-sib.ch](mailto:license@1st-sib.ch)).  
 CC -----  
 DR EMBL; X74750; CAA52769.1;  
 DR PIR; S37141; S37141.  
 KW Ribosomal protein; Repeat; RNA-binding.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 837 MW; 9E18733D58339C9 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 EGE 7  
 DB 6 KGE 8  
 RESULT 8  
 UPAL HUMAN  
 ID CPAL\_HUMAN STANDARD; PRT; 8 AA.  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created).  
 DT 01-APR-1993 (Rel. 25, Last sequence update).  
 DT 16-OCT-2001 (Rel. 40, Last annotation update).  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=94052937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.,  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT NON\_TER 1  
 FT UNSURE 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 944 MW; C01772C455B836DA CRC64;  
 Query Match 28.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 QEGEL 8  
 DB 2 QESNV 6  
 RESULT 9  
 WPI\_PERAT STANDARD; PRT; 9 AA.  
 ID WPI\_PERAT  
 AC P83195;  
 DT 28-FEB-2003 (Rel. 41, Created).  
 DT 28-FEB-2003 (Rel. 41, Last sequence update).  
 DT 28-FEB-2003 (Rel. 41, Last annotation update).  
 DE Wall protein-1 (PKP-1) (Fragment).  
 OS Perkinsus atlanticus.  
 CC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.  
 CC NCBI\_TaxID=106964;  
 RN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=22044350; PubMed=12049410;  
 RA Montes J.F., Durfort M., Ilado A., Garcia-Valero J.,  
 RT "Characterization and immunolocalization of a main proteinaceous  
 RT component of the cell wall of the protozoan parasite Perkinsus  
 RT atlanticus."  
 RL Parasitology 124:477-484(2002).  
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play  
 CC a key role in the organization of the cell wall and in promoting  
 CC the survival of this parasite.  
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell  
 CC wall components.  
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental  
 CC stages.

KW Cell wall.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 765 MW; F1787D87B1AA516 CRC64;  
 Query Match 28.2%; Score 10; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 EG 6  
 DB 4 EG 5  
 RESULT 10  
 PSK DAUCA  
 ID PSK DAUCA STANDARD; PRT; 5 AA.  
 AC P58261;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)]  
 CS Daucus carota (Carrot).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; campanulids; Apiales; Apiaceae; Daucus.  
 CC NCBI\_TaxID=4039;  
 RN [1]  
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
 RC STRAIN:cv. US-Harumakigosun;  
 RX MEDLINE=20212743; PubMed=10750705;  
 RA Harai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,  
 RA Kanada H., Sakagami Y.;  
 RT "A secreted peptide growth factor, phytosulfokine, acting as a  
 RT stimulatory factor of carrot somatic embryo formation";  
 RJ Plant Cell Physiol. 41:27-32(2000).  
 CC FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
 CC EMBRYOS.  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
 CC PUTATIVE NEURANE RECEPTOR BY SIMILARITY.  
 CC SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
 KW Growth factor; 1 4 PHYTOSULFOKINE DATA.  
 FT PEPTIDE 1 1 SULFATION.  
 FT MCD\_RES 1 1  
 FT MCD\_RES 3 3 SULFATION.  
 SQ SEQUENCE 5 AA; 687 MW; 76C1B504B300C01 CRC14;  
 Query Match 25.6%; Score 10; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TO 4  
 DB 4 TO 5  
 RESULT 11  
 EY05 LITRU  
 ID EY05 LITRU STANDARD; PRT; 7 AA.  
 AC P82101;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 5.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 834 MW; 6DC05B076B0B5030 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 EGEL 8  
 DB 3 EPEI 6  
 RESULT 12  
 UC24 MAIZE  
 ID UC24 MAIZE STANDARD; PRT; 7 AA.  
 AC P80630;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein: from 2D-page of etiolated coleoptile (Spot 447);  
 DE (Fragment).  
 OS Zea mays (Maize).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 CC NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Tourlet P., Riccardi F., Moxin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.  
 CC Maize-2DEPAGE: P80630; COLEOPTILE.  
 DR MaizeDB; 123956;  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 STTQ 4  
 DB 1 STAK 4  
 RESULT 13  
 UN06 PINPS  
 ID UN06 PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 CC NCBI\_TaxID=71647;  
 RN [1]

RP SEQUENCE  
 RC TISSUE=Needle;  
 RA MEDLINE=99274C98; PubMed=10344297;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahtman N., Kruze A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem mat:time pine  
 RT proteins";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 523 MW; 69D76724486B574C CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 GEL 8  
 DB 3 GNU 5

## RESULT 14

CRMY CRCL1  
 TD ORMY CRCL1 STANDARD; PRT; 8 AA.  
 AC PB2455;  
 DT 16-OCT-2001 (Rel. 40, Created;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update);  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Orcomyotrophic (CMT).  
 CS Orcomyotrophic limbus (Spinycheek crayfish).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Asacidea;  
 CC Astacidea; Carabidae; Orconectres.  
 OX NCBI\_TaxID=28379;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Hindgut;  
 RX MEDLINE=20411310; PubMed=10952880;  
 RA Dircksen H., Burdick S., Sauter A., Keller R.;  
 RT "Two orckinins and the novel octapeptide orckoyotrocin in the hindgut  
 RT of the crayfish Orconectes limbus: identified myostimulatory  
 RT neuropeptides originating together in neurones of the terminal  
 RT abdominal ganglion";  
 RL J. Exp. Biol. 203:2807-2818(2000).  
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES WITH THE FREQUENCY AND  
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED  
 CC BY ABDOMINAL GANGLIONIC NEURONS  
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD: FAB  
 KW Amidation; Neuropeptide.  
 FT MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 25.6%; Score 10; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+35;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CT 3  
 DB 5 TT 6

## RESULT 15

UH09 RAT  
 ID UH09 RAT STANDARD; PRT; 8 AA.  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 2D-page of heart tissue (Spot P2) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheier C., Regitz-Zagrosek V., Salikov C.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QE 5  
 DB 1 QE 2

Search completed: November 5, 2003, 17:21:08  
 Job time : 13.5 secs

GenCore version 5.1.6  
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CM protein: - protein search, using sw model

Run on: November 5, 2003, 17:18:09 ; Search time 27.5 seconds  
(without alignments)  
75.070 Million ce.] updates/sec

Title: US-09 914-088-2

Perfect score: 39

Sequence: 1 STTCEGEL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 452

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
SPTRMBL23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriopl:
17: sp_archaeap:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16	41.0	8	5 Q94695	Q94695 physarum po
2	14	35.9	8	4 Q16428	Q16428 homo sapien
3	14	35.9	8	5 Q97WH6	Q97WH6 perineretis
4	14	35.9	8	6 Q9MYL5	Q9MYL5 pongo pygma
5	13	33.3	8	13 Q90ZV5	Q90ZV5 fulica leuc
6	12	30.8	7	11 Q63480	Q63480 rattus norv
7	12	30.8	8	2 Q9R9E0	Q9R9E0 bacillus su
8	12	30.8	8	7 Q29810	Q29810 homo sapien
9	11	28.2	7	12 Q65578	Q65578 bovine herp
10	11	28.2	8	2 Q9AGP4	Q9AGP4 arthrobacte
11	11	28.2	8	2 Q68485	Q68485 klebsiella
12	11	28.2	8	4 Q9P285	Q9P285 homo sapien
13	11	28.2	8	6 Q9XSV:	Q9XSV: canis famil
14	11	28.2	8	11 Q35835	Q35835 rattus sp.
15	11	28.2	8	11 P70243	P70243 mus musculu
16	11	28.2	8	11 Q60655	Q60655 mus musculu

#### ALIGNMENTS

##### RESULT 1

```
Q94695 Q94695 PRELIMINARY; PRT; 8 AA.
AC Q94695:
DT 01-FEB-1997 (TREMBLrel. C2, Created)
DT 01-FEB-1997 (TREMBLrel. C2, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. C8, Last annotation update)
DE Actin (Fragment).
GN ARDC.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX MCB1_TaxID=5791;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96182101; PubMed=8622700;
RA Benard M., Lagnel C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum".
RL Mol. Cell.; Biol. 16:968-976(1996).
DR EMBL; M73459; AAC03706.1; -;
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; F4C6C2CAAB187B16 CRC64;
```

Query Match 41.0%; Score 16; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred.No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
DB 2 EGE 4

##### RESULT 2

```
Q16428 Q16428 PRELIMINARY; PRT; 8 AA.
ID Q16428
AC Q16428;
DT 01-NOV-1996 (TREMBLrel. C1, Created)
```





```

RN  SEQUENCE FROM N.A.
RP  MEDLINE=96198747; PubMed=8612486;
RA  Yoshikawa T., Makino S., Gao X.M., Xing S.C., Chuang D.M.,
RT  "Splice variants of rat TR4 orphan receptor: differential expression
RT  of novel sequences in the 5'-untranslated region and C-terminal
RT  domain."
RL  Endocrinology 137:1562-1571(1996);
DR  EMBL: J59125; A802827.1;
KW  Receptor;
FT  NON_TER
SQ  SEQUENCE 7 AA; 758 MW; 672AA278640C535C CRC64;

Query Match 30.8%; Score 12; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GEL 8
DB 5 GDL 7

RESULT 7
Q9R9E0 PRELIMINARY; PRT; 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update);
DE Stage V sporulation protein E (Fragment);
GN SPOVE;
OS Bacillus subtilis;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
CX NCBI_TaxID=1423;
RN [1]_TaxID=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.C., de Lencastre H., Pigot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spoVE is
RT homologous to the ara region of Escherichia coli."
RL Biochimie 74:735-748(1992);
DR EMBL: X64258; CAA4556.1;
FT NON_TER
SQ SEQUENCE 8 AA; 893 MW; E275A1332B18AA CTR04;

Query Match 30.8%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTQE 5
DB 2 TTKK 5

RESULT 8
Q29810 PRELIMINARY; PRT; 8 AA.
AC Q29810;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE HLA class II DR-beta chain (Fragment);
GN HLA-DRB5*5;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo;
CX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=96175156; PubMed=9110934;
RA Svensson A.C., Setterblad N., Pilgrim U., Rask L., Andersson G.;

```

```

RT "Evolutionary relationship between different human major
RT histocompatibility complex HLA-DR haplotypes.";
RL Immunogenetics 43:304-314(1996);
DR EMBL: X88792; CAA61271.1;
FT NON_TER
SQ SEQUENCE 8 AA; 909 MW; 62C6C1A9CAA731A8 CRC64;

Query Match 30.8%; Score 12; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TQE 5
DB 6 TQQ 8

RESULT 9
Q65578 PRELIMINARY; PRT; 7 AA.
AC Q65578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Hypothetical 0.8 kDa protein (Fragment);
OS Bovine herpesvirus 1;
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus;
CX NCBI_TaxID=10320;
RN [1]_TaxID=10320;
RP SEQUENCE FROM N.A.
RC STRAIN=Cooper;
RX MEDLINE=95313343; PubMed=7793062;
RA Vleck C., Beres V., Lu Z., Kutish G.F., Paces V., Rock D.,
RA Letchworth G.J., Schwytzer M.;
RT "Nucleotide sequence analysis of a 30-kb region of the bovine
RT herpesvirus 1 genome which exhibits a colinear gene arrangement with
RT the UL21 to UL4 genes of herpes simplex virus.";
RL Virology 210:100-108(1995);
DR EMBL: Z48053; CAA88130.1;
KW Hypothetical protein;
FT NON_TER
SQ SEQUENCE 7 AA; 756 MW; 6DD33455B1F1B1C0 CRC64;

Query Match 28.2%; Score 11; DB 12; Length 7;
Best Local Similarity 33.3%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTQEG 7
DB 1 TTSHK 6

RESULT 10
Q9AGP4 PRELIMINARY; PRT; 8 AA.
AC Q9AGP4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created);
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update);
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update);
DE Serine hydroxymethyltransferase (Fragment);
GN GLYA;
OS Arthrobacter sp. IIN;
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococccaceae; Arthrobacter;
CX NCBI_TaxID=153502;
RN [1]_TaxID=153502;
RP SEQUENCE FROM N.A.
RC STRAIN=IIN;
RA Meskys R., Harris R.J., Casalte V., Basran J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
RT sarcosine degradation in Arthrobacter spp.: implications for glycine
RT betaine catabolism.";

```

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF229478; AAK16486.1; -  
 KW Nucleoside transferase; transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 898 MW; 631870533372453 CRC64;

Query Match 28.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 6 GE 7  
 Db 7 GE 8

## RESULT 11

ID O68485 PRELIMINARY; PRT; 8 AA.  
 AC O68485;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Amino-glycoside 3'-O-nucleotidyltransferase (Fragment).  
 GN AAD1.  
 OS Klebsiella pneumoniae.  
 OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Bacteri; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella.  
 OX NCB: TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:K1;  
 RX MEDLINE=98287600; PubMed=9624504;  
 RA Centron D., Roy P.H.;  
 RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene  
 ac6'::q from the integrin of a natural multiresistance plasmid".  
 RL Antimicrob. Agents Chemother. 42:506-508(1998).  
 DR EMBL: AF047556; AAC25501.1; -  
 KW Plasmid; transferase.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB:DD256 CRC64;

Query Match 28.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 TIG 4  
 Db 5 STC 8

## RESULT 12

ID Q9P285 PRELIMINARY; PRT; 8 AA.  
 AC Q9P285;  
 DT 01-OCT-2003 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 15, Last annotation update)  
 DE Clotting factor VIII (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCB: TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shibata M., Shima M., Morichika S., Yoshio A.;  
 RT "Human clotting factor VIII gene, junction regions of the deletion of  
 exon 4 through 7".  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AB040872; BAA94312.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 866 MW; IC16987AAB05BDD: CRC64;

Query Match 28.2%; Score 11; DB 4; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 3 TOSG 6  
 Db 3 SEDG 6

## RESULT 13

ID O9XSY1 PRELIMINARY; PRT; 8 AA.  
 AC O9XSY1;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE Retinoblastoma protein (Fragment).  
 GN RBL.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCB: TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97049323; PubMed=8894053;  
 RA Venter P.J., Brouillet J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;  
 RT "Gene-specific universal mammalian sequence-tagged sites: application  
 to the canine genome".  
 RL Biochem. Genet. 34:321-341(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;  
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)  
 gene".  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF155737; AAD38807.1; -  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 895 MW; 14259B18676721E3 CRC64;

Query Match 28.2%; Score 11; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 6 GE 7  
 Db 5 GE 6

## RESULT 14

ID O35835 PRELIMINARY; PRT; 8 AA.  
 AC O35835;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF1 protein.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCB: TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=98008057; PubMed=9581555;  
 RA Hospital V., Prat A., Joule C., Cherif D., Day R., Cohen P.;  
 RT "Human and rat testis express two mRNA species encoding variants of  
 RT NQD convertase, a metalloendopeptidase of the insulinsase family".  
 RL Biochem. J. 327:773-779(1997).  
 DR EMBL: X93208; CAA3695.1; -  
 SQ SEQUENCE 8 AA; 986 MW; EAT8A1B1ADC5A5B6 CRC64;

Query Match 28.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STT 3  
 DB 4 ATT 6

## RESULT 15

P70243 PRELIMINARY; PRT; 5 AA.  
 AC P70243;  
 DT 01-FEB-1997 (TEMBLrel. 02. Created;  
 DT 01-FEB-1997 (TEMBLrel. 02. Last sequence update;  
 DT 01-DEC-2001 (TEMBLrel. 19. Last annotation update;  
 DE Skeletal muscle specific calcium channel (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:129;  
 RA Ophio: R.A.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DFIJ databases.  
 DR EMBL; X98325; CAA66969.1; -.  
 FT NCN\_TFR 1  
 FT NCN\_TFR 8  
 SQ SEQUENCE 9 AA: 565 MW: D9C37DCB1861AD0E LKCG64;

Query Match 28.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GE 7  
 DB 4 GE 5

Search completed: November 5, 2003, 17:22:17  
 Job time : 10.5 secs

GenCore version 5.1.6  
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OX protein - protein search, using sw model

Run on: November 5, 2003, 17:14:39 ; Search time 33.5 Seconds  
(without alignments)  
37,905 Million cell updates/sec

Title: US-09-914-088-2

Perfect score: 39

Sequence: 1: STTQEGEL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 102276

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq 19Jun03.1

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1950.DAT
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1941.DAT
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1942.DAT
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1943.DAT
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1944.DAT
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1945.DAT
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1946.DAT
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1947.DAT
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1948.DAT
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1949.DAT
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1950.DAT
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1951.DAT
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1952.DAT
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1953.DAT
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1954.DAT
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1955.DAT
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1956.DAT
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1957.DAT
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1958.DAT
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1959.DAT
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1960.DAT
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1961.DAT
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1962.DAT
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1963.DAT

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	8	AAB23868	Immunoglobulin E
2	39	100.0	8	AAB23908	IgE C-epitope 2 do
3	39	100.0	8	AAJ16613	Peptide P2 derived
4	39	100.0	8	AAB51024	IgE peptide #2, M
5	39	100.0	8	AAB50218	Human IgE immunoge
6	31	79.5	6	AAB25931	P1 mimotope peptid
7	31	79.5	6	AAU16646	Peptide P2sh deriv
8	31	79.5	6	AAJ00230	Human IgE immunoge
9	21	53.8	5	AAW66615	Proteoglycan

10	21	53.8	6	21	AAW87756	Potato THT protein
11	21	53.8	7	16	AAW21258	Hydroxymethylgluta
12	21	53.8	8	22	ABP13186	HIV A02 super moti
13	21	53.8	8	22	ABP15880	HIV A24 super moti
14	20	51.3	6	22	AAU05503	Synthetic hexapept
15	20	51.3	7	21	AAW23121	Hsp47-binding phag
16	20	51.3	7	21	AAW02936	Nucleotide-binding
17	20	51.3	7	21	AAW02937	Nucleotide-binding
18	20	51.3	7	23	ABP49021	Zinc finger protei
19	20	51.3	7	23	ABP49022	Zinc finger protei
20	20	51.3	7	23	ABP49049	Zinc finger protei
21	19	48.7	6	13	AAW25035	mAb 42 antigenic d
22	19	48.7	7	11	AAW07089	Glycopeptide again
23	19	48.7	7	21	AAW02935	Nucleotide-binding
24	19	48.7	7	23	ABP48708	Zinc finger protei
25	19	48.7	7	23	ABP48963	Zinc finger protei
26	19	48.7	7	23	ABP49023	Zinc finger protei
27	19	48.7	7	23	ABP50013	Zinc finger protei
28	19	48.7	9	14	AAW43434	Ro/SSA epitope 78
29	19	48.7	8	19	AAW58632	Platelet factor 4
30	19	48.7	8	21	AAW10329	S. cerevisiae RNA
31	19	48.7	8	21	AAW10335	S. pombe RNA guar
32	19	48.7	8	21	AAW10341	C. albicans RNA qu
33	19	48.7	8	21	AAW32133	Peptide motif III
34	19	48.7	8	21	AAW32139	Peptide motif III
35	19	48.7	8	21	AAW32145	Human DNA derived
36	19	48.7	8	22	ABU53735	HIV A02 super moti
37	19	48.7	8	22	ABP13227	HIV A24 super moti
38	19	48.7	8	22	ABP15899	HIV B58 super moti
39	19	48.7	8	22	ABP18294	Bacterial conserve
40	19	48.7	8	22	AAU69102	Rat glutamate tran
41	19	48.7	8	22	AAU61188	Peptide motif of R
42	19	48.7	8	23	ABJ05606	Peptide motif of R
43	19	48.7	8	23	ABJ05612	Peptide motif of R
44	19	48.7	8	23	ABJ05618	Peptide motif of R
45	19	48.7	8	23	ABG68930	Signature motif #2

ALIGNMENTS

RESULT 1  
AAB23868  
ID AAB23868 standard; peptide; 8 AA.  
XX  
AC AAB23868;  
XX  
DT 03-JAN-2001 (first entry)  
XX  
XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:6.  
DE  
KW Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; antiallergic; nootropic; neuroprotective;  
KW protozoacide; Alzheimer's disease; allergy.  
XX  
OS Homo sapiens.  
XX  
PN WO2000050077-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 22-FEB-2002; 2000MO-EP01457.  
XX  
PR 25-FEB-1999; 99GB-0004405.  
PR 25-FEB-1999; 99GB-0004408.  
PR 25-FEB-1999; 99GB-0004412.  
XX  
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Coste M, Lobet Y, Van Mechelen MP, Verriest C;



DR WPI: 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases  
 PT  
 XX Example 4; Page 21; 48pp; English.  
 PS  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical, composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU1693 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 39; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STTQEGEL 8  
 Db |||||  
 1 STTQEGEL 8  
 RESULT 4  
 AAB51024  
 ID AAB51024 standard; Peptide; 8 AA.  
 AC AAB51024;  
 XX 21-MAR-2001 (first entry)  
 DE IGE peptide #2.  
 XX Vaccine; immunoglobulin E; IgE; anti-allergy;  
 XX Mammalia.  
 CS WC200074716-A2.  
 PN 14-DEC-2000.  
 PO 06-JUN-2000; 2000WO-EP05164.  
 XX 08-JUN-1999; 99GB-0013327.  
 PR (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Prietels J;  
 XX WPI: 2001-C91150/10.  
 DR New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual  
 PT susceptible to an allergic response  
 XX  
 PS Claim 5; Page 20; 26pp; English.  
 CC The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 CC such peptide from IgE. The composition is useful as a vaccine or for

CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 39; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STTQEGEL 8  
 Db |||||  
 1 STTQEGEL 8  
 RESULT 5  
 AAB300218  
 ID AAB300218 standard; Peptide; 8 AA.  
 XX AAB300218;  
 AC 02-SEP-2002 (first entry)  
 DT Human IgE immunogenic peptide SEQ ID NO: 2.  
 XX  
 DE Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; antiallergic.  
 XX Homo sapiens.  
 OS WO200216409-A2.  
 XX 28-FEB-2002.  
 PD 17-AUG-2001; 2001WO-EP09576.  
 XX 22-AUG-2000; 2005GB-0020717.  
 PR (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX Friede M, Mason S, Turrell WG, Virais Bassols YC;  
 PI WPI: 2002-489648/52.  
 DR Conjugate for use in vaccine for treatment of allergy, comprises  
 XX disulfide bridge cyclized peptide and immunogenic carrier  
 PT Claim 4; Page 9; 45pp; English.  
 PS The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 19; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STTQEGEL 8  
 Db |||||  
 1 STTQEGEL 8  
 RESULT 6  
 AAB25931  
 ID AAB25931 standard; Peptide; 6 AA.  
 XX AAB25931;  
 XX

DT 05-JAN-2001 (first entry)  
 DE P2 mimotope peptide P2sh SEQ ID NO:25.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C epsilon2 domain;  
 KW allergic disease; immunoprophylaxis; immunotherapy; anti-allergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX Homo sapiens.  
 OS  
 XX WO2000050460 A1.  
 XX 31 AUG-2000.  
 XX 22-FEB-2000; 2000WO-EP01455.  
 XX 25-FEB-1999; 99GB-0004405.  
 XX 29-MAR-1999; 99GB-0007151.  
 PR C7-MAY-1999; 99GB-0010537.  
 PR C7-MAY-1999; 99GB-0010538.  
 PR C7-AUG-1999; 99GB-0018594.  
 PR C7-AUG-1999; 99GB-0018663.  
 PR C7-SEP-1999; 99GB-0021046.  
 PR C7-SEP-1999; 99GB-0021047.  
 PR 23-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (SPPT-) PEPTIDE THERAPEUTICS LTD.  
 PA  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lambert A, Mason S;  
 PI Randall R, Turnell WG, Van Mechelen WP, Vinals De Rasco G V;  
 XX WP: 2000-572073/53.  
 DA Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Disclosure; Page 9; 129pp; English.  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (EI) of C epsilon2 domain (II) of  
 CC immunoglobulin E (IGE), or its mimotope. Also defined are (i) an  
 CC immunogen (iii) for treating allergy comprising (i) and (ii), a vaccine (iii)  
 CC for treating allergies comprising (iii) and a human (iv) capable of  
 CC recognising (i); (4) a pharmaceutical composition comprising (iv);  
 CC (5) a peptide (ia) capable of being recognised by (iv); (6) an immunogen  
 CC (iia) comprising (ia); and (7) producing (iii) by producing (ii). (i)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (ii), (iii) and (iv) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (iv) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (i) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (ii), (iii) and (iv) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (iv) is also useful in diagnosing atopy. AAB25927 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 79.5%; Score 31; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TTQEGS 7  
 DB 1 TTQEGS 6

RESULT 7  
 AAU16656  
 ID AAU16656 standard; Peptide; 6 AA.  
 XX  
 AC AAU16656;  
 XX  
 DT C7-NOV-2001 (first entry)  
 XX  
 DE Peptide P2sh derived as mimotope of C epsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; C epsilon2; C epsilon3; C epsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200145745-A2.  
 XX 28-JUN-2001.  
 XX 21-DEC-2000; 2000WO-GB04935.  
 XX 21-DEC-1999; 99GB-0030233.  
 PR 22-FEB-2000; 2000GB-0004096.  
 PR 22-AUG-2000; 2000GB-0020707.  
 PR 22-AUG-2000; 2000GB-0020708.  
 XX (ACAM-) ACAYBIS RES LTD.  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 PI Flinn N, Johnson T;  
 XX WPI; 2001-521967/57.  
 DR  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 PT  
 XX Example 4; Page 21; 48pp; English.  
 PS  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC C epsilon2, C epsilon3 or C epsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptide sequences derived from or mimotopes of  
 CC the C epsilon2/C epsilon3/C epsilon4 region of human IgE.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 79.5%; Score 31; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TTQEGS 7  
 DB 1 TTQEGS 6

RESULT 8  
 ABJ00230  
 ID ABJ00230 standard; Peptide; 6 AA.  
 XX  
 AC ABJ00230;

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XX DT 02-SEP-2002 (first entry)
XX DE Human IgE immunogenic peptide SEQ ID NO: 14.
XX KW Immunogen: human; IgE; immunoglobulin E; allergy; thio-ether linkage;
XX KW vaccine; antiallergic.
XX OS Homo sapiens.
XX PN WO200216409-A2.
XX PD 28 FEB-2002.
XX FF 17-AUG-2001: 2001WO-EP09576.
XX PR 22-AUG-2000: 2000GB-0020717.
XX PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Russell YC.
XX DR WPI: 2002-489648/52.
XX PR Conjugate for use in vaccine for treatment of allergy, comprises
XX PR disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 9; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulfide bridge cyclized peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a peptide immunogen derived from human
XX CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.
XX SQ Sequence 6 AA;
    Query Match 79.5%; Score 11; DR 23; Length 6;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TQEGE 7
Db 1 TQEGE 6
RESULT 9
AAW66615
XX ID AAW66615 standard; peptide; 5 AA.
XX AC AAW66615;
XX DT 27-NOV-1998 (first entry)
XX DE Phosphopeptide.
XX KW casein; calcium phosphate complex; amorphous calcium phosphate; ACP;
XX KW phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency;
XX KW osteoporosis; osteomalacia; tooth; bone disease.
XX OS Synthetic.
XX OS Bos taurus.
XX PH Key location/Qualifiers
XX PH Modified-site 2 /note="Thr(P)"
XX PH Modified-site 3 /note="Thr(P)"
XX PN WO9840406 A1.
XX PD 17-SEP-1998.

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XX PF 13-MAR-1998; 98WO-AU00160.
XX PR 13-MAR-1997; 97AJ-C005662.
XX PA (UYNE) UNIV MELBOURNE.
XX PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.
XX PI Reynolds EC;
XX DR WPI: 1998-520833/44.
XX PT Stable calcium phosphate complex including phospho-peptide
XX PT stabilised amorphous calcium phosphate - useful for treatment of
XX PT dental caries, calcium malabsorption and bone diseases such as
XX PT osteoporosis and osteomalacia.
XX PS Example 2; Page 17; 43pp; English.
XX CC The invention relates to a stable calcium phosphate complex including
XX CC phosphopeptide stabilised amorphous calcium phosphate (ACP) or its
XX CC derivative, where the phosphopeptide includes the amino acid sequence:
XX CC Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the
XX CC phosphopeptides are a delivery vehicle for co-localisation of Ca, form
XX CC P and phosphate at the tooth surface in a slow-release amorphous, form
XX CC producing superior anticaries efficacy over prior art. The amorphous
XX CC phases stabilised by the phosphopeptides are also useful as dietary
XX CC supplements to increase calcium bioavailability and to help prevent
XX CC diseases associated with calcium deficiencies. They are particularly
XX CC useful for treatment or prevention of dental caries, calcium
XX CC malabsorption and bone diseases such as osteoporosis and osteomalacia.
XX CC The compositions are useful in humans and in veterinary medicine in
XX CC domestic animals such as cattle, sheep, horses and companion animals
XX CC e.g. cats and dogs as well as zoo animals. The relationship between the
XX CC phosphopeptide structure and interaction with amorphous calcium
XX CC phosphate was investigated using a series of synthetic peptide homologues
XX CC and analogues (AAW66615-22). These studies showed that the cluster
XX CC sequence Ser(P)-Ser(P)-Glu-Glu- was mainly responsible for the
XX CC interaction with ACP and that all three contiguous Ser(P) residues are
XX CC required for maximal interaction with ACP.
XX SQ Sequence 5 AA;
    Query Match 53.8%; Score 21; DR 19; Length 5;
    Best Local Similarity 80.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STQGE 5
Db 1 STQGE 5
RESULT 10
AAW67756
XX ID AAW67756 standard; Protein; 6 AA.
XX AC AAW67756;
XX DT 17-AUG-2000 (first entry)
XX DE Potato THT protein fragment #5.
XX KW THT protein; transgenic plant; resistance; phytopathogen; oomycete;
XX KW hydroxycinnamic acid-coenzyme A; potato; fungicide; infection;
XX KW tyramine N-hydroxycinnamic acid transferase; tyraminamide biosynthesis.
XX OS Solanum tuberosum.
XX PN DE19846001 A1.
XX PD 27-APR-2000.
XX PF 06-OCT-1998; 94SE-1046001.

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XX 06-OCT-1998; 98CE-1046001.  
 XX (BIOPLANT BIOTECHNOLOGISCHES FORSCHUNGSLAB.  
 PA (IPRP); IPB INST. PFLANZENBIOCHEMIE.  
 XX Scheel D., Rosahl S., Strack D., Schmidt A.  
 XX WPI; 2000-319:17/28.  
 XX Transgenic plant, especially potato, resistant to Phytophthora  
 PT infestans, contains gene for hydroxycinnamic acid:tyramine  
 PT N-hydroxycinnamic acid transferase.  
 XX Claim 5a; Column 11-12; 12pp; German.  
 XX This invention describes a novel transgenic plant with increased  
 CC resistance to infection by phytopathogens, especially Phytophthora  
 CC infestans, contains, in its genome, a gene construct comprising a  
 CC heterologous promoter, and a sequence (1) encoding a hydroxycinnamic  
 CC acid coenzyme A:tyramine N-(hydroxycinnamic acid) transferase (11),  
 CC under the control of the promoter. The products of the invention have  
 CC fungicide activity. (1) is involved in biosynthesis of tyramineamide  
 CC which is incorporated into plant cell walls to provide a chemical  
 CC barrier against pathogens, extracellular tyramineamide inhibits the  
 CC growth of pathogens. The introduction of (11), into tobacco, cotton,  
 CC rape, melon, sugar beet, maize, and especially potato or tomato, is  
 CC used to improve resistance to phytopathogens, particularly P. infestans  
 CC or other Oomycetes. (1) can also be used to express (11) in prokaryotic  
 CC or eukaryotic cells and its fragments can be used to isolate homologous  
 CC sequences from bacteria, fungi, plants and animals. In the antisense  
 CC orientation, (1) and its fragments can be used to inhibit expression of  
 CC (11) in cells. AAY8752-Y8771 represent fragments of the potato  
 CC (11); in cells. AAY8752-Y8771 represent fragments of the potato  
 CC (Solanum tuberosum) THT protein described in the text of the  
 CC invention.  
 XX SQ Sequence 6 AA;  
 Query Match 53.8%; Score 21; DB 21; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TTQES 6  
 |||  
 Db 2 TTNES 6  
 RESULT 1:  
 AAW21258  
 ID AAW21258 standard; peptide; 7 AA.  
 XX AC AAW21258;  
 CT 29 JUL 1997 (first entry)  
 XX Hydroxymethylglutaryl coenzyme A reductase signal oligopeptide #17.  
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; HIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW change; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; thesus;  
 KW gonadolibirin precursor; plasminogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW Treponema pallidum membrane protein; TMA; iso. amyloid polypeptide;  
 KW fibroblast MP1; schistosoma elastase precursor; schistosomin;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX Homo sapiens.  
 OS WC9511568-A1.  
 XX

PD 20-JUL-1995.  
 XX 12-JAN-1995; 95WO-US00575.  
 XX 14-JAN-1994; 94US-0182248.  
 XX (RATH//) RATH M.  
 XX Rath M.  
 XX WPI; 1995-263953/34.  
 XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between protein(s).  
 XX Claim 5; Page 32; 88pp; English.  
 XX The sequences given in AAW21201-56C represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX SQ Sequence 7 AA;  
 Query Match 53.8%; Score 21; DB 16; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STQEE 5  
 |||  
 Db 3 STTEE 7  
 RESULT 12  
 ABP13186  
 ID ABP13186 standard; Peptide; 8 AA.  
 XX AC ABP13186;  
 DT 15-JUL-2002 (first entry)  
 XX HIV A02 super motif pol peptide #101.  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 PN WO200124810-A1.  
 XX 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIMX-) EPIMMUNE INC.  
 XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 138; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 XX Query Match 53.8%; Score 21; DB 22; Length 8;  
 XX Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TQEGEL 8  
 DB 3 TEEAEI 8  
 RESULT 13  
 ABP15880  
 ID ABP15880 standard; Peptide: 8 AA.  
 XX AC ABP15880;  
 XX DT 15-JUL 2002 (first entry)  
 XX DE HIV A24 super motif pol peptide #60.  
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 XX KX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 XX KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX OS Human immunodeficiency virus type 1.  
 XX PN WC200124810-A1.  
 XX XX 12-APR-2001.  
 XX PF 05-OCT-2000; 2000WO-US27766.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX PA (EPIM-) EPIMMUNE INC.  
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 138; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 XX Query Match 53.8%; Score 21; DB 22; Length 8;  
 XX Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TQEGEL 8  
 DB 3 TEEAEI 8

DR WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 194; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 XX Query Match 53.8%; Score 21; DB 22; Length 8;  
 XX Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TQEGEL 8  
 DB 3 TEEAEI 8  
 RESULT 14  
 AAU05503  
 ID AAU05503 standard; Peptide: 6 AA.  
 XX AC AAU05503;  
 XX DT 24-OCT-2001 (first entry)  
 XX DE Synthetic hexapeptide ligand 15.  
 XX KW Hexapeptide ligand; drug design; high throughput screening; HTS; MOSAR;  
 XX KX Multivariate Quantitative Structure Activity relationships.  
 XX OS Synthetic.  
 XX PN WO200136980-A2.  
 XX PD 25-MAY-2001.  
 XX PF 20-NOV-2000; 2000WO-GB04420.  
 XX PR 18-NOV-1999; 99GB-0027346.  
 XX PA (MELA-) MELACURE THERAPEUTICS AB.  
 XX PA (PET/) PETT C P.  
 XX PI Lundstedt T, Andersson P, Wikberg J, Muceniece R, Prusis P;  
 XX WPI: 2001-432565/46.  
 XX A novel method for identifying the interaction site, binding site or  
 PT active site in a macromolecule, using of informative combinatorial

```

chemistry, informative peptide libraries and Multivariate Quantitative
Structure Activity Relationships -
Example 7; Fig 29; 13pp; English
The sequence represents a hexapeptide ligand selected according to
2 ((8-13) fractional factorial design) (cp for step 2 random), which
were used to model the interaction of a ligand with its target. The
invention relates to characterising the interaction between a Ligand Y
and a Target X by obtaining information (e.g Multivariate Quantitative
Structure Activity relationships, MOSAR) representing one or more
physical and/or chemical properties of targets of type X and type Y
to produce a model of interaction. The methods of the invention are
useful for identifying outliers of type X or cut-offs
of type Y, drug design, design or identification of lead compounds (e.g
by high throughput screening, HTS), design of ligands of type Y with
improved affinity and/or selectivity for targets of type X, protein
engineering, design of DNA or RNA molecules, design of artificial targets
of type X/or artificial ligands of type Y, analysis and/or in the
engineering of regions and/or parts of targets of type X and/or ligands
of type Y, design of organic compound, catalyst, pharmaceutical, drug,
macromolecule being capable of binding a molecule, peptidomimetic,
protein, enzyme, antibody, molecule, macromolecule, DNA, RNA or a
carbohydrate. The methods are also useful for designing new ligands for
known targets and/or for new targets.
Sequence 6 AA;
Query March 51.3%; Score 20; DB 22; Length 6;
Res: Local Similarity 80.0%; Pred.No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 2 TTGES 6
DB 2 TTGES 6
RESULT 15
AAB23212
ID AAB23212 standard; peptide; 7 AA.
AC AAB23212;
XY
DT 29-JAN-2001 (first entry)
DE Hsp47 binding phase display hepta-peptide; SEQ ID NO: 4
KW Hsp47 binding heptapeptide; phage display library;
KW Hsp47 external domain; carcinoma; cancer; targeting molecule;
KW therapy; diagnosis; detection; imaging; drug delivery; invasion;
KW migration; metastasis; modulation; tumor; skin; basal cells; colon;
KW large intestine; lung; breast; bladder; oral cancer;
KW head and neck cancer; larynx; nasopharynx; adrenal cortex;
KW apocrine gland; kidney; liver; pancreas; prostate;
OS Synthetic.
XX
XX WO200054805-A1.
PN
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; ZOOO-WO005588.
PF
XX
PR 15-MAR-1999; 99US-0124491.
PP
XX (UNYA-) UNIV MARYLAND BALTIMORE.
PA
XX
XX Sauk Co;
PI
XX
XX WPI; 200C-655997/63.
DR
XX
XX treating, diagnosing or modulating a carcinoma cell, which expresses
PT Heat shock protein 47 on its surface. Involves administering an agent
PT
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GenCore version 5.1.6  
Copyright (c) 1993 2003 CompuGen Ltd.

OM protein protein search, using sw model

Run on: November 5, 2003, 17:22:25 / Search time 22 Seconds  
(without alignments)  
62,454 Million Cell updates/sec

Title: US-09-914-088-2  
Perfect score: 39  
Sequence: 1 STTOEGEL 8

Scoring table: BLOSUM62

Gapcp 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 42362

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications, AA.\*  
1: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/2/pubaa/PCR\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/2/pubaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/2/pubaa/PCRUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/prodata/2/pubaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/2/pubaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/prodata/2/pubaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
15: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
16: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*  
17: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	8	12	US-10-082-014-274
2	39	100.0	8	12	US-10-372-076-128
3	20	51.3	7	9	US-09-989-994-1017
4	20	51.3	7	9	US-09-989-994-1222
5	20	51.3	7	9	US-09-989-994-1231
6	20	51.3	7	11	US-09-990-186-1017
7	20	51.3	7	11	US-09-990-186-1222
8	20	51.3	7	11	US-09-990-186-1231
9	20	51.3	7	11	US-09-989-994-1017
10	20	51.3	7	11	US-09-989-994-1222
11	20	51.3	7	11	US-09-989-994-1231
12	19	48.7	7	9	US-09-989-994-708
13	19	48.7	7	9	US-09-989-994-793
14	19	48.7	7	9	US-09-989-994-813
15	19	48.7	7	9	US-09-989-994-2617

16	19	48.7	7	11	US-09-990-186-708	Sequence 708, App
17	19	48.7	7	11	US-09-990-186-793	Sequence 793, App
18	19	48.7	7	11	US-09-990-186-813	Sequence 813, App
19	19	48.7	7	11	US-09-990-186-2617	Sequence 2617, App
20	19	48.7	7	11	US-09-989-994-708	Sequence 708, App
21	19	48.7	7	11	US-09-989-994-793	Sequence 793, App
22	19	48.7	7	11	US-09-989-994-813	Sequence 813, App
23	19	48.7	7	11	US-09-989-994-2617	Sequence 2617, App
24	19	48.7	7	12	US-09-990-832C-33	Sequence 33, App1
25	19	48.7	8	12	US-10-167-831-4	Sequence 4, App1
26	19	48.7	8	12	US-10-167-831-10	Sequence 10, App1
27	19	48.7	8	12	US-10-167-831-16	Sequence 16, App1
28	19	48.7	8	12	US-10-167-831-88	Sequence 88, App1
29	19	48.7	8	12	US-10-167-831-17	Sequence 17, App1
30	19	48.7	5	15	US-10-205-270-14	Sequence 14, App1
31	19	46.2	6	9	US-09-736-611-17	Sequence 17, App1
32	19	46.2	6	9	US-09-740-359-8	Sequence 8, App1
33	19	46.2	6	10	US-09-894-711-8	Sequence 8, App1
34	19	46.2	6	12	US-10-205-110-6	Sequence 6, App1
35	19	46.2	6	12	US-10-205-110-46	Sequence 46, App1
36	19	46.2	6	12	US-10-299-183A-2	Sequence 2, App1
37	19	46.2	6	12	US-10-128-587A-64	Sequence 64, App1
38	19	46.2	6	12	US-10-316-421-17	Sequence 17, App1
39	19	46.2	6	15	US-10-166-241-2	Sequence 2, App1
40	19	46.2	6	15	US-10-128-590-64	Sequence 64, App1
41	19	46.2	7	9	US-09-765-086-145	Sequence 145, App
42	19	46.2	7	9	US-09-812-471-16	Sequence 16, App1
43	19	46.2	7	10	US-09-812-633-16	Sequence 16, App1
44	19	46.2	7	10	US-09-988-117-16	Sequence 16, App1
45	19	46.2	7	12	US-10-375-992-145	Sequence 145, App

## ALIGNMENTS

### RESULT 1

US-10-082-014-274  
; Sequence 274, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 274  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-274

Query Match 100.0%; Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTOEGEL 8  
|:|||||  
DB 1 STTOEGEL 8

### RESULT 2

US-10-372-076-128  
; Sequence 128, Application US/10372076  
; Publication No. US20030198645A;  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,295  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 128  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10 372-076-128

Query Match 100.0%; Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTCEGEL 8  
| | | | |  
Db 1 STTCEGEL 8

RESULT 3  
US-09-989-789-1017  
; Sequence 1017, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1017  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-1017

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CEGEL 8  
| | | |  
Db 1 CEGEL 5

RESULT 4  
US-09-989 789-1222  
; Sequence 1222, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1222  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP

US-09-989-789-1222

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CEGEL 8  
| | | |  
Db 1 CEGEL 5

RESULT 5  
US-09-989 789-1231  
; Sequence 1231, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1231  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-1231

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CEGEL 8  
| | | |  
Db 1 CEGEL 5

RESULT 6  
US-09-990-186-1017  
; Sequence 1017, Application US/09990186  
; Publication No. US20030368675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2003-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1017  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1017

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CEGEL 8  
| | | |  
Db 1 CEGEL 5

RESULT 7  
US-09-990-186-1222

; Sequence 1222, Application US/09990186  
; Publication No. US20030668675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1222  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1222

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

## RESULT 4

US-09-990-186-1231  
; Sequence 1231, Application US/09990186  
; Publication No. US20030668675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1231  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1231

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

## RESULT 9

US-09-989-994-1017  
; Sequence 1017, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1017  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1017

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1017

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

## RESULT 10

US-09-989-994-1222  
; Sequence 1222, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1222  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1222

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

## RESULT 11

US-09-989-994-1231  
; Sequence 1231, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1231  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1231

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

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RESULT 12
US-09-989-789-708
; Sequence 728, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 708
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-728

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCGEL 8
DB      1 QTGEL 5

RESULT 13
US-09-989-789-793
; Sequence 793, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 793
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-793

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCGEL 8
DB      1 QTGEL 5

RESULT 14
US-09-989-789-813
; Sequence 813, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
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; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 813
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-813

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCGEL 8
DB      1 QTGEL 5

RESULT 15
US-09-989-789-2617
; Sequence 2617, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2617
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-2617

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCGEL 8
DB      1 QTGEL 5

Search completed: November 5, 2003, 17:30:35
Job time : 22 secs
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GenCore version: 5.0.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein: - protein search, using sw model

Run on: November 5, 2003, 17:19:19 : Search time 14 Seconds  
(without alignments)  
24.178 Million cell updates/sec

Title: US-09-914-088-2

Perfect score: 39

Sequence: 1 STTQEGEL 8

Scoring table: BLCSM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4230958 residues

Total number of hits satisfying chosen parameters: 61971

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:

- 1: /cgn2\_6/prodata/1/iaa/5A COMB pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B COMB pep.\*
- 3: /cgn2\_6/prodata/1/iaa/5A COMB pep.\*
- 4: /cgn2\_6/prodata/1/iaa/5B COMB pep.\*
- 5: /cgn2\_6/prodata/1/iaa/5C COMB pep.\*
- 6: /cgn2\_6/prodata/1/iaa/5D COMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.8	7	2	US-09-128-362-2	Sequence 9, Appl
2	53.8	7	3	US-09-128-362-2	Sequence 9, Appl
3	51.3	7	3	US-09-173-941-76	Sequence 77, Appl
4	51.3	7	3	US-09-173-941-76	Sequence 78, Appl
5	48.7	6	1	US-08-253-854-91	Sequence 91, Appl
6	48.7	7	3	US-09-173-941-76	Sequence 76, Appl
7	48.7	8	1	US-08-259-550A-90	Sequence 90, Appl
8	48.7	8	3	US-09-188-573-2	Sequence 2, Appl
9	48.7	8	3	US-09-188-573-2	Sequence 9, Appl
10	48.7	8	3	US-09-188-573-2	Sequence 14, Appl
11	48.7	8	3	US-09-315-444-2	Sequence 2, Appl
12	48.7	8	3	US-09-315-444-2	Sequence 8, Appl
13	48.7	8	3	US-09-315-444-2	Sequence 14, Appl
14	48.7	8	4	US-09-320-548-10	Sequence 2, Appl
15	48.7	8	4	US-09-321-362-2	Sequence 2, Appl
16	48.7	8	4	US-09-321-362-2	Sequence 8, Appl
17	48.7	8	4	US-09-321-362-2	Sequence 14, Appl
18	48.7	8	4	US-09-752-165-16	Sequence 4, Appl
19	48.7	8	4	US-09-752-165-16	Sequence 10, Appl
20	48.7	8	4	US-09-752-165-16	Sequence 16, Appl
21	48.7	8	4	US-09-752-165-16	Sequence 88, Appl
22	46.2	5	1	US-08-704-170-64	Sequence 64, Appl
23	46.2	5	1	US-08-704-170-64	Sequence 109, Appl
24	46.2	5	5	PCT-US94-02631-64	Sequence 64, Appl
25	46.2	5	5	PCT-US94-02631-169	Sequence 109, Appl
26	46.2	6	3	US-09-012-669F-44	Sequence 44, Appl
27	46.2	6	4	US-08-057-430A-31	Sequence 31, Appl

Sequence 2, Appl  
Sequence 17, Appl  
Sequence 145, Appl  
Sequence 29, Appl  
Sequence 145, Appl  
Sequence 145, Appl  
Sequence 9, Appl  
Sequence 15, Appl  
Sequence 60, Appl  
Sequence 27, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 45, Appl  
Sequence 45, Appl  
Sequence 15, Appl  
Sequence 174, Appl  
Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-869-506-9  
; Sequence 9, Application US/08869506  
; Patent No. 5827710  
; GENERAL INFORMATION:  
; APPLICANT: Uchida, Kohji  
; APPLICANT: Matsukawa, Hirokazu  
; APPLICANT: Matuo, Yushi  
; APPLICANT: Fujita, Tsuchi  
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
; TITLE OF INVENTION: LACTATE DEHYDROGENASE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 No. 5827710th Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/869,506  
; FILING DATE: 05-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: JP 73797/1996  
; FILING DATE: 29-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 159-43  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEC ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-869-506-9

Query Match 53.8%, Score 21; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 4 QCEG 7
   1
Db 3 QCEG 6

RESULT 2
US 09 128-967-9
; Sequence 9, Application US/09128967
; Patent No. 605714
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuc, Yushi
; APPLICANT: Fujita, Tutos;
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
; TITLE OF INVENTION: LACTATE DEHYDROGENASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 605714th Grebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/869,506
; FILING DATE: 05-JUN-1997
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US 09 128-967-9

Query Match 53.8%; Score 21; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QCEG 7
   1
Db 3 QCEG 6

RESULT 3
US 09-173-941-77
; Sequence 77, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NC000815
; CURRENT APPLICATION NUMBER: US/09/173,941
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; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-77

Query Match 51.3%; Score 20; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QCEG 8
   1
Db 1 QCEG 5

RESULT 4
US-09-173-941-78
; Sequence 78, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NC000815
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-78

Query Match 51.3%; Score 20; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QCEG 8
   1
Db 1 QCEG 5

RESULT 5
US-08-253-854-91
; Sequence 91, Application US/08253854
; Patent No. 5504190
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Cuervo, Julio H.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Appel Jr., Jon R.
; APPLICANT: Blondelle, Silvie
; TITLE OF INVENTION: Synthesis Of Equimolar Multiple
; TITLE OF INVENTION: Oligomer Mixtures, Especially Of Oligopeptide Mixtures
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milwaukee, Ltd.
; STREET: 180 No. 5504190th Stetson Avenue, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60601
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: PRL-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-253-854-91

Query Match: 48.7%; Score 19; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 STTCGG 6
Db 1 STTCGG 6

RESULT 6
US-09-173-941-76
; Sequence 76, Application US/09173941
; Patent No. 614308:
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NCVO0815
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 76
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US 09-173-941-76

Query Match: 48.7%; Score 19; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8
Db 4 QEGEL 5

RESULT 7
US-08-259-550A-90
; Sequence 90, Application US/0825955CA
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
```

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; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-259-550A-90

Query Match: 48.7%; Score 19; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTQEGE 7
Db 1 TTQEGE 6

RESULT 8
US-09-188-579-2
; Sequence 2, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Motif III of RNA guanylyltransferase.
US-09-188-579-2

Query Match: 48.7%; Score 19; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8
Db 1 TTQEGEL 7

RESULT 9
US-09-188-579-8
; Sequence 8, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
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Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
SEQUENCE ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-8

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 10  
US-09-315-444-8  
Sequence 14, Application US/091885798  
Patent No. 6107040  
GENERAL INFORMATION:  
APPLICANT: Shuman, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
SEQUENCE ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Candida albicans  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-8

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 11  
US-09-315-444-2  
Sequence 2, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuman, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
SEQUENCE ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-2

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7  
RESULT 12  
US-09-315-444-6  
Sequence 8, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuman, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
SEQUENCE ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-6

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 13  
US-09-315-444-14  
Sequence 14, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuman, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
SEQUENCE ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Candida albicans  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-14

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 14  
US-09-230-549-10  
Sequence 10, Application US/09230548  
Patent No. 6326466  
GENERAL INFORMATION:  
APPLICANT: Barraco, Donald P

? APPLICANT: Petryshyn, Raymond  
 ? APPLICANT: The Government of the United States of America  
 ? APPLICANT: as represented by The Secretary,  
 ? APPLICANT: Department of Health and Human Services  
 ? TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived  
 ? TITLE OF INVENTION: Peptides to Promote Proliferation of Cells and Tissues  
 ? TITLE OF INVENTION: in a Controlled Manner  
 ? FILE REFERENCE: 015280-286200US  
 ? CURRENT APPLICATION NUMBER: US/09/230,548  
 ? CURRENT FILING DATE: 1999-07-23  
 ? EARLIER APPLICATION NUMBER: US 60/323,307  
 ? EARLIER FILING DATE: 1996-07-30  
 ? EARLIER APPLICATION NUMBER: WO PCT/US97/14350  
 ? EARLIER FILING DATE: 1997-07-29  
 ? NUMBER OF SEQ ID NOS: 31  
 ? SOFTWARE: Patent In. Ver. 2.1  
 ? SEQ ID NO 10  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: double-stranded  
 ? OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide  
 ? OTHER INFORMATION: antagonist  
 ? US-09-230,548-10

Query Match 48.7% Score 19; DB 4; Length 8;  
 Best Local Similarity 57.1% Pred. No. 2.5e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STQGE 7  
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 Db 2 STQGE 8

RESULT 15  
 US-09-721,362-2  
 ? Sequence 2, Application US/09721362  
 ? Patent No. 6423163  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Shuman, Stewart  
 ? TITLE OF INVENTION: Pharmacological Targeting of tRNA Cap Formation  
 ? FILE REFERENCE: 06185CIP/C  
 ? CURRENT APPLICATION NUMBER: US/09/721,362  
 ? CURRENT FILING DATE: 2000-11-22  
 ? PRIOR APPLICATION NUMBER: US 09/315,444  
 ? PRIOR FILING DATE: 1999-05-20  
 ? NUMBER OF SEQ ID NOS: 116  
 ? SEQ ID NO 2  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Saccharomyces cerevisiae  
 ? FEATURE:  
 ? OTHER INFORMATION: Motif III of RNA guanylyltransferase  
 ? US-09-721,362-2

Query Match 48.7% Score 19; DB 4; Length 8;  
 Best Local Similarity 57.1% Pred. No. 2.5e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
 1 1 1 1  
 Db 1 TLLDDEL 7

Search completed: November 5, 2003, 17:23:15  
 Job time : 14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:29:45 / Search time 11 seconds  
(without alignments)  
87,426 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57

Sequence: 1 SQKHWLSDRT 10

Scoring table: BLOSUM62

Gapcp 10.0, Gapext 0.5

Searched: 283:08 seqs, 96:68682 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAR:ES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	40.4	10	2 A49187	gonadotropin-relea
2	20	35.1	10	1 RHPCS	gonadolibetin - pi
3	20	35.1	10	1 RHSHG	gonadolibetin - sh
4	20	35.1	10	1 PHAQ	gonadolibetin I -
5	20	35.1	10	1 RHAQT	gonadolibetin II -
6	20	35.1	10	1 A61126	gonadolibetin - sp
7	20	35.1	10	2 B46530	gonadolibetin I -
8	20	35.1	10	2 A46530	gonadolibetin -
9	20	35.1	10	2 A21114	gonadolibetin - ch
10	19	33.3	10	2 PQ0177	neurokinin C - lac
11	19	33.3	10	2 A60647	neurokinin C - bov
12	18	31.6	10	2 PT0289	Ig heavy chain CRD
13	17	29.8	6	2 S29881	Na+/K+-exchanging
14	16	28.1	7	2 PT0576	T-cell receptor be
15	16	28.1	8	2 T14306	hypothetical prote
16	16	28.1	9	2 A43848	cell surface adhes
17	16	28.1	9	2 PT0231	Ig heavy chain CDR
18	16	28.1	10	2 T17054	cytochrome-c oxida
19	15	26.3	5	2 PT0672	T-cell receptor be
20	15	26.3	7	2 S33567	tubulin beta-3 cha
21	15	26.3	7	4 A58725	virotoxin - destro
22	15	26.3	9	2 A6C108	exotoxin A - Strept
23	15	26.3	9	2 PT0324	Ig heavy chain CRD
24	15	26.3	9	2 A37027	macrophage chemota
25	15	26.3	9	2 PT0562	T-cell receptor be
26	15	26.3	10	2 L40532	trpE protein - Bac
27	15	26.3	10	2 T17375	cytochrome-c oxida
28	15	26.3	10	2 T17563	cytochrome-c oxida
29	15	26.3	10	2 T12325	cytochrome-c oxida

30 15 26.3 10 2 T12329  
31 15 26.3 10 2 T14212  
32 15 26.3 10 2 T14215  
33 15 26.3 10 2 T14223  
34 14.5 25.4 10 2 JC1367  
35 14 24.6 5 2 PT0565  
36 14 24.6 6 2 PT0532  
37 14 24.6 6 2 PT0650  
38 14 24.6 9 2 JS0302  
39 14 24.6 9 2 A60320  
40 14 24.6 9 2 S65933  
41 14 24.6 9 2 S78420  
42 14 24.6 9 4 S78450  
43 14 24.6 10 2 S09387  
44 14 24.6 10 2 S13224  
45 14 24.6 10 2 C39191

# ALIGNMENTS

## RESULT 1

A49187  
gonadotropin-releasing hormone III - sea lamprey  
C:Species: Petromyzon marinus (sea lamprey)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: A49187  
R:Sower, S.A.; Chiang, Y.C.; Lovas, S.; Conlon, J.M.  
Endocrinology 132, 1125-1131, 1993

A:Title: Primary structure and biological activity of a third gonadotropin-releasing hormone  
A:Reference number: A49187; MUID:93178316; PMID:8440174  
A:Accession: A49187

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SOW>

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:126381)

Query Match 40.4%; Score 23; DB 2; Length 10;  
Best: Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KHWLSD S  
DB 1 RHSHG 6

## RESULT 2

RHPGG

gonadolibetin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 18-Mar-1997

C:Accession: A01411

R:Baba, Y.; Yatsuo, H.; Schally, A.V.

Biochem. Biophys. Res. Commun. 44, 459-463, 1971

A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of th

A:Reference number: A90172; MUID:72114303; PMID:4946067

A:Accession: A01411

A:Molecule type: protein

A:Residues: 1-10 <BAB>

R:Matsuoka, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 822-827, 1971

A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase meth

A:Reference number: A90176; MUID:72065376; PMID:4946276

A:Contents: annotation; synthesis

A:Note: the synthetic and natural hormones have the same physicochemical and biological

R:Baba, Y.; Arimura, A.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 483-487, 1971

A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.

A:Reference number: A90175; MUID:72117544; PMID:4946275

A:Contents: annotation

A:Note: Trp-3 appears to be essential for biological activity

C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and f

cytochrome-c oxida  
cytochrome-c oxida  
cytochrome-c oxida  
cytochrome-c oxida  
thyroliberin poten  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
xenopsin-related p  
xenopsin-related p  
pyrimidine synthe  
ribosomal protein  
hemoglobin alpha c  
virG protein - num  
hypothetical prote

C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

RESULT 3  
 RHAQ1  
 gonadoliberin - sheep  
 C:Species: Ovis orientalis aries (domestic sheep)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 18-Mar-1997  
 C:Accession: A93780; A01411  
 R:Burgas, R.; Butcher, M.; Amoss, M.; Ling, N.; Mohanan, V.; Rivier, J.; Fellows, R.; Bl  
 Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972  
 A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing facto  
 A:Reference number: A93780; MUID:72094314; PMID:4550508  
 A:Accession: A93780  
 A:Molecule type: protein  
 A:Residues: 1-10 <BUR>  
 A:Note: the natural and synthetic hormones have the same biological activity  
 C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo  
 C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

RESULT 4  
 RHAQ1  
 gonadoliberin I - American alligator  
 N:Alternate names: gonadotropin-releasing hormone I  
 C:Species: Alligator mississippiensis (American alligator)  
 C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C:Accession: A60066  
 R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanso  
 Regul. Pept. 33, 105-116, 1991  
 A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of  
 A:Reference number: A60066; MUID:91352338; PMID:1882082  
 A:Accession: A60066  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOV>  
 C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

RESULT 5  
 RHAQ2  
 gonadoliberin II - American alligator  
 N:Alternate names: gonadotropin-releasing hormone II  
 C:Species: Alligator mississippiensis (American alligator)  
 C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C:Accession: B60066  
 R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanso  
 Regul. Pept. 33, 105-116, 1991  
 A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o  
 A:Reference number: A60066; MUID:91352338; PMID:1882082  
 A:Accession: B60066  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOV>  
 C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

gonadoliberin II - American alligator  
 N:Alternate names: gonadotropin-releasing hormone II  
 C:Species: Alligator mississippiensis (American alligator)  
 C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C:Accession: B60066  
 R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanso  
 Regul. Pept. 33, 105-116, 1991  
 A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o  
 A:Reference number: A60066; MUID:91352338; PMID:1882082  
 A:Accession: B60066  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOV>  
 C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

RESULT 6  
 A61126  
 gonadoliberin - spotted rattlesnake  
 N:Alternate names: gonadotropin-releasing hormone  
 C:Species: Hydrogaleus collieri (spotted rattlesnake)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 18-Mar-1997  
 C:Accession: A61126  
 R:Lovejoy, D.A.; Sherwood, N.W.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.  
 Gen. Comp. Endocrinol. 82, 152-161, 1991  
 A:Title: Primary structure of gonadotropin-releasing hormone from the brain of a holoco  
 A:Reference number: A61126; MUID:91340067; PMID:1678723  
 A:Accession: A61126  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOV>  
 A:Experimental source: brain  
 C:Superfamily: gonadoliberin  
 C:Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 :||  
 Db 1 QHW 3

RESULT 7  
 B46030  
 gonadoliberin I - spiny dogfish  
 N:Alternate names: gonadotropin-releasing hormone  
 C:Species: Squalus acanthias (spiny dogfish)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jan-2003  
 C:Accession: B46030  
 R:Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter,  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
 A:Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pr  
 A:Reference number: A46030; MUID:92335300; PMID:1631133  
 A:Accession: B46030  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOV>  
 C:Superfamily: gonadoliberin  
 C:Keywords: hormone; pyroglutamic acid  
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+03;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 2  
 A46030  
 gonadolibetin I - spiny dogfish  
 A:Alternate names: gonadotropin-releasing hormone  
 C:Species: Squalus acanthias (spiny dogfish);  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Dec 1998  
 C:Accession: A46030  
 R:Lovejoy, D.A.; Fischer, W.H.; Neamvongchot, S.; Craig, A.G.; Naborniak, C.S.; Peter, R.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
 A:Title: Distinct sequence of gonadotropin-releasing hormone (GRH) in dogfish brain pro  
 A:Reference number: A46030; MUID:92335300; PMID:1631133  
 C:Accession: A46030  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOW>  
 C:Keywords: hormone; pyroglutamic acid  
 F:/Modified site: pyroglutamic acid (GLN, #status experimental;

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+03;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 3  
 A21114  
 gonadolibetin - chum salmon  
 C:Species: Oncorhynchus keta (chum salmon);  
 C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 18 Jun 1993  
 C:Accession: A21114  
 R:Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983  
 A:Title: Characterization of a teleost gonadotropin-releasing hormone.  
 A:Reference number: A21114; MUID:83195140; PMID:6341097  
 C:Accession: A21114  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <SHE>

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+04;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 10  
 P00177  
 neuromedin C - laughing frog  
 C:Species: Rana ridibunda (laughing frog)  
 C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 11-Jan-2000  
 C:Accession: P00177  
 R:Corlison, C.M.; Ciharte, F.; Vaudry, H.  
 Biochem. Biophys. Res. Commun. 178, 528-530, 1991  
 A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that b  
 A:Reference number: P00177; MUID:91315477; PMID 1855415  
 C:Accession: P00177  
 A:Molecule type: protein

A:Residues: 1-10 <CON>  
 A:Experimental source: brain  
 C:Superfamily: gastrin-releasing peptide  
 C:Keywords: amidated carboxyl end  
 F:/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 33.3%; Score 19; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 1.7e+03;  
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HW 5  
 :  
 Db 3 HW 4

RESULT 11  
 A60647  
 neuroedin C - bovine  
 C:Species: Bos primigenius taurus (cattle);  
 C>Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
 C:Accession: A60647  
 R:Lemaire, S.; Trifaro, J.M.; Chodunard, L.; Cecyre, D.; Dessureault, J.; Mercier, P.;  
 Peptides 10, 355-360, 1989  
 A:Title: Structural identification, subcellular localization and secretion of bovine ac  
 A:Reference number: A60647; MUID:89331342; PMID:2755876  
 C:Accession: A60647  
 A:Molecule type: protein  
 A:Residues: 1-10 <LEM>  
 A>Note: this neuropeptide was purified from secretory granules of cells in the adrenal  
 C:Superfamily: gastrin releasing peptide  
 C:Keywords: adrenal gland; neuropeptide

Query Match: 33.3%; Score 19; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 1.7e+03;  
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HW 5  
 :  
 Db 3 HW 4

RESULT 12  
 PT0289  
 Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0289  
 R:Yamada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91102337; PMID:1899102  
 C:Accession: PT0289  
 A:Molecule type: DNA  
 A:Residues: 1-10 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 31.6%; Score 18; DB 2; Length 10;  
 Best Local Similarity: 50.0%; Pred. No. 2.6e+03;  
 Matches: 2; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HWLS 7  
 :  
 Db 3 NWS 6

RESULT 13  
 S29881  
 Na+/K+-exchanging ATPase (EC 3.6.3.9; alpha chain - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 13-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 19-Apr-2002  
 C:Accession: S29881  
 R:Walterhaug, M.O.; Peier, P.; Saccorani, G.; Leonard, R.T.; Briskin, D.P.

J. Biol. Chem. 265, 3852-3859, 1985  
 A:Title: Structural relatedness of three ion-transport adenine triphosphatases around  
 A:Reference number: S29881; MUID:95131201; PMID:3156136  
 A:Accession: S29881

A:Molecule type: Protein  
 A:Residues: 1-6 <WAL>  
 A:Experimental source: kidney  
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
 F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 29.8%; Score 17; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SDPT 10

DB 3 SDKT 6

#### RESULT 14

PT0576

T-cell receptor beta chain V-D-J region (142-13); - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 10 May 1997

C:Accession: PT0576

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:9277601; PMID:171359

A:Accession: PT0576

A>Status: translation not shown

A:Molecule type: tRNA

A:Residues: 1-7 <FE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 28.1%; Score 16; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FRT 10

DB 5 DRT 7

#### RESULT 15

T14906

Hypothetical protein - parsley

C:Species: Petroselinum crispum (parsley)

C:Date: 20-Sep-1999 #sequence\_revision 20 Sep 1999 #text\_change 20 Sep 1999

C:Accession: T14906

R:Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Hart, K.; Weisshaar, B.

Plant Cell 6, 1607-1621, 1994

A:Title: Functional analysis of a light-responsive plant tZIP transcriptional regulator.

A:Reference number: Z18259; MUID:95128172; PMID:7827494

A:Accession: T14906

A>Status: preliminary; translated from GB/EXSL/EDB1

A:Molecule type: DNA

A:Residues: 1-8 <FEL>

A:Cross-references: EXBL:S75395; NID:q913201; P:ID:el9424

Query Match 28.1%; Score 16; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWJS 7

DB 2 KHTLT 6

Search completed: November 5, 2003, 17:35:21

Job time : 12 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:23:40 ; Search time 2.3433 Seconds  
(without alignments)  
64.127 Million cell updates/sec

Title: US-09-914-088-3  
Perfect score: 57  
Sequence: 1 SQKHWSLDRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 372

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	23	40.4	10	1	GON3_PETMA	P30948
2	20	35.1	10	1	GON1_ALLMI	P37041
3	20	35.1	10	1	GON1_CHEPR	P36677
4	20	35.1	10	1	GON1_CUEPA	P31749
5	20	35.1	10	1	GON2_CHEPR	P36678
6	20	35.1	10	1	GON2_CHEPR	P36678
7	20	35.1	10	1	GON3_CHEPR	P36678
8	20	35.1	10	1	GON3_CHEPR	P36678
9	20	35.1	10	1	GON3_CHEPR	P36678
10	18	31.6	9	1	DI_NEPNO	P36678
11	17	29.8	10	1	MP2_MICOR	P36678
12	16	28.1	10	1	FAR5_MACRS	P31278
13	15	26.3	8	1	FAR3_ROMAN	P41486
14	14	24.6	9	1	CONV_CONVE	P31247
15	13	22.8	5	1	UF01_MOUSE	P36639
16	13	22.8	6	1	E101_LITRU	P36639
17	13	22.8	7	1	FAR2_ASCSU	P31890
18	13	22.8	8	1	CKKN_MACSU	P30369
19	13	22.8	10	1	BPP2_ROTIN	P30422
20	13	22.8	10	1	BPP2_ROTIN	P30422
21	13	22.8	10	1	CAER_LITXA	P36264
22	13	22.8	10	1	URA6_HUMAN	P32083
23	12	21.1	7	1	TPFY_PACTA	P31455
24	12	21.1	8	1	FAR2_MACRS	P31278
25	12	21.1	8	1	HTF1_PERAY	P31278
26	12	21.1	8	1	HTF2_PERAY	P31278
27	12	21.1	8	1	HTF1_PERAY	P31278
28	12	21.1	8	1	LITO_LITAU	P32945
29	12	21.1	9	1	NEUX_HUMAN	P34277
30	12	21.1	10	1	AEGL_AGRAR	P31465
31	12	21.1	10	1	AEGL_AGRAR	P31465
32	12	21.1	10	1	AEGL_AGRAR	P31465
33	12	21.1	10	1	HTF1_ROMMI	P31278

34	12	21.1	10	1	HTF2_CARMO	P11385
35	12	21.1	10	1	TRU1_UREUN	P40751
36	12	21.1	10	1	TPIS_NICPL	P19118
37	11	19.3	4	1	CCP3_OCTMI	P58649
38	11	19.3	5	1	BPP7_BOTIN	P30425
39	11	19.3	6	1	LOK1_LOCM1	P41491
40	11	19.3	7	1	BRP2_CONIM	P58803
41	11	19.3	7	1	FAR1_MACRS	P31278
42	11	19.3	7	1	FAR2_PROCL	P31278
43	11	19.3	7	1	TY5_LITRU	P82065
44	11	19.3	7	1	JP04_MOUSE	P36642
45	11	19.3	7	1	WWA1_ACHFU	P35919

ALIGNMENTS

RESULT 1  
GON3\_PETMA STANDARD: PRT: 10 AA.  
AC P30948;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)  
DE (Luliberin III)  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
OX NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93178316; PubMed=8440174;  
RA Sower S.A., Chiang Y.-C., Iovas S., Conlon J.M.;  
RT "Primary structure and biological activity of a third gonadotropin-releasing hormone from lamprey brain";  
RL Endocrinology 132:1125-1131(1993).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR InterPro: IPR002012; GNRH.  
DR Pfam: PF03446; GNRH; 1.  
DR PROSITE: PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1 10 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MOD\_RES 12 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1277 MW; 284356237AAIFSA3 CRC64;  
Query March 40.4%; Score 23; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 KHWLSD 2  
Db 1 QHWSHD 6  
RESULT 2  
GON1\_ALLMI STANDARD: PRT: 10 AA.  
AC P37041; P20407;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)  
DE (Luliberin I)  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylia; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;

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RN PP SEQUENCE.
RC 1:SSUR=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McGorry J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT first brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC 1: FUNCTION: Stimulates the secretion of gonadotropins.
CC 1: SUBCELLULAR LOCATION: Secreted.
CC 1: SIMILARITY: Belongs to the GnRH family.
DR PIR: A60066; RHA01.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 28482307286845A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5
DB 1 QHW 3

RESULT 3
CON: CHEPR
ID _GON1_CHEPR STANDARD; PRT; 10 AA.
AC P80677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH I)
DE (Luliberin I).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
PY SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC 1: FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle stimulating
CC hormones.
CC 1: SUBCELLULAR LOCATION: Secreted.
CC 1: TISSUE SPECIFICITY: GnRH neurons lie within hypothalamus close to
CC the neurohypophysis and gonads in both juveniles and adults, implying
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC 1: MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC 1: SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 2848363928585A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5

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DB 1 QHW 3

RESULT 4
CON: CLUPA
ID _GON1_CLUPA STANDARD; PRT; 10 AA.
AC P81749;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH)
DE (Luliberin I).
GN GnRH1.
CS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724;
PY SEQUENCE.
RX MEDLINE=20114351; PubMed=13650929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC 1: FUNCTION: Stimulates the secretion of gonadotropins.
CC 1: SUBCELLULAR LOCATION: Secreted.
CC 1: SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 284820872871F5A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5
DB 1 QHW 3

RESULT 5
CON: CHEPR
ID _GON2_CHEPR STANDARD; PRT; 10 AA.
AC P80678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
DE (Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
PY SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC 1: FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC 1: SUBUNIT: Homodimer; disulfide-linked.

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CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO  
 CC THE CONDUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING  
 CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.  
 CC -1- MASS SPECTROMETRY: MW=1117.52; METHCD=VALDI.  
 CC -1- SIMILARITY: Belongs to the GnRH family  
 DR InterPro: IPR02012; GnRH.  
 DR PROSITE: PS0473; GnRH; 1.  
 KW Hormone; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 6 6 INTERCHAIN.  
 FT MOD\_RES 10 10 AMIDATION [BY SIMILARITY].  
 SQ SEQUENCE 10 AA; 1135 MW; 284819D1EB735A3 CRC64.  
 Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KHW 5  
 DB 1 QHW 3  
 RESULT 6  
 GON3\_CHICK STANDARD; PRT; 10 AA.  
 AC P37043; P20408; P81750;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)  
 DE (LH-RH II) (Luliberin II).  
 CS Gallus gallus (Chicken).  
 CS Alligator mississippiensis (American alligator).  
 OS Squatus acanthias (Spiny dogfish).  
 OS Hydrolagus collieri (Spotted ratfish) (Pacific ratfish), and  
 OS Clupea pallasii (Pacific herring).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archostralia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 CX NCBI\_TaxID=9031, 8496, 7797, 7673, 30724;  
 RN [1]  
 RN SEQUENCE.  
 RC SPECIES=Chicken; TISSUE=Hypothalamus;  
 RX MEDLINE=84222059; PubMed=6427779;  
 RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi Y., Kurojima K.,  
 RA Matsuo H.;  
 RT "Identification of the second gonadotropin-releasing hormone in  
 RT chicken hypothalamus: evidence that gonadotropin secretion is  
 RT probably controlled by two distinct gonadotropin-releasing hormones  
 RT in avian species."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:1874-1878(1984).  
 RN [2]  
 RN SEQUENCE.  
 RC SPECIES=A.mississippiensis; TISSUE=Brain;  
 RX MEDLINE=91352338; PubMed=1882082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone  
 RT from brains of the American alligator (Alligator mississippiensis)."  
 RL Regul. Pept. 33:105-116(1991).  
 RN [3]  
 RN SEQUENCE.  
 RC SPECIES=S. acanthias; TISSUE=Brain;  
 RX MEDLINE=92335300; PubMed=1631133;  
 RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
 RA Nahrniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;  
 RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in  
 RT dogfish brain provides insight into GnRH evolution."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).  
 RN [4]  
 RN SEQUENCE.  
 RC SPECIES=H. collieri; TISSUE=Brain;

RX MEDLINE=91340067; PubMed=1678723;  
 RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,  
 RA Lee T.;  
 RT "Primary structure of gonadotropin-releasing hormone from the brain  
 RT of a holoccephalan (ratfish: Hydrolagus collieri).";  
 RL Gen. Comp. Endocrinol. 82:152-161(1991).  
 RN [5]  
 RN SEQUENCE, AND FUNCTION.  
 RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring."  
 RL Endocrinology 141:505-512(2000).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the GnRH family.  
 DR PIR; A61126; A61126.  
 DR PIR; B46030; B46030.  
 DR PIR; B60366; RHAQ2.  
 DR InterPro: IPR02012; GnRH.  
 DR Pfam: PF00446; GnRH; 1.  
 DR PROSITE: PS00473; GnRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;  
 Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KHW 5  
 DB 1 QHW 3  
 RESULT 7  
 GON3\_ONCKE STANDARD; PRT; 10 AA.  
 AC P20367; P81751;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-  
 DE RH III) (Luliberin III).  
 DE GnRH3.  
 OS Oncorhynchus keta (Chum salmon), and  
 OS Clupea pallasii (Pacific herring).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 CX NCBI\_TaxID=8018, 30724;  
 RN [1]  
 RN SEQUENCE.  
 RC SPECIES=O. keta;  
 RX MEDLINE=83195140; PubMed=6341999;  
 RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;  
 RT "Characterization of a teleost gonadotropin-releasing hormone."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).  
 RN [2]  
 RN SEQUENCE, AND FUNCTION.  
 RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring."  
 RL Endocrinology 141:505-512(2000).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 CC the secretion of both luteinizing and follicle-stimulating  
 CC hormones.

CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR: A21114; A21114.  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.  
 DR PROSITE: PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1230 MW; 284B3233786545A3 CR64;  
 Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KHW 5  
 DB : QHW 3  
 RESULT 8  
 GRNLSQUAC  
 ID GRNLSQUAC STANDARD; PRT; 10 AA.  
 AC P27429;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)  
 DE (Laliberin).  
 CS Squalea acanthias (Spiny dogfish).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 CC Elasmobranchii; Squalea; Squaleidae; Squalidae; Squales.  
 CX NCBI\_TaxID=7737;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92335300; PubMed=611133;  
 RA Lovejoy D.A., Fischer W.H., Namwongchon S., Craig A.G.,  
 RA Nakajima C.S., Peter R.E., Rivier J.E., Sherwood N.M.,  
 RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in  
 RT dogfish brain provides insight into GNRH evolution".  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:6171-6174 (1992).  
 CC 1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR: A46037; A46037.  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.  
 DR PROSITE: PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1204 MW; 284B3233786545A3 CR64;  
 Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 DB : QHW 3  
 RESULT 9  
 GRP\_RANRI  
 ID GRP\_RANRI STANDARD; PRT; 10 AA.  
 AC P23260;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neomedin C.  
 CC Neomedin C.  
 CC Rana ridibunda (Laughing frog) (Marsh frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Extraneostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 CX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91315477; PubMed=199413;  
 RA Conlon J.M., O'Harte F., Vaudry H.,  
 RT "Primary structures of the bombesin-like neuropeptides in frog brain  
 RT show that bombesin is not the amphibian gastrin-releasing peptide".  
 RT Biochem. Biophys. Res. Commun. 178:526-530 (1991).  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR: PQ0177; PQ0177.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862C3C371 CR64;

Query Match 33.3%; Score 19; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 5  
 DB : KHW 4

RESULT 10  
 D1\_NEPNO  
 ID D1\_NEPNO STANDARD; PRT; 9 AA.  
 AC P24816;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Gastrin/cholecystokinin-like peptide D1.  
 OS Nephrops norvegicus (Norway lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea.  
 CC Nephropoidea; Nephropidae; Nephrops.  
 CX NCBI\_TaxID=6829;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Stomach;  
 RX MEDLINE=92082847; PubMed=1747388;  
 RA Favrel P., Kegel G., Sedlmeyer D., Keller R., van Wormhoudt A.,  
 RT "Structure and biological activity of crustacean gastrointestinal  
 RT peptides identified with antibodies to gastrin/cholecystokinin".  
 RL Biochimie 73:1233-1239 (1991).  
 CC 1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.  
 CC 1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR: S47432; S47432.  
 KW Hormone.  
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB5D8787B CR64;

Query Match 31.6%; Score 18; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGFWL 6  
 DB : QGFWL 9

RESULT 11  
 MP2\_MICOC  
 ID MP2\_MICOC STANDARD; PRT; 10 AA.  
 AC P81533;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE M22 protein (Fragment).  
 OS Microplitis ocellatae (Braconid wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neuroptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Microgastrinae; Microplitis.  
 OX NCBI\_TaxID=99573;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RA Takahashi M., Quicke D.L.J.;  
 RL Submitted (CCT-1998) to the SWISS-PROT data bank.  
 CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.  
 CC -!- DEVELOPMENTAL STAGE: LARVAL.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1255 MW; FE4FD33366C41AFA CRC64;  
 Query Match 29.8%; Score 17; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 KHW 6  
 Db 5 RQW 8  
 RESULT 12  
 FARS\_MACRS STANDARD; PRT; 10 AA.  
 AC P83278;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CE FMRamide-like neuropeptide FLPS (DTPALRSP-amide)  
 OS Macrobrachium rosenbergii (Giant fresh water prawn)  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Sarathongkum W., Jandeechuey S., Jongyart S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii".  
 RL Comp. Biochem. Physiol. 120B:587-595 (1992).  
 CC -!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO:0007218; P:neuropeptide signaling pathway; FARP.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC711 CRC64;  
 Query Match 28.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 DRT 10  
 Db 1 DRT 3  
 RESULT 13  
 FARS\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 CE FMRamide-like neuropeptide 3 (Fu: 3) (F2).  
 OS FMRamide-like neuropeptide 3 (Fu: 3) (F2).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=86116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRamide-like immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RJ J. Comp. Neurol. 268:16-26 (1987).  
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 NM  
 CC -!- POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;  
 Query Match 26.3%; Score 15; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 SCR 9  
 Db 1 SDR 3  
 RESULT 14  
 COM\_CONVE STANDARD; PRT; 9 AA.  
 AC P83347;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Contryphan-Vn.  
 OS Conus ventricosus (Mediterranean cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apeogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=17992;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=21547785; PubMed=11688995;  
 RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;  
 RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean  
 RT snail Conus ventricosus".  
 RL Biochem. Biophys. Res. Commun. 285:908-913 (2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Amidation; D-amino acid.  
 FT DISULFID 3 9  
 FT MOD\_RES 5 5  
 FT MOD\_RES 9 9  
 SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;  
 Query Match 24.6%; Score 14; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 KHW 5  
 Db 6 KPW 8  
 RESULT 15  
 UF01\_MOUSE STANDARD; PRT; 5 AA.  
 ID UF01\_MOUSE  
 AC P38639;

DT 31-OCT-1994 (Rel: 30, Created:  
 DT 31-OCT-1994 (Rel: 30, Last sequence update)  
 DT 31-FEB-1995 (Rel: 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment)  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7521108;  
 RA Merrick B.A., Patterson R.M., Richter L.D., Ho C., Wolpert J.K.  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis."  
 RL Electrophoresis 15:735-745(1994)  
 CC 1: MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.  
 FT NON TER 5  
 SQ SEQUENCE 5 AA; 717 MW; 736408704110000 CRC64;

Query Match 22.81; Score 13; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred No. 1,36-05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WL 6  
 DE : WI 2

Search completed: November 5, 2003, 17:33:04  
 Job time : 8.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:29:05 ; Search time 26 seconds  
(without alignments)  
99.251 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57 SQHMLSRT 10

Sequence: 1 SQHMLSRT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052654 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPRMBL23:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_ricent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacterioph:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	21	36.8	9	Q8W8X4	Q8W8X4 diadema mex
2	20	35.1	8	Q8W8X7	Q8W8X7 iomis hirta
3	20	35.1	9	Q8W8X6	Q8W8X6 procambartus
4	20	35.1	10	Q8W8X5	Q8W8X5 helicobacte
5	19	33.3	8	Q8W8X3	Q8W8X3 oryctolagus
6	19	33.3	9	Q8W8X2	Q8W8X2 varanus gfg
7	19	33.3	10	Q8W8X1	Q8W8X1 bradypodion
8	19	33.3	10	Q8W8X0	Q8W8X0 rana muscos
9	19	33.3	10	Q8W8X8	Q8W8X8 escherichia
10	19	33.3	10	Q8W8X9	Q8W8X9 acinetobact
11	18	31.6	9	Q8W8X4	Q8W8X4 diadema mex
12	18	31.6	9	Q8W8X7	Q8W8X7 iomis hirta
13	18	31.6	10	Q8W8X6	Q8W8X6 procambartus
14	18	31.6	10	Q8W8X5	Q8W8X5 helicobacte
15	18	31.6	10	Q8W8X3	Q8W8X3 oryctolagus
16	18	31.6	10	Q8W8X2	Q8W8X2 varanus gfg

17	29.9	8	11	Q99MN0	Q99MN0 mus musculu
18	29.9	9	4	Q9H326	Q9H326 homo sapien
19	29.8	9	12	P90359	P90359 barley mild
20	29.8	10	2	Q47561	Q47561 escherichia
21	29.8	10	8	Q9XMB4	Q9XMB4 aequilops ta
22	29.8	10	8	Q94VD5	Q94VD5 varanus oli
23	29.8	10	8	Q9G362	Q9G362 acanthosaur
24	28.1	9	4	Q15890	Q15890 homo sapien
25	28.1	8	6	Q95M23	Q95M23 sus scrofa
26	28.1	9	2	Q9R5M1	Q9R5M1 staphylococ
27	28.1	10	3	Q8T8G8	Q8T8G8 pleurotus o
28	28.1	10	6	Q3TU33	Q3TU33 canis famil
29	28.1	10	8	Q8T8P3	Q8T8P3 liolaemus a
30	28.1	10	8	Q9T8L9	Q9T8L9 liolaemus f
31	28.1	10	8	Q9T8W5	Q9T8W5 liolaemus r
32	28.1	10	8	Q8W916	Q8W916 liolaemus m
33	28.1	10	8	Q9T8N7	Q9T8N7 liolaemus o
34	28.1	10	8	Q9T8H8	Q9T8H8 basiliscus
35	28.1	10	8	Q9T8P0	Q9T8P0 liolaemus f
36	28.1	10	13	Q42355	Q42355 brachydanio
37	28.1	10	13	Q90Y93	Q90Y93 gallus gall
38	26.3	7	11	Q8K3H6	Q8K3H6 rattus norv
39	26.3	8	9	Q94V88	Q94V88 varanus tri
40	26.3	8	9	Q94VJ4	Q94VJ4 varanus ben
41	26.3	8	8	Q94V91	Q94V91 varanus tim
42	26.3	8	8	Q94V54	Q94V54 varanus mel
43	26.3	8	8	Q94VF9	Q94VF9 varanus ind
44	26.3	8	11	Q62721	Q62721 rattus norv
45	26.3	8	12	Q64971	Q64971 alfalfa mos

#### ALIGNMENTS

RESULT 1

Q8W8X4 PRELIMINARY; PRT; 9 AA.

AC Q8W8X4: 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Cytochrome oxidase subunit 1 (Fragment).  
GN COI.  
OS Diadema mexicanum.  
OG Mitochondrion.  
OC Sukariyota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinozoa; Diadematacea; Diadematoida; Diadematidae.  
OC Diadema.  
OX NCBI\_TaxID=105353;  
RN 111\_TaxID=105353;  
RP SEQUENCE FROM N.A.  
RC STRAIN=CC70, and CC117;  
RX MEDLINE=21323357; PubMed=11430656;  
RA Lessios H.A., Kessing B.D., Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global  
phylogeography of the sea urchin Diadema";  
RL Evolution 55:955-975(2001).

RN 121  
RP SEQUENCE FROM N.A.  
RC STRAIN=CC70, and CC117;  
RX MEDLINE=21561594; PubMed=11703875;  
RA Lessios H.A., Garrido M.J., Kessing B.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on  
Caribbean reefs";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
DR EMBL: AY012921; AAL33844.1;  
KW Mitochondrion.  
FT NCN TER 1  
SQ SEQUENCE 9 AA; 1174 MW; 2873173846DDC2D3 CRC64;  
Query Match 36.8%; Score 21; DB 8; Length 9;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HMLS 7  
| |  
DL : HWVA 4

## RESULT 2

Q8WGD7 PRELIMINARY; PRT; 8 AA.  
AC Q8WGD7;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update;  
DE Cytochrome oxidase subunit 1 (Fragment).  
OS *Leishmania*.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Lomidae;  
OC Lomidae; Lomis.  
OX NCBI\_TaxID=177234;  
RN [1];  
RP SEQUENCE FROM N.A.  
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
RA Cunningham C.W.;  
RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
RT evolution to the crab-like form."  
RL Submitted (JCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF436035; AAL31611.1;  
KW Mitochondrion.  
FT NON-TER 1  
FT NON-TER 8  
SQ SEQUENCE 8 AA; 1038 MW; C5B5B9C733640321 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 8;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
| |  
DB 2 KRWL 5

## RESULT 3

Q8WGE6 PRELIMINARY; PRT; 8 AA.  
AC Q8WGE6;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update;  
DE Cytochrome oxidase subunit 1 (Fragment).  
OS *Procambarus clarkii* (Red swamp crayfish).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Astacoidea; Cambaridae; Procambarus.  
OX NCBI\_TaxID=6728;  
RN [1];  
RP SEQUENCE FROM N.A.  
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
RA Cunningham C.W.;  
RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
RT evolution to the crab-like form."  
RL Submitted (JCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF436024; AAL31599.1;  
KW Mitochondrion.  
FT NON-TER 1  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 1185 MW; 936B5C733640321 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
| |  
DB 3 KRWL 6

## RESULT 4

Q9F9H5 PRELIMINARY; PRT; 10 AA.  
AC Q9F9H5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created;  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update;  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update;  
DE Glutamate racemase (fragment).  
OS *Glut.*  
OC Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1];  
RP SEQUENCE FROM N.A.  
RA STRAIN=India75A;  
RX MEDLINE=20270152; PubMed=10809702;  
RA Kersulyte D., Mukhopadhyay A.K., Velapattino B., Su W.W., Pan Z.J.,  
RA Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,  
RA Gao H., Alarcon T., Lopez-Brea M., Balakrishna R., Chowdhury A.,  
RA Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,  
RA Lam S.K., Olfat F.O., Boren T., Engstrand L., Torres O., Schneider R.,  
RA Thomas J.E., Czinn S., Berg D.E.;  
RT "Differences in genotypes of Helicobacter pylori from different human  
RT populations."  
RL J. Bacteriol. 182:3210-3218(2000).  
DR EMBL: AF190663; AAG18486.1;  
FT NON-TER 1  
SQ SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;

Query Match 35.1%; Score 20; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
| |  
DB 5 KRWL 8

## RESULT 5

G02831 PRELIMINARY; PRT; 8 AA.  
AC G02831;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created;  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Pro alpha 1 type III collagen protein (fragment).  
OS *Oryctolagus cuniculus* (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1];  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96377339; PubMed=8783186;  
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
RA Vuorio E.;  
RT "Evidence for insufficient chondrocytic differentiation during repair  
RT of full-thickness defects of articular cartilage."  
RL Matrix Biol. 15:39-47(1996).  
DR EMBL: S83372; AAC4433.1;  
KW Collagen.  
FT NON-TER 1  
SQ SEQUENCE 8 AA; 1028 MW; B859C727EA77371 CRC64;

Query Match 33.3%; Score 19; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

QY 4 HW 5
Db 1 HW 2

RESULT 6
Q94VIC PRELIMINARY; PRT; 9 AA.
AC Q94VIC;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI
OS Varanus giganteus.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
CX NCBI_TaxID=62041;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001);
DR EMBL; AF407498; AAL10048.1; -.
KW Mitochondrion.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1138 MW; 9C4CB7336411A9C1 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 6 WLS 8

RESULT 7
Q94VG5 PRELIMINARY; PRT; 10 AA.
AC Q94VG5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI
OS Varanus griseus griseus.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
CX NCBI_TaxID=169828;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001);
DR EMBL; AF407503; AAL10063.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1219 MW; C97CCB7336411R2 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 6 WLS 8

RESULT 8

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```

Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI
OS Bradypodion tavetanum.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Bradypodion.
CX NCBI_TaxID=179888;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF448733; AAL90472.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1327 MW; 5E2180C733641597 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 2 WLS 4

RESULT 9
Q958J9 PRELIMINARY; PRT; 10 AA.
AC Q958J9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI
OS Rana muscosa.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
CX NCBI_TaxID=162500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184280; PubMed=1285498;
RA Macey S.R., Strasburg J.L., Brissan J.A., Vredenburg V.T.,
RA Jennings M., Larson A.;
RT "Molecular Phylogenetics of Western North American Frogs of the Rana
Mol. Phylogenetic Evol. 13:131-143(2001);
DR EMBL; AF34026; AAK56898.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1335 MW; C0D380C9D371F1A9 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HW 5
Db 5 HW 6

RESULT 10
Q7056C PRELIMINARY; PRT; 10 AA.
ID Q7056C

```

```
AC 076580;
DT C1-AUG-1998 (TrEMBLrel. 07, Created;
DE C1-AUG-1998 (TrEMBLrel. 07, Last sequence update);
GN C1-XAR-2003 (TrEMBLrel. 20, Last annotation update);
OS Carbonic anhydrase III (Fragment);
OC CA3 OR CAR3 OR CA3;
OX NCBI_TaxID=10390;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=21604134; PubMed=11763242;
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ002785; CAC82977.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;

Query Match 31.6%; Score 19; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KHWLSDRT 10
DB 3 KHWLSDRT 10

RESULT 11
Q937H9 PRELIMINARY; PRT; 9 AA.
AC Q937H9
DT C1-DEC-2001 (TrEMBLrel. 19, Created;
DE C1-DEC-2001 (TrEMBLrel. 19, Last sequence update);
GN Putative transposition protein TniQ (Fragment);
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=CH210; TRANSPOSON=TN5057;
RA Minakhin L.S., Kholodii G.Y., Gortenko Z.M., Minakhina S.V.,
RA Yurieva O.V., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ002785; CAC82977.1;
FT NON TER 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match 31.6%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9
DB 1 QNDGLSDK 8

RESULT 12
Q937H9 PRELIMINARY; PRT; 9 AA.
AC Q937H9
DT C1-DEC-2001 (TrEMBLrel. 19, Created;
DE C1-DEC-2001 (TrEMBLrel. 19, Last sequence update);
GN Putative transposition protein TniQ (Fragment);
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=CH210; TRANSPOSON=TN5057;
RA Minakhin L.S., Kholodii G.Y., Gortenko Z.M., Minakhina S.V.,
RA Yurieva O.V., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ002785; CAC82977.1;
FT NON TER 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match 31.6%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9
DB 1 QNDGLSDK 8
```

```
DT 01-XAR-2002 (TrEMBLrel. 20, Last annotation update);
DE Putative TniQ protein (Fragment);
GN TniQ;
OS Enterobacter sp. CH2-4;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=143777;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=CH2-4; TRANSPOSON=TN5057v1;
RA Minakhin L.S., Kholodii G.Y., Gortenko Z.M., Minakhina S.V.,
RA Yurieva O.V., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ291727; CAC83017.1;
FT NON TER 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9
DB 1 QNDGLSDK 8

RESULT 13
Q937H9 PRELIMINARY; PRT; 10 AA.
AC Q937H9
DT C1-DEC-2001 (TrEMBLrel. 19, Created;
DE C1-DEC-2001 (TrEMBLrel. 19, Last sequence update);
GN Putative transposition protein TniQ (Fragment);
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=48296;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=YM0160; TRANSPOSON=class 1 integron;
RA Yum J.H., Yong E., Lee K., Chong Y., Livermore D.M.;
RT "A 2.2 kb beta-lactamase gene containing integron in an
RT Acinetobacter (possible) genomespecies 3) clinical isolate.";
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169871; AA054205.1;
FT NON TER 10
SQ SEQUENCE 10 AA; 1178 MW; 25287BC729C73378 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6
DB 2 KHWL 5

RESULT 14
Q79915 PRELIMINARY; PRT; 10 AA.
AC Q79915
DT 01-NOV-1998 (TrEMBLrel. 08, Created;
DE 01-NOV-1998 (TrEMBLrel. 08, Last sequence update);
GN Cytochrome c oxidase subunit I (fragment);
OS Leptotrichia bellicosa.
```

OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leiolepidinae;  
OC Leiolepis.  
OX NCBI\_TaxID=52196;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97115309; PubMed=9169559;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.D.;  
RT "Evolutionary shifts in three major structural features of the  
RT Mitochondria: genome among iguanian lizards";  
RL J. Mol. Evol. 44:650-674(1997);  
DR EMBL: U82689; AAC62287.1;  
KW Mitochondrion.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA: 1297 MW: 1A358C73364:400 CRGG;  
  
Query Match 31.6% Score 18; DP 8; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 3; Gaps 0;  
  
QY 1 SQHWL 6  
QB 2 SIRRWL 7  
  
RESULT 15  
Q8SHG2 PRELIMINARY; PRT, 10 AA.  
AC Q8SHG2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
ST 01-JUN-2002 (TrEMBLrel. 21, Last sequence update);  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Chamaeleo jacksonii.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=116114;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Townsend T.M., Larson A.B.;  
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the  
RT Chamaeleonidae (Reptilia, Squamata)";  
RL Submitted (NCV-2001) to the EMBL/GenBank/CCDB data bases  
DR EMBL: AF448753; AAJ90541.1;  
KW Mitochondrion.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA: 1368 MW: C7218C71364:36 S 3.4;  
  
Query Match 31.6% Score 18; DP 8; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 3; Gaps 0;  
  
QY 2 QXHWL 6  
QB 3 QLAWL 7

Search completed: November 5, 2003, 17:34:16  
Job time : 28 secs

GenCore version 5.1.6  
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# OM protein protein search, using sw model

Run on: November 5, 2003, 17:23:00 / Search time 33.3333 Seconds  
(without alignments)  
47.618 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57

Sequence: 1 SQKHWLSDRF:10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 251420

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A: Geneseq\_19Jun03.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
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- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	21	AAB20869 Immunoglobulin E e
2	57	100.0	10	21	AAB25909 Ige C-epsilon-2 do
3	57	100.0	10	22	AAU16634 Peptide P3 derived
4	57	100.0	10	22	AAB51025 Ige peptide #1. M
5	57	100.0	10	23	ABJ09219 Human Ige immunoge
6	48	84.2	8	20	AA42618 Human Ige peptide
7	48	84.2	8	21	AA485217 Human Ige mutant #
8	48	84.2	8	21	AA485250 Human Ige mutant #
9	37	64.9	9	24	AAE35074 Human immunoglobul

10	37	64.9	9	24	ABP96578 Human immunoglobul
11	35	61.4	8	14	AAE33325 Ige Kabat residue
12	35	61.4	9	24	AAE35054 Immunoglobulin E (
13	35	61.4	9	24	AAE35063 Human immunoglobul
14	35	61.4	9	24	ABP96567 Human immunoglobul
15	30	52.6	9	24	ABR18853 Human cancer-relat
16	30	52.6	9	24	ABR19200 Human cancer-relat
17	30	52.6	9	24	ABR19431 Human cancer-relat
18	30	52.6	10	24	ABR18895 Human cancer-relat
19	30	52.6	10	24	ABR18960 Human cancer-relat
20	30	52.6	10	24	ABR19294 Human cancer-relat
21	30	52.6	10	24	ABR19341 Human cancer-relat
22	30	52.6	10	24	ABR19520 Human cancer-relat
23	30	52.6	10	24	ABR19521 Human cancer-relat
24	30	52.6	10	24	ABR19533 Human cancer-relat
25	30	52.6	10	24	ABR19705 Human cancer-relat
26	30	52.6	10	24	ABR19752 Human cancer-relat
27	30	52.6	10	24	ABR19764 Human cancer-relat
28	28	49.1	7	23	AAU81676 Enterokinase recog
29	27	47.4	9	20	AA48076 Immunogenic peptid
30	27	47.4	9	23	AAE31171 Human epi100 peptid
31	27	47.4	9	23	AAE16429 Mouse antibody 2A4
32	27	47.4	9	24	ABP60558 Murine antibody 14
33	27	47.4	9	24	ABP74204 Human GPI00 epitop
34	27	47.4	9	24	ABP74209 Human GPI00 epitop
35	27	47.4	10	16	AA82181 Melanoma-specific
36	27	47.4	10	20	AA47116 Immunogenic peptid
37	27	47.4	10	22	AAB92045 Growth factor pept
38	27	47.4	10	24	ABP74205 Human GPI00 epitop
39	27	47.4	10	24	ABP74210 Human GPI00 epitop
40	26	45.6	5	15	AAE66135 Peptide derived fr
41	26	45.6	7	21	AAE84981 Amino acid sequenc
42	26	45.6	9	22	ABP12734 HIV A02 super moti
43	26	45.6	9	22	ABP15684 HIV A24 super moti
44	26	45.6	9	22	ABP15725 HIV A24 super moti
45	26	45.6	9	22	ABP17169 HIV R27 super moti

## ALIGNMENTS

RESULT 1  
AAB20869  
ID AAB20869 standard; peptide; 10 AA.  
XX AAB20869;  
XX AC  
XX DT 01-JAN-2003 (first entry)  
XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:7.  
DE Immunoglobulin E; Ige; immunogenic; immunogen; Protein D; carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytotoxic; anti-allergic; neurotropic; neuroprotective;  
KW protozoacide; Alzheimer's disease; allergy.  
XX Homo sapiens.  
XX OS  
XX PN WO2000050077-A1.  
XX PD  
XX PF 31-AUG-2000.  
XX PF 22-FEB-2000; 2000WC-EP01457.  
XX PR 25-FEB-1999; 99GB-0004405.  
XX PR 25-FEB-1999; 99GB-0004408.  
XX PR 25-FEB-1999; 99GB-0004412.  
XX PR 13-AUG-1999; 99GB-0019260.  
XX (SMIK ; SMITHKLINE BEECHAM BIOLOGICALS.  
XX Coste M, Lobet Y, Van-Mechelen MP, Verriest C;  
XX

DR WPI; 2000-572040/53.

XX Immunogens and vaccine comprising the immunogen useful for preventing  
XX and treating infectious diseases e.g. malaria and chronic disease e.g.  
XX cancer, comprises peptide and carrier from protein D of influenzae  
XX  
XX Claim 9; Page 37; 53pp; English.

XX The present invention describes an immunogen (I) comprising a peptide  
XX (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae  
XX or its fragment. Also described are: (1) a vaccine comprising (I), and  
XX to protein D or its fragment; and (3) preparation of a vaccine of (I),  
XX comprising formulating (I) with an excipient. (I) has cytostatic,  
XX anti-allergic, nontropic, neuroprotective and procoagulative activities.  
XX (I) and the vaccine are useful for the manufacture of a medicament for  
XX preventing and treating infectious diseases such as malaria or chronic  
XX disease such as cancer, Alzheimer's disease or allergy in a patient.  
XX Unlike prior art immunogens, (I) induces high levels of antipeptide  
XX immune responses while inducing a moderate humoral response against the  
XX carrier. The present sequence represents a specifically claimed  
XX immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can  
XX be used in an immunogen of the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQKHWSJSDRT 10

DB 1 SQKHWSJSDRT 10

RESULT 2

AAB25909

ID AAB25909 standard; Peptide; 10 AA.

AC AAB25909;

DT 05-JAN-2001 (first entry)

DE IgE C-epsilon-2 domain surface exposed epitope peptide P3 SEQ ID NO:3.

XX Epitope; Mimotope; human; immunoglobulin E; IgE C-epsilon-2 domain;  
XX allergic disease; immunophylaxis; immunotherapy; anti-allergic;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.

CS Homo sapiens.

PN WC25050463-A1.

XX 31-AUG-2000.

PF 22-FEB-2000; 2000WO-EP01455.

PR 25-FEB-1999; 93GB-0004405.

PR 29-MAR-1999; 93GB-0007151.

PR 07-MAY-1999; 93GB-0010537.

PR 07-MAY-1999; 93GB-0010538.

PR 07-AUG-1999; 93GB-0018594.

PR 07-AUG-1999; 93GB-0018603.

PR 07-SEP-1999; 93GB-0021046.

PR 07-SEP-1999; 93GB-0021047.

PR 23-OCT-1999; 93GB-0025619.

PR 23-NOV-1999; 93GB-0027698.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEP) PEPTIDE THERAPEUTICS LTD.

PI Dyson M, Friede M, Greenwood J, Hewitt E, Lament A, Mason S;

PI Randall R, Turnell WG, Van Meetele MP, Vinals De Bassols YC,  
XX WPI; 2000-572073/53.

XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.

XX Claim 4; Page 5; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (E) of C-epsilon-2 domain (D) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
XX immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
XX for treating allergies comprising (II); (3) a ligand (IV) capable of  
XX recognising E; (4) a pharmaceutical composition (PC) comprising (IV);  
XX (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
XX (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)  
XX can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (IV) is useful for identifying mimotopes of P1,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (I) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (I), (II) and (III) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQKHWSJSDRT 10

DB 1 SQKHWSJSDRT 10

RESULT 3

AACU16634

ID AACU16634 standard; Peptide; 10 AA.

AC AACU16634;

DT 07-NOV-2001 (first entry)

DE Peptide P3 derived from Cepsilon2 region of human IgE.

XX Human; linkage technology; conjugated compound; carrier vehicle;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.

OS Homo sapiens.

PN WO200145745-A2.

XX 28-JUN-2001.

PF 21-DEC-2000; 2000WO-GB04935.

PR 21-DEC-1999; 99GB-0030233.

PR 22-FEB-2000; 2000GB-0004096.

PR 22-AUG-2000; 2000GB-0020707.

PR 22-AUG-2000; 2000GB-0020708.

XX (ACAM) ACAM-BIS RES LTD.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Flinn N, Johnson T;

DR WPI; 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 XX  
 XX Example 4; Page 21; 48pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides; to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB |||||  
 1 SQKHWSLSDRT 10  
 RESULT 4  
 AAB51025  
 ID AAB51025 standard; Peptide; 10 AA.  
 AC AAB51025;  
 DT 21-MAR-2002 (first entry)  
 XX IGE peptide #3.  
 DE Vaccine; immunoglobulin E; IgE; anti-allergy.  
 KW Mammalia.  
 OS WO2000074716 A2.  
 FN 14-DEC-2000.  
 FD 06-JUN-2000; 2003WO-EP0516A.  
 DF 08-JUN-1999; 93GB-0013327.  
 PR (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Prieels J;  
 XX WPI; 2001-091150/10.  
 XX New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual  
 PT susceptible to an allergic response.  
 XX Claim 5; Page 20; 26pp; English.  
 XX The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is the  
 CC such peptide from IgE. The composition is useful as a vaccine or for

CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB |||||  
 1 SQKHWSLSDRT 10  
 RESULT 5  
 ABJ00219  
 ID ABJ00219 standard; Peptide; 10 AA.  
 AC ABJ00219;  
 DT 02-SEP-2002 (first entry)  
 XX Human IGE immunogenic peptide SEQ ID NO: 3.  
 DE Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; anti-allergic.  
 OS Homo sapiens.  
 PN WO200216403-A2.  
 XX 28-FEB-2002.  
 PD 17-AUG-2001; 2001WO-EP09576.  
 PF 22-AUG-2000; 2000GB-0020717.  
 PR (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
 DR WPI; 2002-489648/52.  
 XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.  
 PS Claim 4; Page 3; 45pp; English.  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB |||||  
 1 SQKHWSLSDRT 10  
 RESULT 6  
 AAY42608  
 ID AAY42608 standard; peptide; 8 AA.  
 XX AAY42608.  
 AC AAY42608.  
 XX

DT 10-JAN-2000 (first entry);  
 XX Human IgE peptide fragment.

DE Immunoglobulin E; IgE; antagonist; FcεpsilonR1 receptor; human; Fcε;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.

XX Homo sapiens.

OS

XX US965709 A.

PN 12-OCT-1999.

XX 21-APR 1994; 94US 0232539.

XX 14-AUG-1991; 91US-0744768.

PR 27-JAN-1994; 94US-0178583.

XX (GETH ) GENENTECH INC.

XX Gardieu PM, Presta LG;

DR WPI; 1999-579541/49.

XX Immunoglobulin E variants as peptide antagonists useful for raising and

PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and

PT purification of FcεpsilonR1 receptor and in the treatment of allergic

PT diseases -

XX Example 1; Column 37-38; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one

CC or more of the FcεpsilonR1 receptor-binding determinant sites of human

CC IgE. The antagonists include IgE variants comprising an immunoglobulin

CC template and binding determinant sequences (bds); CDRs, EFBDs and the

CC sequence shown in AAY42581. The CDRs (CD loop binding determinant

CC sequence) are selected from the sequences shown in AAY42567 Y42577 and

CC the EFBDs (EF loop binding determinant sequence) are selected from

CC sequences shown in AAY42578-Y42580. The variants are useful in raising

CC and screening anti-IgE antibodies, in the isolation and purification of

CC FcεpsilonR1 receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 8 AA:

QY 2 QKHMLSDR 9

DB 1 QKHMLSDR 8

RESULT 7

AAAY85217

ID AAY85217 standard; protein; 8 AA.

XX AAY85217;

XX 29-JUN-2000 (first entry)

XX Human IgE mutant #15 fragment amino acid sequence.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcεL; FcεH;

XX low affinity binding receptor; high affinity binding receptor; allergy;

PD 14-MAR-2000.

XX 06-JUN-1995; 95US-0466151.

XX 15-MAR-1995; 95US-0405617.

PR 14-AUG-1992; 92WO-US06860.

PR 26-JAN-1994; 94US-0185899.

XX (GETH ) GENENTECH INC.

XX Presta LG, Jardieu PM;

PI WPI; 2000-269933/23.

XX New bispecific antibodies, useful for treating immunoglobulin

XX E-mediated disease, binds to IgE, but only when on the low affinity

XX receptor, and to an antigen other than IgE -

XX Example 2; Column 33; 48pp; English.

XX This sequence represents a fragment of an amino acid sequence encoding a

CC mutant human immunoglobulin E (IgE). The mutant IgE is used to test the

CC binding of IgE to its receptors. The invention relates to a bispecific

CC antibody that binds specifically to IgE when IgE is bound to its low

CC affinity receptor (FcεL), but does not bind to IgE. When IgE is bound to

CC its high affinity receptor (FcεH), the bispecific antibody comprises an

CC IgE-binding arm with human framework residues of a recipient human

CC antibody and donor murine CDR (complementarity determining region)

CC residues, but with at least one human CDR residue replacing the analogous

CC murine residue. The antibody also comprises an Fv that is specific for a

CC predetermined antigen other than IgE. The antibodies work by displacing

CC bound IgE from its receptor, or via competitive inhibition of its

CC binding. The bispecific antibodies are used for diagnosis, treatment and

CC prevention of allergy and other IgE-mediated diseases, also, when

CC immobilised for the isolation of FcεL from cells (for research or

CC therapy). The bispecific antibodies of the invention do not cause

CC granulation or release of histamine from mast cells.

XX Sequence 8 AA:

QY 2 QKHMLSDR 9

DB 1 QKHMLSDR 8

RESULT 8

AAAY85250

ID AAY85250 standard; peptide; 8 AA.

XX AAY85250;

XX 29-JUN-2000 (first entry)

XX Human IgE mutant #31 fragment amino acid sequence.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcεL; FcεH;

XX low affinity binding receptor; high affinity binding receptor; allergy;

DT 10-JAN-2000 (first entry);  
 XX Human IgE peptide fragment.

DE Immunoglobulin E; IgE; antagonist; FcεpsilonR1 receptor; human; Fcε;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.

XX Homo sapiens.

OS

XX US965709 A.

PN 12-OCT-1999.

XX 21-APR 1994; 94US 0232539.

XX 14-AUG-1991; 91US-0744768.

PR 27-JAN-1994; 94US-0178583.

XX (GETH ) GENENTECH INC.

XX Gardieu PM, Presta LG;

DR WPI; 1999-579541/49.

XX Immunoglobulin E variants as peptide antagonists useful for raising and

PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and

PT purification of FcεpsilonR1 receptor and in the treatment of allergic

PT diseases -

XX Example 1; Column 37-38; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one

CC or more of the FcεpsilonR1 receptor-binding determinant sites of human

CC IgE. The antagonists include IgE variants comprising an immunoglobulin

CC template and binding determinant sequences (bds); CDRs, EFBDs and the

CC sequence shown in AAY42581. The CDRs (CD loop binding determinant

CC sequence) are selected from the sequences shown in AAY42567 Y42577 and

CC the EFBDs (EF loop binding determinant sequence) are selected from

CC sequences shown in AAY42578-Y42580. The variants are useful in raising

CC and screening anti-IgE antibodies, in the isolation and purification of

CC FcεpsilonR1 receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 8 AA:

QY 2 QKHMLSDR 9

DB 1 QKHMLSDR 8

RESULT 7

AAAY85217

ID AAY85217 standard; protein; 8 AA.

XX AAY85217;

XX 29-JUN-2000 (first entry)

XX Human IgE mutant #15 fragment amino acid sequence.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcεL; FcεH;

XX low affinity binding receptor; high affinity binding receptor; allergy;

PR 26-JAN-1994; 94US-0185899.  
 XX (GETH) GENENTECH INC.  
 PA  
 PT Presta LG, Jardieu PX;  
 PI  
 XX WPI; 2800-269913/23.  
 DR  
 XX New bispecific antibodies, useful for treating immunoglobulin  
 PT E-mediated disease, binds to IgE, but only when on the low affinity  
 PT receptor, and to an antigen other than IgE.  
 PT  
 PS Example 5; Column 43; 49pp; English.  
 XX  
 CC This sequence represents a fragment of an amino acid sequence encoding a  
 CC mutant human immunoglobulin E (IgE). The mutant IgE is used to test the  
 CC binding of the anti-IgE antibodies of the invention. The invention  
 CC relates to a bispecific antibody that binds specifically to IgE when IgE  
 CC is bound to its low affinity receptor (FcεR1), but does not bind to IgE,  
 CC when IgE is bound to its high affinity receptor (FcεR2). The bispecific  
 CC antibody comprises an IgE-binding arm with human framework residues of a  
 CC recipient human antibody and donor murine CDR (complementarity  
 CC determining region) residues, but with at least one human CDR residue  
 CC replacing the analogous murine residue. The antibody also comprises an Fc  
 CC that is specific for a predetermined antigen other than IgE. The  
 CC antibodies work by displacing bound IgE from its receptor, or via  
 CC competitive inhibition of its binding. The bispecific antibodies are used  
 CC for diagnosis, treatment and prevention of allergy and other IgE-mediated  
 CC diseases, also, when immobilized, for the isolation of FcεR1 from cells  
 CC (for research or therapy). The bispecific antibodies of the invention do  
 CC not cause granulation or release of histamine from mast cells.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 84.2%; Score 48; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QKHWSLR 9  
 Db 1 QKHWSLR 8  
 |||||  
 |||||  
 RESULT 9  
 AAE35074 standard; peptide; 9 AA.  
 ID AAE35074  
 AC AAE35074;  
 XX  
 DT 25-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E (IgE) HLA A2 peptide binding motif  
 XX  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KW transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200292773-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 FF 13-MAY-2002; 2002WO-US15341.  
 XX  
 PR 15-MAY-2001; 2001US-291300P.  
 XX  
 PA (CRTH) CRTHO-MCNEL PHARM INC.  
 XX  
 PI Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Leqraw J;

XX WPI; 2003-120673/11.  
 XX  
 PT Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T the cell  
 PT epitopes.  
 XX  
 PS Example 3; Column 47; 49pp; English.  
 XX  
 CC The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 64.9%; Score 37; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWL 6  
 Db 4 SQKHWL 9  
 |||||  
 |||||  
 RESULT 10  
 ABP96578 standard; peptide; 9 AA.  
 ID ABP96578  
 AC ABP96578;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E related peptide SEQ ID NO:17.  
 XX  
 KW Immune response; IgE; cytotoxic T lymphocyte response;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US26986.  
 XX  
 PR 13-AUG-2001; 2001US-312120P.  
 XX  
 PA (IGET-) IGE THERAPEUTICS INC.  
 XX  
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 XX WPI; 2003-268242/26.  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE



PT peptides naturally presented by major histocompatibility complex class  
 PT I protein  
 XX  
 TS Example 5; Page 70; 187pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T1) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T1) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I1) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I1); and  
 CC (C3) comprising antigen-presenting cells that recognize at least one (I1).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides, C1-3 have anti-allergic, anti-asthmatic, immunosuppressive,  
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis), and urticaria  
 CC hives). The present sequence represents a peptide which is used in an  
 CC example from the present invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 64.9%; Score 37; DB 24; Length 8;  
 ID AAE33054 standard; peptide; 9 AA.  
 Best Local Similarity 120.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQRWLSDR 6  
 |||||  
 Db 4 QKRWLSDR 9

RESULT 11  
 AAE33325  
 ID AAE33325 standard; peptide; 8 AA.  
 AC AAE33325;  
 DE 25-MAR-2003 (updated);  
 DT 05-JUL-1993 (first entry);  
 XX  
 XX IgE Kibab residue no. 329-336.  
 XX  
 XX High affinity; FCEH; low affinity; FCEH; Padlan;  
 KW IgE receptor; Fc; IgG1.  
 XX  
 XX Homo sapiens.  
 CS  
 XX WC9304173-A1.  
 PN  
 XX C4-MAR-1993.  
 PC  
 XX 14-AUG-1992; 92WO-006860.  
 PF  
 XX 14-AUG-1991; 91US-0744768.  
 PR 07-MAY-1992; 92US-0879495.  
 XX  
 XX (GETH) GENENTECH INC.  
 PA  
 XX Jardieu PX; Presta LG;  
 PT WPI; 1993-094024/11.  
 XX  
 XX Polypeptide(s) binding to specific Fc epsilon receptors act as

PT IgE antagonists; useful for treating and preventing IgE-mediated  
 PT disorders e.g. allergies  
 XX  
 PS Disclosure; Page 57; 113pp; English.  
 XX  
 CC Based on the model of IgE Fc by Padlan & Davies (Mol. Immun.,  
 CC 23:1063-1075 (1986)), which is based on the crystal structure of  
 CC human IgG1Fc (Deisenhofer, Biochem. 20:2361-2370 (1981)), a series  
 CC of mutants were designed which could be used to test the binding of  
 CC human IgE to its receptors. These mutants are designated Emut 1-13.  
 CC The sequence of AAE33325 (amino acids 329-336 of IgE - numbering  
 CC according to Kabat) was replaced by the sequence of AAE33326 to give  
 CC mutant 13. Mutant 13 shows +ve and +ve binding to Fc epsilon RI.  
 CC The mutant IgEs were transiently expressed in human kidney 293 cells,  
 CC purified on a mouse anti-human IgE antibody affinity column and samples  
 CC run using SDS-PAGE to ascertain that the mutant proteins were of the  
 CC proper mol. wt.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 8 AA;  
 Query Match 61.4%; Score 35; DB 14; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKRWLSDR 9  
 |||||  
 Db 1 QKRWLSDR 8

RESULT 12  
 AAE33054  
 ID AAE33054 standard; peptide; 9 AA.  
 AC AAE33054;  
 DE 28-MAY-2003 (first entry);  
 XX  
 XX Immunoglobulin E (IgE) antigenic peptide, IgE 185.  
 XX  
 XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KW transplant rejection; immunoglobulin 5; IgE; antigen.  
 XX  
 XX Unidentified.  
 OS  
 XX WC200292773-A2.  
 PN  
 XX 21-NOV-2002.  
 PD  
 XX 13-MAY-2002; 2002WC-US15341.  
 PF  
 XX 15-MAY-2001; 2001US-29130CP.  
 PR  
 XX (ORTH) ORTHO-MCNEIL PHARM INC.  
 XX  
 XX Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;  
 PI  
 XX WPI; 2003-120673/11.  
 DR  
 XX

PT Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T cell  
 PT epitopes  
 XX  
 XX Example 4; Column 52; 49pp; English.  
 PS  
 XX The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class

CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is immunoglobulin E (IgE) antigenic peptide.  
 CC This peptide is used in the exemplification of the invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 WLSRDT 10  
 Db 1 WLSRDT 6  
 |||||

RESULT 13  
 AAE35063  
 ID AAE35063 standard; peptide; 9 AA.  
 XX AAE35063;  
 AC  
 XX  
 DT 28-MAY-2003 (first entry)  
 DE Human immunoglobulin E (IgE) HLA-A2 peptide motif #1.  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KW transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200292773-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 13-MAY-2002; 2002WO-US:5341.  
 XX  
 PR 15-MAY-2001; 2001US-29:300P.  
 XX  
 PA (CITE) ORTHO-McNEIL PHARM INC.  
 XX  
 PI Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Legraw G;  
 XX  
 DR WPI; 2003-123673/11.  
 XX  
 PT Producing cytotoxic T lymphocytes for treating end. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T the cell  
 PT epitopes -  
 XX  
 PS Example 3; Column 47; 49pp; English.  
 XX  
 CC The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes.  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic

CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 WLSRDT 10  
 Db 1 WLSRDT 6  
 |||||

RESULT 14  
 ABP96567  
 ID ABP96567 standard; peptide; 9 AA.  
 XX ABP96567;  
 AC  
 XX  
 DT 28-MAY-2003 (first entry)  
 DE Human immunoglobulin E related peptide SEQ ID NO:6.  
 XX  
 KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Homo sapiens.  
 CS Synthetic.  
 XX  
 PN WO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US26986.  
 XX  
 PR 13-AUG-2001; 2001US-312120P.  
 XX  
 PA (IGET-) IGE THERAPEUTICS INC.  
 XX  
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 XX  
 DR WPI; 2003-268242/26.  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class  
 PT I protein -  
 XX  
 PS Example 5; Page 70; 187pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in

CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and uterine  
 CC cramps). The present sequence represents a peptide which is used in an  
 CC example from the present invention.

SQ Sequence 9 AA;

Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLSRDT 10  
 |||||  
 DB : WLSRDT 6

RESULT 15

ABR18853  
 ID ABR18853 standard; Peptide; 9 AA.

XX ABR18853;

DT 19 MAY-2003 (first entry)

DE Human cancer-related protein 184P1310 HLA peptide #48.

KW Human; Cytostatic; vaccine; cancer; immune response; HLA;

KX human leukocyte antigen.

CS Homo sapiens.

PN WC200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.

PR 10-APR-2002; 2001US-282739P.

PR 10-APR-2002; 2001US-283112P.

XX 25-APR-2002; 2001US-286630P.

PA (AGN-); AGENSYS INC.

PI Jakobovits A, Chailita-Eid PM, Faris M, Ge W, Hahnel PS;

PI Morrison K, Morrison RK, Raitano AB;

XX WP; 2003 075555/07.

PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients.

PS Claim 13; Page 304; 1021pp; English.

XX The present invention relates to novel human cancer related genes and  
 CC proteins (AB278120-AB278168 and ABR01799-ABR01861); the genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

SQ Sequence 9 AA;  
 Query Match 52.6%; Score 30; DB 24; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 HWLSD 8  
 |||||  
 DB 4 HWLSD 8

Search completed: November 5, 2003, 17:32:29  
 Job time : 34.3333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: November 5, 2003, 17:34:46 / Search time 21 Seconds  
without alignment  
at 785 Million cell updates/sec

Title: US-09-914-088-3  
Perfect score: 57  
Sequence: 1 QKHWLSDR 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 81926

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUSCOMB.pep.
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUSCOMB.pep.
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.
- 6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUSCOMB.pep.
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.
- 8: /cgn2\_6/ptodata/2/pubaa/US09\_PUSCOMB.pep.
- 9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUSCOMB.pep.
- 10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUSCOMB.pep.
- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUSCOMB.pep.
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUSCOMB.pep.
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUSCOMB.pep.
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUSCOMB.pep.
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.
- 17: /cgn2\_6/ptodata/2/pubaa/US0C\_NEW\_PUB.pep.
- 18: /cgn2\_6/ptodata/2/pubaa/US06\_PUB.pep.

Pred. No. is the number of results predicted by a model to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	48	84.2	8	9 US-09-802-077-24	Sequence 24, Appl
2	48	84.2	8	9 US-09-802-077-57	Sequence 57, Appl
3	48	84.2	8	9 US-09-802-077-24	Sequence 24, Appl
4	48	84.2	8	9 US-09-802-077-57	Sequence 57, Appl
5	48	84.2	8	11 US-09-925-179-24	Sequence 24, Appl
6	48	84.2	8	11 US-09-925-179-57	Sequence 57, Appl
7	37	64.9	9	15 US-10-214-524-17	Sequence 17, Appl
8	35	61.4	9	12 US-10-144-588-52	Sequence 52, Appl
9	35	61.4	9	15 US-10-214-524-17	Sequence 6, Appl
10	28	49.1	7	10 US-09-884-767A-14	Sequence 143, App
11	26	45.6	7	12 US-10-285-457-40	Sequence 43, Appl
12	26	45.6	10	10 US-09-751-378-455	Sequence 455, App
13	26	45.6	10	10 US-09-851-138-193	Sequence 193, App
14	25	43.9	9	15 US-10-351-644-9	Sequence 9, Appl
15	24	42.1	5	9 US-09-817-661-34	Sequence 34, Appl

16	24	42.1	7	12	US-10-193-764-20	Sequence 20, Appl
17	24	42.1	8	9	US-09-848-164-78	Sequence 78, Appl
18	24	42.1	8	9	US-09-848-164-86	Sequence 86, Appl
19	24	42.1	8	10	US-09-900-379-78	Sequence 78, Appl
20	24	42.1	8	10	US-09-900-379-86	Sequence 86, Appl
21	24	42.1	9	12	US-10-177-725-110	Sequence 110, App
22	24	42.1	9	12	US-10-221-984-4	Sequence 4, Appl
23	24	42.1	9	12	US-10-286-457-440	Sequence 440, App
24	24	42.1	9	12	US-10-144-188-53	Sequence 53, Appl
25	24	42.1	10	12	US-10-190-082-565	Sequence 565, App
26	24	42.1	10	12	US-10-353-929-142	Sequence 142, App
27	24	42.1	10	12	US-10-353-929-154	Sequence 154, App
28	24	42.1	10	12	US-10-200-708-260	Sequence 260, App
29	24	42.1	10	14	US-10-054-552-2	Sequence 2, Appl
30	23	40.4	5	12	US-10-205-110-42	Sequence 42, Appl
31	23	40.4	6	9	US-09-735-995-102	Sequence 102, App
32	23	40.4	6	9	US-09-735-995-103	Sequence 103, App
33	23	40.4	6	9	US-09-735-995-106	Sequence 106, App
34	23	40.4	6	9	US-09-735-995-107	Sequence 107, App
35	23	40.4	7	10	US-09-884-767A-15	Sequence 15, Appl
36	23	40.4	7	12	US-10-052-578-167	Sequence 167, App
37	23	40.4	7	12	US-10-205-110-43	Sequence 43, Appl
38	23	40.4	7	12	US-10-193-082-476	Sequence 476, App
39	23	40.4	7	12	US-10-053-520-167	Sequence 167, App
40	23	40.4	7	12	US-10-053-498B-167	Sequence 167, App
41	23	40.4	8	12	US-10-044-896-12	Sequence 12, Appl
42	23	40.4	8	15	US-10-193-768-21	Sequence 21, Appl
43	23	40.4	9	9	US-09-765-527-200	Sequence 200, App
44	23	40.4	9	9	US-09-881-490-168	Sequence 168, App
45	23	40.4	9	12	US-10-205-110-27	Sequence 27, Appl

## ALIGNMENTS

RESULT 1  
US-09-802-077-24  
; Sequence 24, Application US/09802077  
; Patent No. US20010033842A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardiou, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C2US  
; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 24  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-077-24

Query Match 84.2% Score 48; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QKHWLSDR 9  
Db 1 QKHWLSDR 9

RESULT 2

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US-09-802-096-57
; Sequence 57, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-57

Query Match      84.2%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      2 QKHWSLDR 9
DB      1 QKHWSLDR 8

RESULT 3
US-09-802-096-57
; Sequence 57, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-57

Query Match      84.2%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      2 QKHWSLDR 9
DB      1 QKHWSLDR 8

US-09-802-096-57
; Sequence 57, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-04-08
; PRIOR APPLICATION NUMBER: US 08/465,163
; PRIOR FILING DATE: 1995-06-04
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-179-24

Query Match      84.2%; Score 48; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      2 QKHWSLDR 9
DB      1 QKHWSLDR 9

US-09-925-179-24
; Sequence 24, Application US/09925179
; Publication No. US20010044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-04-08
; PRIOR APPLICATION NUMBER: US 08/465,163
; PRIOR FILING DATE: 1995-06-04
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-179-24

Query Match      84.2%; Score 48; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      2 QKHWSLDR 9
DB      1 QKHWSLDR 9
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Db      2 QKHWLSDR 8

RESULT 6
US-09-925-179-57
; Sequence 57, Application US/09925179
; Publication No. US20030044958A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1JS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/0696C
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-179-57

Query Match      84.2%; Score 46; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2 QKHWLSDR 9
Db      1 QKHWLSDR 8

RESULT 7
US-10-214-524-17
; Sequence 17, Application US/0214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-17

Query Match      64.9%; Score 37; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SCXHWL 6
Db      4 SCXHWL 9

RESULT 8
US-10-144-188-52
; Sequence 52, Application US/10144188
; Publication No. US20030170212A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Shi, Weixing
; APPLICANT: Kong, Yan
; APPLICANT: Degraw, Juli
; TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific
; FILE REFERENCE: P10010 ORT-1627
; CURRENT APPLICATION NUMBER: US/10/144,188
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/291,300
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144-188-52

Query Match      61.4%; Score 35; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 WLSDR 10
Db      1 WLSDR 6

RESULT 9
US-10-214-524-6
; Sequence 6, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-6

Query Match      61.4%; Score 35; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 WLSDR 10
Db      1 WLSDR 6

RESULT 10
US-C9-884-767A-43
; Sequence 43, Application US/09984767A
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Publication No. US20020192789A1  
GENERAL INFORMATION:  
APPLICANT: DVAX Corp.  
APPLICANT: Jey, Arthur C.  
APPLICANT: Lunau, Christopher J.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: NOVEL ENZYMOLOGICAL SEQUENCES  
FILE REFERENCE: DEX-012.1 US, DEX-012.1 PCT  
CURRENT APPLICATION NUMBER: US/09/884,767A  
CURRENT FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 09/597,321  
PRIOR FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 143  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US 09-884 767A-143

Query Match 49.1%; Score 28; DB 10; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5; 0; 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLSUR 9  
| | |  
Cb 2 WLSUR 6

RESULT 11  
US-10-286-457-40  
Sequence 40, Application US/10286457  
Publication No. US2003016604A;  
GENERAL INFORMATION:  
APPLICANT: JENC GYRIS et al.  
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
FILE REFERENCE: GPCI-P01-178  
CURRENT APPLICATION NUMBER: US/10/284,457  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: 60/334822  
PRIOR FILING DATE: 2001-11-01  
NUMBER OF SEQ ID NOS: 684  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 40  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: artificial sequences designed to bind to endothelial cells  
US-10-286-457-40

Query Match 45.6%; Score 26; DB 12; Length 7;  
Best Local Similarity 66.7%; Pred. No. 5; 0; 0;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HWLSUR 9  
| | |  
Cb 2 HWASPR 7

RESULT 12  
US-09-791-378-455  
Sequence 455, Application US/09791378  
Patent No. US20020142303A1  
GENERAL INFORMATION:  
APPLICANT: Parekh, Rajesh  
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
FILE REFERENCE: SCHIZOPHRENIA  
CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/750,395  
PRIOR FILING DATE: 2000-12-28  
NUMBER OF SEQ ID NOS: 677  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-791-378-455

Query Match 45.6%; Score 26; DB 10; Length 10;  
Best Local Similarity 62.5%; Pred. No. 5; 0; 0;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXWLSUR 9  
| | |  
Cb 3 QYHYLLOR 10

RESULT 13  
US-09-851-138-193  
Sequence 193, Application US/09851138  
Publication No. US20020193508A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
STUYVER, LIEVEN  
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
AGENTS  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6.0 / ASCII text output  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,138  
FILING DATE: 09-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,075  
FILING DATE: <UNKNOWN>  
APPLICATION NUMBER: EP 94870166.9  
FILING DATE: 21 Oct 1994  
APPLICATION NUMBER: EP 95870076.7  
FILING DATE: 28 Jun 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KAMMERER, PATRICIA A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: INNS:004  
INFORMATION FOR SEQ ID NO: 193:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 193:  
US-09-851-138-193

Query Match 45.6%; Score 26; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 5; 0; 0;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOKHW 5  
| | |  
Cb 2 SRRHW 6

Search completed: November 5, 2003, 17:46:07  
Job time : 22 secs

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RESULT 14
US-10-301-644-9
; Sequence 9, Application US/0301644
; Publication No. US2003012413A1
; GENERAL INFORMATION:
; APPLICANT: Phalipot, Armelle
; APPLICANT: Sansonetti, Philippe
; APPLICANT: Felici, Franco
; APPLICANT: Cortese, Riccardo
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDES THAT MIMIC A SURFACE
; TITLE OF INVENTION: POLYSACCHARIDE ANTIGEN OF A PATHOGENIC MICROORGANISM,
; TITLE OF INVENTION: METHOD FOR OBTAINING THE SAME, AND THEIR USE IN VACCINE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 03495-0176
; CURRENT APPLICATION NUMBER: US/10/301,644
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/057,906
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide used to induce an immune response against
; OTHER INFORMATION: pathogenic microorganisms
US-10-301-644-9

```

```

Query Match 43.9%; Score 25; DB 15; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 QKHWLSDR 9
Db 1 KRHFSLQR 8

```

```

RESULT 15
US-09-917-661-34
; Sequence 34, Application US/09917661
; Patent No. US20020276692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane
; APPLICANT: Holst, Thor
; TITLE OF INVENTION: Improvements to ribosome display
; FILE REFERENCE: 84633
; CURRENT APPLICATION NUMBER: US/09/917,661
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/193,822
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutagenized
; OTHER INFORMATION: sequence
US-09-917-661-34

```

```

Query Match 42.1%; Score 24; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 HWLSD 8
Db 1 HWQTD 5

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:30:40 ; Search time 12.333 Seconds  
(without alignments)  
34.396 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57

Sequence: 1 SQKWLSDRT 10

Scoring table: E-OSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 10058

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pept.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pept.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pept.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pept.\*
- 5: /cgn2\_6/ptodata/1/1aa/7CUS.COMB.pept.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfltest.pept.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	84.2	8	2	US-08-232-539D-42
2	48	84.2	8	2	US-08-469-141A-16
3	48	84.2	8	3	US-08-469-141A-60
4	48	84.2	8	3	US-09-104-337A-353
5	48	84.2	8	4	US-09-626-581D-59
6	48	84.2	8	4	US-09-415-765B-59
7	26	45.6	10	3	US-08-469-141A-60
8	25	43.9	8	2	US-08-816-075A-153
9	25	43.9	9	4	US-09-144-283-9
10	24	42.1	4	3	US-08-924-446A-10
11	24	42.1	5	1	US-07-973-235A-19
12	24	42.1	5	2	US-08-469-141A-62
13	24	42.1	6	1	US-08-489-006-63
14	24	42.1	6	2	US-08-488-659A-67
15	24	42.1	6	4	US-08-877-605-172
16	24	42.1	7	3	US-08-469-141A-62
17	24	42.1	7	4	US-09-206-942-23
18	24	42.1	7	5	PCT-US95-13794-62
19	24	42.1	8	2	US-08-596-387B-78
20	24	42.1	8	2	US-08-596-387B-78
21	24	42.1	8	3	US-08-596-387B-78
22	24	42.1	8	4	US-09-067-615-39
23	24	42.1	8	4	US-09-067-615-39
24	24	42.1	8	4	PCT-US95-09816A-78
25	24	42.1	8	5	PCT-US95-09816A-78
26	24	42.1	8	5	PCT-US95-13794-61
27	24	42.1	9	2	US-08-350-262A-153

Sequence 3, Appli  
Sequence 60, Appli  
Sequence 353, App  
Sequence 59, Appl  
Sequence 59, Appl  
Sequence 59, Appl  
Sequence 3, Appli  
Sequence 60, Appli  
Sequence 2, Appli  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 160, App  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 67, Appl  
Sequence 68, Appl  
Sequence 71, Appl  
Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-08-232-539D-42  
; Sequence 42, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula N.  
; TITLE OF INVENTION: Ige Antagonists  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.539D  
; FILING DATE: 31-Apr-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179583  
; FILING DATE: 07-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: PCT:8P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-232-539D-42

Query Match 84.2% Score 48; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 CQKWLSDR 9

```

DB      1 CKHWLSR 8
US-08-464-025A-16
RESULT 2
US-08-464-025A-16
Sequence 16, Application US/08464025A
Patent No. 5994314
GENERAL INFORMATION:
APPLICANT: Cardieu et al.
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464-025A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P371B-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-464-025A-16
Query Match          84.2%; Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      2 CKHWLSR 9
DB      1 CKHWLSR 8
US-08-466-151-57
RESULT 3
US-08-466-151-57
Sequence 24, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466-151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-163B-57

```

```

Query Match      84.2%, Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

```

```

RESULT 5
US-08-466-163B-24
; Sequence 24, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466-163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-24

```

```

Query Match      84.2%, Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

```

```

RESULT 6
US-08-466-163B-57
; Sequence 57, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1

```

```

; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-57

```

```

Query Match      84.2%, Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

```

```

RESULT 7
US-08-836-075A-193
; Sequence 193, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & BURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04:55
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-193

```

Query Match 45.6%; Score 26; DB 3; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 SOKHW 5  
DB 2 SHRW 6

RESULT 8  
US-08-669-284B-20  
; Sequence 20, Application US/08669284B  
; Patent No. 5939534  
; GENERAL INFORMATION:  
; APPLICANT: Iroue, Makoto  
; APPLICANT: Kikuchi, Kaoru  
; APPLICANT: Ishige, Yoko  
; APPLICANT: Ito, Akira  
; APPLICANT: Kimura, Toru  
; APPLICANT: Nakayama, Chikao  
; APPLICANT: No. 5939534uchi, Hiroshi  
; TITLE OF INVENTION: NOVEL HUMAN CELLULAR NEUROTROPIC FACTORS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.10  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,284B  
; FILING DATE: 28-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/02269  
; FILING DATE: 27-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-268281  
; FILING DATE: 05-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-261564  
; FILING DATE: 02-AUG-1994  
; APPLICATION NUMBER: JP 05-150344  
; FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Dean H.  
; REGISTRATION NUMBER: 33,981  
; REFERENCE/DOCKET NUMBER: G-42041  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-669-284B-20

Query Match 43.9%; Score 25; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 5 WLSDR 10  
DB 2 WLDXT 7

RESULT 9  
US-09-144-280-9  
; Sequence 9, Application US/09144280A  
; Patent No. 6528061  
; GENERAL INFORMATION:  
; APPLICANT: Phalipon, Armelle  
; APPLICANT: Sansonetti, Philippe  
; APPLICANT: Felici, Franco  
; APPLICANT: Cortese, Riccardo  
; APPLICANT: Kraehenbuhl, Jean-Pierre  
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDES THAT MIMIC A SURFACE  
; TITLE OF INVENTION: POLYSACCHARIDE ANTIGEN OF A PATHOGENIC MICROORGANISM,  
; TITLE OF INVENTION: METHOD FOR OBTAINING THE SAME, AND THEIR USE IN VACCINE  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 03495-0176  
; CURRENT APPLICATION NUMBER: US/09/144,280A  
; CURRENT FILING DATE: 1998-08-31  
; EARLIER APPLICATION NUMBER: 60/057,906  
; EARLIER FILING DATE: 1997-09-04  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide used to induce an immune response against  
; OTHER INFORMATION: pathogenic microorganisms  
US-09-144-280-9

Query Match 43.9%; Score 25; DB 4; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 2 QKHWLSDR 9  
DB 1 KRHFLSOR 8

RESULT 10  
US-08-904-446A-10  
; Sequence 10, Application US/08904446A  
; Patent No. 6029114  
; GENERAL INFORMATION:  
; APPLICANT: Sharovsky, Igor L.  
; APPLICANT: Ross, Gregory M.  
; APPLICANT: Riopelle, Richard J.  
; APPLICANT: Weaver, Donald F.  
; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor  
; TITLE OF INVENTION: Binding  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dowell & Dowell, P.C.  
; STREET: 1215 Jefferson Davis Highway, Suite 309  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/904,446A  
; FILING DATE: 31-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9616105.4  
; FILING DATE: 31-JUL-1996  
; ATTORNEY/AGENT INFORMATION:

NAME: RALPH A. DOWELL  
REGISTRATION NUMBER: 26868  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 415-2555  
TELEFAX: (703) 415-2559  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURES:  
NAME/KEY: Peptide  
LOCATION: 1..4  
OTHER INFORMATION: /note= "Residues 74-77 of human NGF, mouse NGF or delta 3 9 mutant of mouse NGF"  
US-09-914-446A-10

Query Match 42.1%; Score 24; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
|||  
DB 1 KHW 3

RESULT 1:  
US-07-973-235A-19  
Sequence 19, Application US/07973235A  
Patent No. 5491130  
GENERAL INFORMATION:  
APPLICANT: David D. Roberts, et al.  
TITLE OF INVENTION: Peptide Inhibitors of Fibrinectin and  
TITLE OF INVENTION: Related Collagen-Binding Proteins  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect, Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/973-235A  
FILING DATE: 19921110  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert L. Price  
REGISTRATION NUMBER: 22,685  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 684-1111  
TELEFAX: (703) 684-1124  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACIDS  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-973-235A-19

Query Match 42.1%; Score 24; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5

DB 3 KHW 5  
|||

RESULT 12  
US-08-462-720-19  
Sequence 19, Application US/08462720  
Patent No. 5849761  
GENERAL INFORMATION:  
APPLICANT: Roberts, David D.  
APPLICANT: Kruttsch, Henry C.  
APPLICANT: Sipes, John M.  
APPLICANT: Gao, Neng-hua  
APPLICANT: Nesre, Eric  
TITLE OF INVENTION: Peptide Inhibitors of Fibrinectin and  
TITLE OF INVENTION: Related Collagen-Binding Proteins  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In. Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,720  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 015280-023110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2430  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-720-19

Query Match 42.1%; Score 24; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
|||  
DB 3 KHW 5

RESULT 13  
US-08-487-006-67  
Sequence 67, Application US/08487006  
Patent No. 5641861  
GENERAL INFORMATION:  
APPLICANT: Dooley, Colette I.  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: No. 5641861; Mu Opioid Receptor Ligands:  
TITLE OF INVENTION: Agonists and Antagonists  
NUMBER OF SEQUENCES: 222  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California

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1 COUNTRY: USA
2 ZIP: 92122
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: PatentIn Release #1.0, Version #1.25
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/487,066
12 FILING DATE: 07-JUN-1995
13 CLASSIFICATION: 530
14
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Campbell, Cathryn A.
17 REGISTRATION NUMBER: 31,815
18 REFERENCE/DOCKET NUMBER: P-TP 1706
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (619) 535-9001
21 TELEFAX: (619) 535-8949
22
23 INFORMATION FOR SEQ ID NO: 67:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 6 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 FEATURE:
30 NAME/KEY: Peptide
31 LOCATION: 6
32
33 OTHER INFORMATION: /note= "Amino acid is amidated at
34 the C-terminal."
35
36 US-08 487-066-67
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GenCore version 5.1.6  
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OM protein: protein search, using sw model

Run on: November 5, 2003, 17:29:45 ; Search time 11 seconds  
(without alignment)  
27,426 Million cell updates/sec

Title: US-09 914-088-4  
Perfect score: 55  
Sequence: 1 GHTFEDSTKK 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 293308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 1100  
Minimum DB seq length: 0  
Maximum DB seq length: 10  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	38.2	10	2 A60476	S-layer protein
2	19	34.5	9	2 A31576	xylose isomerase
3	17	30.9	8	2 S43971	tumor-associated a
4	17	30.9	8	2 A43972	tumor-associated a
5	17	30.9	8	2 I54812	transferrin
6	17	30.9	10	2 A27613	triglyceride phosphatidyl
7	16	29.1	5	2 S73615	alpha 1,4 beta-xyl
8	16	29.1	10	2 XGHE	erythrocyte membra
9	15	27.3	5	2 A26830	mitosis inhibiting
10	15	27.3	8	2 A28719	thyroid tumor fac
11	15	27.3	8	2 S69165	feiredoxin a2 - ja
12	15	27.3	9	2 A60427	macrophage cytoctox
13	15	27.3	10	2 GXHU1	gastric juice pept
14	15	27.3	10	2 A59272	peptide-M4-IN-acet
15	15	27.3	10	2 A43977	FMRFamide-like pro
16	14	25.5	3	3 GXHU	growth-modulating
17	14	25.5	4	2 PL0142	carbon-monoxide de
18	14	25.5	4	2 I38888	COI thron 16 prot
19	14	25.5	5	2 D62774	major protein anti
20	14	25.5	6	2 A61419	sarcosine dehydrog
21	14	25.5	6	2 B56979	collagen alpha 1(I
22	14	25.5	7	2 S42407	gramicidin S synth
23	14	25.5	7	2 S68004	muscin, 75K chain
24	14	25.5	8	2 D61512	variant surface gi
25	14	25.5	8	2 PH0803	T-cell receptor a2
26	14	25.5	9	2 A24244	adipokinetic hormo
27	14	25.5	9	2 S07205	hormon 2 Glu - Au
28	14	25.5	9	2 S07204	hormon 1 - Austr
29	14	25.5	9	2 S07241	hormon Rohde's

RESULT 1  
A60476  
S-layer protein - Bacillus thuringiensis (fragment)  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1993 #sequence\_revison: 20-Feb-1993 #text\_change 12-Mar-1993  
C:Accession: A60476  
J. Luckevich, M.D.; Beveridge, T.J.  
J. Bacteriol. 171, 6656-6667, 1989  
A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.  
A:Reference number: A60476, MUID:90078111; PMID:2592346  
A:Accession: A60476  
A:Molecule type: protein  
A:Residues: 1-10 <LTC>  
C:Comment: The S-layer, or surface array, is the outermost component of several archaei

Query Match 38.2% Score 21; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. NC. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTFED 6  
DB 2 GHTFPD 7

RESULT 2  
A31576  
xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment)  
C:Species: Streptomyces sp.  
C:Date: 31-Mar-1990 #sequence\_revison: 31-Mar-1990 #text\_change 28-Apr-1993  
C:Accession: A31576  
R.Pawar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G.  
Biochem. Biophys. Res. Commun. 155, 411-417, 1988  
A:Title: Purification and characterisation of glucose (xylose) isomerase from Chainia  
A:Reference number: A31576; MUID:88326335; PMID:3415697  
A:Contents: Chainia sp. NCL 82-5-1  
A:Accession: A31576  
A:Molecule type: protein  
A:Residues: 1-9 <PAW>  
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 34.5% Score 19; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4  
DB 7 HTP 9

RESULT 3  
S43971  
tumor-associated antigen MUT1 - mouse

30 14 25.5 9 2 JQ1202 leader peptide - p  
31 14 25.5 9 2 PT0315 1g heavy chain CRD  
32 14 25.5 9 2 A42266 peptidylglycine mo  
33 14 25.5 9 2 S39437 D-amino-acid oxida  
34 14 25.5 10 1 GMRO12 leucosulfakinin-II  
35 14 25.5 10 2 A61289 streptopain (EC 3.  
36 14 25.5 10 2 PQ0177 neuromedin C - lau  
37 14 25.5 10 2 A60647 neuromedin C - bov  
38 14 25.5 10 2 A32543 leucosulfakinin I  
39 14 25.5 10 2 B60656 cardioexcitatory n  
40 14 25.5 10 2 A56633 leucosulfakinin I  
41 14 25.5 10 2 A30823 neovosuppressin -  
42 14 25.5 10 2 PH0895 bothrostoxin - ja  
43 14 25.5 10 2 A59173 T-cell receptor be  
44 14 25.5 6 2 A46474 nuclelease Bn1 (EC 3  
45 13 23.6 7 1 NYPG7 Fc epsilon RIIB -  
hypothalamic hepta

## ALIGNMENTS

```

C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C:Accession: S43971
R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
A:Reference number: S43971; PMID:8421781; PMID:8164742
A:Accession: S43971
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAK>
C:Superfamily: unassigned animal peptides

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FEQST 8
DB 1 FEQNT 5

RESULT 4
S43972
tumor-associated antigen WUT2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C:Accession: S43972
R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
A:Reference number: S43971; PMID:8421781; PMID:8164742
A:Accession: S43972
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <XAN>
C:Superfamily: unassigned animal peptides

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FEQST 8
DB 1 FEQNT 5

RESULT 5
164832
Ca2+-transporting ATPase (EC 3.6.3.9) rat brain
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-Apr-2002
C:Accession: 164832
R:Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of cDNA and protein encoding Ca2+-ATPase 1
A:Reference number: 151892
A:Accession: 164832
A>Status: preliminary; translated from GB/EWH/0082
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:M99223; NID:9203644; PMID:8444091; PMID:9203646
C:Genetics:
A:Gene: SERCA1b
C:Keywords: hydrolase

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 EDSTKK 10
DB 3 EDENRR 8

RESULT 6
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C:Accession: A27617
R:Bauw, G.; De Loose, W.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4866-4870, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino aci-
A:Reference number: A94167
A:Accession: A27617
A:Molecule type: protein
A:Residues: 1-10 <BAU>
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pen-

Query Match 30.9%; Score 17; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTF 4
DB 1 GRTP 4

RESULT 7
S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragm
N:Alternate names: xylanase
C:Species: Streptomyces sp.
A:Variety: Chainia sp. NCL 82.5.1
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S70615
R:Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A:Title: Structural environment of an essential cysteine residue of xylanase from Chai
A:Reference number: S70615; PMID:96265041; PMID:8670151
A:Accession: S70615
A:Molecule type: protein
A:Residues: 1-5 <RAO>
A:Experimental source: Chainia sp. strain NCL 82.5.1
A>Note: the source is designated as Chainia sp.
C:Function:
A:Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A:Pathway: fermentation of hemicellulose into ethanol
C:Keywords: glycosidase; hydrolase

Query Match 29.1%; Score 16; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TFED 6
DB 2 TFSD 5

RESULT 8
XGHUE
erythrocyte membrane glycopeptide - human
C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A03187
R:Weiss, J.B.; Lote, C.J.; Bobinski, H.
Nature New Biol. 234, 25-26, 1971
A:Title: New low molecular weight glycopeptide containing triglycosylcysteine in human
A:Reference number: A03187; PMID:72034940; PMID:528658
A:Accession: A03187
A:Molecule type: protein
A:Residues: 1-10 <WEI>
C:Comment: The identity of the glycoprotein from which this peptide is derived is unkn-
found (see PR:XGHUE).
C:Superfamily: unassigned animal peptides

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C:Keywords: glycoprotein  
F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : GHTE 5  
DB : 3 GHSHD ?

## RESULT 9

A6830  
macrosis inhibiting peptide - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Nov-1988 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: A26810  
R:Reichelt, K.; Elgjo, K.; Edmonson, P.D.;  
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987  
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.  
A:Reference number: A26830; MUID:87298602; PMID:3619940  
A:Accession: A26830  
A:Molecule type: protein  
A:Residues: 1-5 <REL>  
C:Superfamily: unassigned animal peptides  
C:Keywords: blocked amino end; pyroglutamic acid  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 2 EDS 4

## RESULT 10

A28719  
thymic humoral factor gamma-2 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1999 #text\_change 18-Jun-1993  
C:Accession: A28719  
R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.;  
Biochemistry 27, 4666-4071, 1988  
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immun  
A:Reference number: A28719; MUID:88326320; PMID:3261994  
A:Accession: A28719  
A:Molecule type: Protein  
A:Residues: 1-8 <PUR>

Query Match 27.3%; Score 15; DB 2; Length 3;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 EDSK 9  
DB 2 EDGPK 6

## RESULT 11

S69165  
ferredoxin a2 - Japanese radish (fragment)  
C:Species: Kaiware daikon (Japanese radish)  
C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998  
C:Accession: S69165  
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shim, M.;  
Arch. Biochem. Biophys. 316, 797-802, 1995  
A:Title: Four ferredoxins from Japanese radish leaves.  
A:Reference number: S69164; MUID:95168667; PMID:7861635  
A:Accession: S69165  
A:Molecule type: protein

A:Residues: 1-8 <OBA>

C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 27.3%; Score 15; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HTFED 6  
DB 2 HREED 6

## RESULT 12

A60427  
macrophage cytotoxicity-inducing factor, 29K - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
C:Accession: A60427  
R:Jones, C.M.; Prince, C.A.; Williams, J.S.;  
Exp. Hematol. 19, 704-709, 1991  
A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induc  
A:Reference number: A60427; MUID:91372335; PMID:1909970  
A:Accession: A60427  
A:Molecule type: protein  
A:Residues: 1-9 <JON>  
A:Note: the sequence from the text on page 706 is inconsistent with that from page 708  
C:Keywords: cytokine

Query Match 27.3%; Score 15; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 6 EDS 8

## RESULT 13

GXHU:  
gastric juice peptide - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A01628  
R:Heathcote, J.G.; Washington, R.J.;  
Int. J. Protein Res. 2, 117-126, 1970  
A:Title: Peptides of normal human gastric juice.  
A:Reference number: A01628; MUID:75150968; PMID:5538395  
A:Accession: A01628  
A:Molecule type: protein  
A:Residues: 1-10 <HEA>  
A:Note: a second peptide lacking 1-Leu, but otherwise identical in composition with th  
C:Superfamily: unassigned animal peptides  
C:Keywords: stomach

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 7 EDS 9

## RESULT 14

A59272  
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain  
N:Alternate names: peptide N-glycosidase  
C:Species: Prunus dulcis var. sativa (sweet almond)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000  
C:Accession: A59272  
R:Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.;  
Eur. J. Biochem. 252, 118-123, 1998  
A:Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase

A:Reference number: A59272; PMID:98181894; PMID:9523720  
A:Accession: A59272  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <ALT>  
C:Keywords: hydrolase

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFD 6  
|:  
Db 6 HSWAD 10

## RESULT 15

A43977  
FMRamide-like protein - tobacco hornworm  
C:Species: Manduca sexta (tobacco hornworm)  
C:Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text change 17-Mar-1999  
C:Accession: A43977  
R:Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Rehm, C.P.; Rao, K.R.; Hildebrand, J.G.;  
Peptides 11, 849-856, 1990  
A:Title: A new peptide in the FMRamide family isolated from the CNS of the hawkmoth, *Manduca sexta*  
A:Reference number: A43977; PMID:91045350; PMID:2235684  
A:Accession: A43977  
A:Molecule type: protein  
A:Residues: 1-10 <K1>  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
P:1/Modified site: pyroglutamic acid (Gln); #status experimental  
P:10/Modified site: amidated carboxyl end (Phe); #status experimental

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4  
|:  
Db 5 HSF 7

Search completed: November 5, 2003, 17:35:21  
-Gb time : 11 secs

GenCore version 5.1.6  
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QM protein: protein search, using sw mode

Run on: November 5, 2003, 17:23:40 : Search time 7.33333 seconds  
(without alignments)  
64.127 Million cell updates/sec

Title: US-09-914-088-4

Perfect score: 55

Sequence: 1 GHTFEDSTKK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scatched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 112

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	21	38.2	1	SLAP_BACTG
2	19	34.5	9	XYLA_STRSQ
3	17	30.9	10	TPIS_NICPL
4	17	30.9	10	UPA7_HUMAN
5	16	29.1	10	GLEM_HUMAN
6	15	27.3	10	FARP_VANSE
7	15	27.3	10	GATJ_HUMAN
8	15	27.3	10	SPL_EALRC
9	14	25.5	3	GRAM_HUMAN
10	14	25.5	4	DMPL_PSECH
11	14	25.5	9	LITO_LITAU
12	14	25.5	9	LITR_PHYRC
13	14	25.5	9	NSKI_SABRU
14	14	25.5	10	AVEN_BELAY
15	14	25.5	10	FARP_LOCM
16	14	25.5	10	GRP_FANRC
17	14	25.5	10	LCMS_LEIMA
18	14	25.5	10	LSK2_LEIMA
19	13	23.6	7	HV7_PIG
20	13	23.6	7	UC22_VAIZE
21	13	23.6	8	ALL5_CYDPO
22	13	23.6	8	ANG2_9OTTA
23	13	23.6	9	FLA2_TREHY
24	13	23.6	9	PPK1_PERRA
25	13	23.6	10	ANG1_BCTJA
26	13	23.6	10	ANGT_BOVIN
27	13	23.6	10	ANGT_CHICK
28	13	23.6	10	ESTA_SCHGA
29	13	23.6	10	TKNK_FIG
30	13	23.6	10	UPA9_HUMAN
31	12	21.8	8	RT34_BOVIN
32	12	21.8	9	FARP_VANSE
33	12	21.8	10	COX6_RAT

34	12	21.8	10	1	FARP_MYTED
35	12	21.8	10	1	SP34_DICMU
36	12	21.8	10	1	UPA4_HUMAN
37	11	20.0	4	1	ACH1_ACHFU
38	11	20.0	5	1	BIOA_CITFR
39	11	20.0	5	1	UC22_VAIZE
40	11	20.0	6	1	FARP_WONEX
41	11	20.0	8	1	AKF_TARAT
42	11	20.0	8	1	HTF2_FERAM
43	11	20.0	8	1	NS3_MYTCT
44	11	20.0	8	1	UPA4_HUMAN
45	11	20.0	8	1	WPI_PERRAT

ALIGNMENTS

RESULT 1  
SLAP\_BACTG STANDARD; PRT; 10 AA.  
ID SLAP\_BACTG STANDARD; PRT; 10 AA.  
AC P49325; Rel. 33, Created  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE S-layer protein (Surface layer protein) (Fragment)  
OS Bacillus thuringiensis (subsp. galleriae)  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
CX NCBI\_TaxID:23338;  
RN [1]  
RP SEQUENCE  
RC STRAIN=NPRL 4045;  
RX MEDLINE=90078111; PubMed=2592346;  
RA Luckeivich M.D., Beveridge T.J.;  
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";  
RL J. Bacteriol. 171:6656-6667(1989);  
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
S-LAYER WITH OBLIQUE (P2) SYMMETRY.  
DR P.R; A60476; A60476.  
KW Cell wall; S-layer.  
FT MON PER 10 10  
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;  
Query Match 38.2%; Score 21; DB 1; Length 10;  
Best Loca: Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 2; Gaps 0;

OY : GHTFED 6  
DB 2 GHTFED 7  
RESULT 2  
XYLA\_STRSQ STANDARD; PRT; 9 AA.  
ID XYLA\_STRSQ STANDARD; PRT; 9 AA.  
AC P19149;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Xylose isomerase (EC 5.3.1.5) (Fragment)  
GN XYLA.  
OS Streptomyces sp. (strain NC 82-5-1).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.  
CX NCBI\_TaxID:1931;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=88126315; PubMed=3415697;  
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;  
RT "Purification and characterisation of glucose (xylose) isomerase from  
Chaetia sp. (NC 82-5-1)."  
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).

CC 1 FUNCTION: Involved in D-xylose catabolism.  
 CC 2 CATABOLIC ACTIVITY: D-xylose = D-xv:ulose.  
 CC 3 CATALYST: Binds 2 magnesium ions per subunit (P07entia.1).  
 CC 4 SUBUNIT: Homotetramer.  
 CC 5 SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.  
 DR PIR: A1576; A1576.  
 DR HAMAP: MF02455; 1.  
 DR INTERPRO: IPR001938; Xylose isom.  
 DR PROSITE: PS0172; XYLOSE\_ISOMERASE\_2; PARTIAL.  
 DR PROSITE: PS0173; XYLOSE\_ISOMERASE\_2; PARTIAL.  
 KW Isomertase; Pentose shunt; Xylose metabolism; Metal binding; Vagovision.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 983 MW; F64BA1RUC58V1C1 CRC64;

Query Match 34.5% Score 19; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 HTF 4  
 DB 7 HTF 9

RESULT 3  
 TPIS\_NICPL STANDARD; PRT: 10 AA.  
 AC P14618;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM, Pfam00118).  
 OS Nicotiana glaucaefolia (Leadwort-leaved tobacco).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core Eudicotyledons;  
 CC Asteridae; Lamiaceae; Solanaceae; Solanaceae; Nicotiana.  
 CC NCBI\_TaxID: 4092;  
 RN 1;  
 PP SEQUENCE.  
 RA Baum G., de Jouse M., Inze D., van Montagu M., Van der Kame C.  
 RT "Alterations in the phenotype of plant cells studied by NMR terminal  
 RT amino acid-sequence analysis of proteins electroeluted from two  
 RT dimensional gel-separated total extracts."  
 RI Proc. Natl. Acad. Sci. U.S.A. 84:4896-4899 (1987).  
 CC 1 CATABOLIC ACTIVITY: D-glyceraldehyde 3 phosphate = glyceraldehyde  
 CC phosphate.  
 CC 2 PATHWAY: Plays an important role in several metabolic pathways.  
 CC 3 SUBUNIT: Homotrimer.  
 CC 4 SUBCELLULAR LOCATION: Cytoplasmic; P14618.  
 CC 5 MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TIM: CYTOSOLIC AND  
 CC AND PLASTID.  
 CC 6 SIMILARITY: BELONGS TO THE TRIOSPHOSPHATE ISOMERASE FAMILY.  
 DR PIR: A27637; A27637.  
 DR INTERPRO: IPR000652; Triophos.isomse  
 DR PROSITE: PS0017; TIM; PARTIAL.  
 KW Isomertase; Glycolysis; Gluconeogenesis; Early amino acid synthesis;  
 KW Pentose shunt.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1140 MW; 82E9D37362C0791 CRC64.

Query Match 30.9% Score 17; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HTF 4  
 DB 1 HTF 4

RESULT 4  
 URAT\_HUMAN STANDARD; PRT: 10 AA.  
 AC P14618;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-036HC)  
 DE (fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID: 9606;  
 RN 1;  
 PP SEQUENCE.  
 RA Gozaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer G.,  
 RA Balant L., Hochstrasser D.F.;  
 RL Submitted (FEB-1994) to the SWISS PROT data bank.  
 CC 1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 4.77, ITS MW IS: 26 kDa.  
 DR SWISS-2DPAGE; P34990; HUMAN.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match 30.9% Score 17; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTF 6  
 DB 4 GENPXD 9  
 ID GLEM\_HUMAN STANDARD; PRT: 10 AA.  
 AC P02728;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Erythrocyte membrane glycoprotein.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID: 9606;  
 RN 1;  
 PP SEQUENCE.  
 RA MEDLINE: 72044940; PubMed: 5256858.  
 RA Weiss C.B., Lote C.C., Borinski H.;  
 RT "New low molecular weight glycoprotein containing triglucoylcysteine  
 RT in human erythrocyte membrane."  
 RL Nature New Biol. 244:25-26 (1973).  
 CC 1 MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS  
 CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
 CC ATTRIBUTED.  
 DR PIR: A01187; XCHUE.  
 DR Glycoprotein; Erythrocyte.  
 FT CARBOHYD 1  
 SQ SEQUENCE 10 AA; 1049 MW; 235EFEEA1F581E8 CRC64;

Query Match 29.1% Score 16; DB 1; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HTF 5  
 DB 3 GRND 7

RESULT 6  
 FARP\_MANSE STANDARD; PRT: 10 AA.  
 AC F14618;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

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SPI_HALRO
ID ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10397;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragrant)
OS Halocynthia roretzi (Sea squirt)
OC Eukaryota; Metazoa; Chordata; Trochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID:7723;
RN [1]
RP SEQUENCE.
RT 7:SSUE:Hemolymph;
RX MEDLINE:96321313; PubMed:8759235;
RA Shiohara F., Abe T., Ohtake S., Tanaka K.
RT "Purification and characterization of a 58,000-Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halocynthia
roretzi";
RL Comp. Biochem. Physiol. 114B:1-9(1996);
CC -- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -- SUBUNIT: Monomer.
CC -- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR INTERPRO: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NCN TER 10
SQ SEQUENCE 10 AA; 1104 MW; 4225G73B1B197AA3 CRC64;

Query Match: 27.5%; Score 15; DB 1; length 10;
Best Local Similarity 100.0%; Pred. No. 3,Re+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY A TKK 10
DB I TKK 3

RESULT 3
GRWM_HUMAN
ID GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 31, Created)
DT 21-JUL-1986 (Rel. 31, Last sequence update)
DT 21-JUL-1986 (Rel. 31, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE.
RT 7:SSUE:77162169; PubMed 85+366;
RX Schlesinger D.H., Hickart L., Thaler M.M.
RT "Growth-modulating serum tripeptide is glycyl histidyl-lysine.";
EX Experientia 33:324-325(1977);
CC -- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO: G0300158; Regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 631EB10000000000 CRC64;

Query Match: 25.5%; Score 14; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1,Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY I GH 2
DB I GH 2

RESULT 1
DML_PSECH
ID DML_PSECH STANDARD; PRT; 4 AA.

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CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cecidomyiidae;  
CC Sarcophagidae; Sarcophaga.  
CX NCBI TaxID=7186;

PP SEQUENCE  
PP TISSUE=Heart;  
PP MEDLINE=3308111; PubMed1350367;  
RA Family A.; Schodts M.; Proost P.; Van Damme G.; de Loof A.;  
RT "Isolation and primary structure of two sulfakinin-like peptides from  
RT the fruit fly, *Nephelocerla bullata*.";  
PI Temp. Biochem. Physiol. 103C:135-142(1997).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYLMINE FAMILY.  
CC INTERFERON (PEPTIDE); Gastrin.  
DR PROSITE: PS00259; GASTRIN; 1.  
KW Neuropeptide; 4 4 SULFATION (POTENTIAL);  
FT NUC RES 9 9 AMIDATION (POTENTIAL);  
SQ SEQUENCE 9 AA; 1197 MW; 8B0AC591E86FAAA CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.8e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GH 2

DB 5 GH 6

## RESULT 14

AMPK\_HLHAM  
ID AVEN HELAM STANDARD; PRT; 10 AA  
AC F81731;  
DT 30 MAY 2000 (Rel. 39, Last sequence update);  
DT 28-FEB-2001 (Rel. 41, Last annotation update);  
LE Aminopeptidase N (EC 3.4.11.2) (CRYIA1) receptor fragment;  
CS Helicoverpa armigera (Cotton bollworm);  
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuidae;  
CC Noctuidae; Heliothinae; Helicoverpa.  
CX NCBI TaxID=29056;

PP SEQUENCE  
PP TISSUE=Midgut;  
RA Indle S.S.; Triwast N.; Prasad R.; Rao K.K.; Chaitan R.S.;  
PT "Aminopeptidase N as a receptor for *Battus thurinus* Cytine  
PT toxin from *Helicoverpa armigera*.";  
RI Submitted (MAR-1999) to the SWISS PRO database.  
CC -!- FUNCTION: ACTS AS A RECEPTOR FOR BUTTERFLY AND MOTTH  
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa  
CC Xbb, from a peptide, amide or amide, but not ester, when a  
CC may be most amino acids including proline which when a  
CC terminal hydrophobic residue is followed by a hydroxy residue, the  
CC two may be released as an intact Xaa-Pro dipeptide.  
CC -!- COFACTOR: Binds 1 zinc ion (5y similarity).  
CC -!- SIMILARITY: Belongs to peptidase family M.  
DR InterPro: IPR006295; Zn\_MTPeptide.  
DR PROSITE: PS0142; ZINC\_PROTEASE; PARTIAL.  
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1093 MW; 05042E8B7B11F1FB CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.8e-03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HTFDS 7

DB 3 YTHEGS 8

## RESULT 15

FARP\_LOCOMI  
ID FARP LOCOMI STANDARD; PRT; 10 AA  
AC P38553;  
DT 01-OCT-1994 (Rel. 30, Created);  
DT 01-OCT-1994 (Rel. 30, Last sequence update);  
DT 30-MAY-2003 (Rel. 39, Last annotation update);  
DE Schistoflavinamide (FVDHFLRFamide, [cardioexcitatory neuropeptide];  
CS Locusta migratoria (migratory locust), and  
CS Schistocerca gregaria (desert locust);  
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Orthoptera; Caelifera; Acridomorpha;  
CC Acridoidea; Acrididae; Caelipodinae; Locusta.  
CX NCBI TaxID=7004; 5310;  
PP SEQUENCE  
PP SPECIES=L. migratoria; TISSUE=Brain;  
RX MEDLINE=9332430; PubMed=7682352;  
RA Schodts M.; Holman G.M.; Paemen E.; Veelaert D.; Amelincx M.;  
RA de Loof A.;  
RT "Isolation, identification, and synthesis of FVDHFLRFamide  
RT (Schistoflavinamide) in *Locusta migratoria* and its association with the  
RT male accessory glands, the salivary glands, the heart, and the  
RT oviduct.";  
RL Peptides 14:409-421(1993);

RN 12;  
RP SEQUENCE  
RC SPECIES=S. gregaria; TISSUE=Thoracic nervous system;  
RX MEDLINE=9324543; PubMed=2719702;  
RA Robb S.; Packman J.C.; Evans P.D.;  
RT "Isolation, primary structure and bioactivity of schistoflavinamide, a  
RT FMRF-amide-like neuropeptide from the locust, *Schistocerca*  
RT gregaria.";  
RL Biochem. Biophys. Res. Commun. 163:850-856(1989);  
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL  
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND  
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.  
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,  
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.

DR PIR; A32543; A32543;  
KW Neuropeptide; Amidation;  
FT MOD RES 10 10  
SQ SEQUENCE 10 AA; 1244 MW; D3C51729C2C1EAB2 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 5.8e-03;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HCF 4

DB 5 HVF 7

Search completed: November 5, 2003, 17:33:04  
Job time : 7.33333 secs

GenCore version 5.1.6  
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Query protein protein search, using sw mode:

Run on: November 5, 2003, 17:33:05 / Search time 26 Seconds  
Without alignments:  
99,251 Million cell updates/sec

Title: US-09-914-088-4  
Perfect score: 55  
Sequence: 1 GHTFADSTK 10

Scoring table: EFASTJ62  
Gapop 10.0, Gapext 0.5

Searched: 83525 seqs, 25852604 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 38  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mbs.\*
- 8: sp\_organalle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_virus.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacterioph.\*
- 17: sp\_archaeap.\*

Pred. Num is the number of results predicted by the search engine. A score greater than or equal to the score of the best hit being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	length	DB	ID	Description
1	20	36.4	7	10	P82445	P82445 nicotiana t
2	18	32.7	10	2	Q93002	Q93002 escherichia
3	18	32.7	10	15	Q8UT83	Q8UT83 human immun
4	17	30.9	9	12	Q93622	Q93622 human vail
5	16	29.1	8	2	Q95950	Q95950 bacillus su
6	16	29.1	8	13	Q90204	Q90204 tulica leuc
7	16	29.1	9	2	Q93E20	Q93E20 streptococ
8	16	29.1	9	4	Q96F97	Q96F97 homo sapien
9	16	29.1	10	2	Q8VX85	Q8VX85 helicobacte
10	15	27.3	8	2	Q93SH0	Q93SH0 staphylococ
11	15	27.3	8	4	Q93J50	Q93J50 homo sapien
12	15	27.3	8	4	Q93PK3	Q93PK3 homo sapien
13	15	27.3	8	11	Q62034	Q62034 staphylococ
14	15	27.3	9	11	Q8CG34	Q8CG34 staphylococ
15	15	27.3	10	2	Q42561	Q42561 staphylococ
16	15	27.3	10	5	P82445	P82445 nicotiana t

17	15	27.3	10	6	Q9TU33	Q9TU33 canis fami
18	15	27.3	10	10	P81899	P81899 prunus dulc
19	15	27.3	10	13	Q9PRY8	Q9PRY8 triakis scy
20	14	25.5	9	2	Q51349	Q51349 pseudomona
21	14	25.5	9	2	Q47410	Q47410 escherichia
22	14	25.5	9	4	Q14277	Q14277 homo sapien
23	14	25.5	9	11	Q89779	Q89779 mus musculu
24	14	25.5	10	2	Q9R7J9	Q9R7J9 helicobacte
25	14	25.5	10	3	Q9UVW2	Q9UVW2 schizosyl
26	14	25.5	10	4	Q81Z42	Q81Z42 homo sapien
27	14	25.5	10	6	Q9TRS3	Q9TRS3 sus scrofa
28	14	25.5	10	6	Q95NB1	Q95NB1 eulemur fu
29	14	25.5	10	6	Q95NR0	Q95NR0 eulemur fu
30	14	25.5	10	6	Q8M552	Q8M552 equus caba
31	14	25.5	10	8	P82136	P82136 spinacia o
32	14	25.5	10	10	Q9FS93	Q9FS93 silene pent
33	14	25.5	10	10	Q95936	Q95936 beta vulgar
34	14	25.5	10	10	P82434	P82434 nicotiana t
35	14	25.5	10	11	Q8V118	Q8V118 mus musculu
36	13	23.6	6	10	P82541	P82541 spinacia o
37	13	23.6	7	2	P70804	P70804 azotobacter
38	13	23.6	8	2	Q45615	Q45615 bacillus su
39	13	23.6	8	2	Q9R517	Q9R517 clostridium
40	13	23.6	8	2	P83156	P83156 anabaena sp
41	13	23.6	8	4	Q9HCQ0	Q9HCQ0 homo sapien
42	13	23.6	8	6	Q9T778	Q9T778 canis fami
43	13	23.6	8	8	Q36898	Q36898 nicotiana p
44	13	23.6	8	11	Q9ERC2	Q9ERC2 mus musculu
45	13	23.6	9	11	Q8CJ03	Q8CJ03 mus musculu

ALIGNMENTS

RESULT 1  
P82445  
ID P82445 PRELIMINARY; PPT: 7 AA.  
AC P82445  
DT 01-JUN-2000 (TREMBL) 14, Created)  
DT 01-JUN-2000 (TREMBL) 14, Last sequence update)  
DT 01-JUN-2000 (TREMBL) 14, Last annotation update)  
DE 10 kDa cell wall protein (Fragment).  
OS Nicotiana glauca (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot.  
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI TaxID=4337;  
RY [1]  
RP SEQUENCE.  
RC STRAIN: CV, PETIT HAVANA,  
RA Pile K.A., Bochar V.A., Marchetti G.P., Robertson D., Slabas A.P.,  
RA Wotaszek P., Bolwell G.P.;  
PT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture";  
RL Plantae 10-0-22000;  
CC -1- SUBCELLULAR LOCATION: CELL WALL.  
CC -1- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON TER 7 7  
SC SEQUENCE 7 AA; 758 MW; 637201E642D1E2AC CRC64;

Query Match: 36.4%; Score 20; DB 10; Length 7;  
Best Local Similarity: 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTF 4

DB 4 GHTF 7

RESULT 2

Q93002  
ID Q93002 PRELIMINARY; PPT: 18 AA.





RL AAK116248-255(2001);  
 DR EXBL: AF307898; AAK43537.1; --  
 KW Kinase;  
 FT NON TER 1  
 FI NFN TER 8

SQ SEQUENCE 9 AA; 994 MW; 9633309CE1B1946 CRC64;  
 Query Match 29.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Query Match 29.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHTFE 5  
 DB 2 GHTFE 6

RESULT 7

ID Q31E20 PRELIMINARY; PRT; 9 AA.  
 AC Q31E20  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SCGB (Fragment)  
 GN SCGB  
 OS Streptococcus agalactiae  
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 CC Streptococcus  
 CX NCBI\_TaxID:1311;  
 PN 1  
 PP SEQUENCE FROM N.A.  
 RC STRAIN:6907;  
 RX MEDLINE:21454698; PubMed:1532154;  
 RA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,  
 RA Lattacker R., Spellerberg H.,  
 RA Podbielski A., Lattacker R., Spellerberg H.,  
 RT "Horizontal gene transfer and host specificity of beta-haemolytic  
 RT streptococci: the role of a putative composite transposon containing  
 RT scgB and lmb."  
 RL Mol. Microbiol. 4:925-935(2001).  
 DR EXBL: AF327852; AAL10713.1;  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1146 MW; 54371AB1326C401 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;  
 Best Local Similarity 50.3%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DSTKK 10  
 DB 4 QSTTK 9

RESULT 8

ID Q36P97 PRELIMINARY; PRT; 9 AA.  
 AC Q36P97  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Reptin52 protein (Fragment)  
 GN Homo sapiens (Human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae;  
 CX NCBI\_TaxID:9606;  
 PN 1  
 PP SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y., Jung H.M., Jun D.Y., Suh T.H., Kim Y.H.;  
 RT "Characterization of TPA-responsive genes in C927 cells using ordered  
 RT differential display PCR."  
 PL Submitted JUL-2001 to the EXBL/GenBank/DBJ databases.  
 DR EXBL: AF401216; AAL02172.1;  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 981 MW; 5CDDAA651AB187A CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHTFDS 7  
 DB 3 GHTFDS 9

RESULT 9

ID Q8VN85 PRELIMINARY; PRT; 13 AA.  
 AC Q8VN85  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Urease accessory protein  
 GN UREP  
 OS Helicobacter pylori (Campylobacter pylori)  
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 CC Helicobacteraceae; Helicobacter  
 CX NCBI\_TaxID:210;  
 RN 1  
 PP SEQUENCE FROM N.A.  
 RC STRAIN:NQ267;  
 RX MEDLINE:21625040; PubMed:11742075;  
 RA Falush D., Kraft C., Taylor N.S., Correa P., Fox J.G., Achtman M.,  
 RA Suerbaum S.;  
 RT "Recombination and mutation during long-term gastric colonization by  
 RT Helicobacter pylori: Estimates of clock rates, recombination size and  
 RT transmission age."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061(2001).  
 DR EXBL: A048329; CAD1229.1;  
 SQ SEQUENCE 10 AA; 1329 MW; 81E8034C332411 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 10;  
 Best Local Similarity 60.3%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DSTKK 10  
 DB 2 DTRKK 6

RESULT 10

ID Q93SR0 PRELIMINARY; PRT; 8 AA.  
 AC Q93SR0  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Beta lactamase repressor B1a1 (Fragment)  
 GN BLA1  
 OS Staphylococcus epidermidis  
 CG Plasmid pST6  
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus  
 CX NCBI\_TaxID:1282;  
 RN 1  
 PP SEQUENCE FROM N.A.  
 RC STRAIN:6;  
 RA Sidhu M.S., Hair E., Sorum H., Heick A.L.;  
 RT "Genetic linkage between quaternary ammonium compound and beta-lactam  
 RT resistance in Staphylococcus isolated from food."  
 RL Submitted (MAR-2001) to the FMBL/GenBank/DBJ databases.  
 DR EMBL: AY028779; AAK38453.1;  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 930 MW; 4F3325H05AA44720 CRC64;

Query Match 27.3%; Score 15; DB 2; Length 8;  
 Best Local Similarity 60.3%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 60.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 FDSST 8  
DB 4 FDSST 8

RESULT 13

Q62933 PRELIMINARY; PRT: 9 AA.  
ID Q62933  
AC Q62933  
DT 01-MAY-2000 (TRENBLER: 13, Created;  
DT 01-MAY-2000 (TRENBLER: 13, Last sequence update;  
DE Cytrophilin 2 (Fragment)  
GN C6H11  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:99153747; PubMed:1030676;  
RA White G.R.M., Varley J.M., Heigway J.  
RT "Isolation and characterisation of a human homologue of the  
RT latrophilin gene from a region of 1p11.1 implicated in breast  
RT cancer."  
RL Cytogene 17:3513-3519(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:202254517; PubMed:10760572;  
RA White G.R.M., Varley J.M., Heigway J.  
RT "Genomic structure and expression profile of LPHN1, a GPCR gene  
RT variably expressed in breast cancer cell lines."  
RL Biochim Biophys Acta 1491:75-92(2000).  
DR EMBL: AJ244509; CAB6204.1;  
FT NON TER  
FT NON TER  
SQ SEQUENCE 8 AA; 1025 MW; 4D530763344AARCB CRC64;

Query Match 27.3%; Score 15; DB 11; Length 8;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FDSST 8  
DB 2 ENST 6

RESULT 14

Q8CG39 PRELIMINARY; PRT: 9 AA.  
ID Q8CG39  
AC Q8CG39  
DT 01-MAR-2003 (TRENBLER: 23, Created;  
DT 01-MAR-2003 (TRENBLER: 23, Last sequence update;  
DT 01-MAR-2003 (TRENBLER: 23, Last annotation update;  
DE Histamine N-tele-methyltransferase (Fragment)  
GN Histamine N-tele-methyltransferase (Fragment)  
OS Rattus norvegicus (Rat)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID:10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN:Sprague Dawley; Tissue=Liver;  
RX MEDLINE=96342418; PubMed=8750766;  
RA Takeuchi M., Yamachi K., Yamatogami A.  
RT "Structural analysis of histamine N-methyltransferase gene."  
RL Methods find. Exp. Clin. Pharmacol 17:114(1995).  
DR EMBL: S82579; AA86745.1;  
KW Transferase; Methyltransferase.  
FT NON TER  
FT NON TER  
SQ SEQUENCE 9 AA; 1060 MW; 4223818C42EB053 CRC64;

Query Match 27.3%; Score 15; DB 11; Length 9;  
Best Local Similarity 56.7%; Pred. No. 8.3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4  
DB 7 NSF 9

Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FDSST 7  
DB 1 YEN 4

RESULT 12

Q9P0K3 PRELIMINARY; PRT: 9 AA.  
ID Q9P0K3  
AC Q9P0K3  
DT 01-OCT-2000 (TRENBLER: 15, Created;  
DT 01-OCT-2000 (TRENBLER: 15, Last sequence update;  
DT 01-OCT-2000 (TRENBLER: 15, Last annotation update;  
DE cAMP specific phosphodiesterase PDE5A (Fragment)  
GN PDE5A  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20145478; PubMed:10679249;  
RA Jin C.H., Lau A., Tu R., Jue T.F.  
RT "Identification of three alternative first exons in an intronic  
RT promoter of human PDE5A gene."  
RL Biochem Biophys Res. Commun. 268:596-600(2000).  
DR EMBL: AF551955; AAF40302.1;  
FT NON TER  
FT NON TER  
SQ SEQUENCE 9 AA; 908 MW; EBA3AAB7497E926 FDSST;

Query Match 27.3%; Score 15; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FDSST 7  
DB 1 YEN 4

Query Match 27.3%; Score 15; DB 4; Length 8;

```

RESULT 15
Q4756: PRELIMINARY; PRT: 10 AA
ID Q4756:
AC Q4756:
DT 01-NOV-1996 (TRENBLrel: 01, Created)
DE 01-NOV-1996 (TRENBLrel: C1, Last sequence update)
DR 01-JAN-1999 (TRENBLrel: C9, Last annotation update)
DE Hypothetical: 1.1 kDa protein (fragment).
CS Escherichia coli.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID:562;
RN [1]
RP SEQUENCE FROM NLA
RC STRAIN:K 12;
RX MEDLINE:94162733; PubMed:764507;
RA Yamada M., Yanai S., Talkner A.;
RT "Analysis of products of the Escherichia coli genome: genes and
RT regulation of their expressions: an applicable procedure for genomic
RT analysis of other microorganisms."
RD Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL: D21431; BAA04679.1; -.
KW Hypothetical protein.
FT NON-TER 1
FT NON-TER 10 13
SQ SEQUENCE 10 AA: 1109 MW; 2D1B5B5F87D2D33 CRC64;
Query March 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred No 2.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY : GHZ 3
DB : 6 GHS 8

```

Search completed: November 5, 2003, 17:34:37  
 Job time: 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM Protein - protein search, using sw model

Run on: November 5, 2003, 17:23:00 / Search time: 31.033 seconds  
(without alignment)  
47,618 Million cell updates/sec

Title: us-09-914-088-4

Perfect score: 65

Sequence: 1 GTFPLSTKK 10

Scoring table:

Gapop 12.0, Gapext 2.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 11420

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq 19Jun03:\*

1	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
2	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
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4	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
5	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
6	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
7	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
8	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
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10	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
11	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
12	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
13	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
14	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
15	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT
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24	/S/DS1/gcgdata/geneseq/geneseq-emb/AA1941.DAT

Prod. No. is the number of results predicted by choice to have a score greater than or equal to the score of the hit it being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	55	100.0	10	21	AA025910		Inf. Cys-glycin-2 do
2	55	100.0	10	22	AAU16035		Peptide P4 derived
3	58	100.0	10	23	AB023220		Human IgE Immune
4	28	50.9	8	22	AA089420		Human IgE supermotif
5	27	49.1	9	23	AB034507		Inf. epitope HLA pe
6	27	49.1	9	23	AB034507		Inf. epitope HLA pe
7	27	49.1	9	23	AB034507		Inf. epitope HLA pe
8	27	49.1	10	23	AB034507		Inf. epitope HLA pe
9	26	47.3	8	13	AA025994		Inf. epitope HLA pe

10	26	47.3	9	23	AB046949		Human BlyS binding
11	26	47.3	10	22	AAG86567		Saccharomyces cere
12	26	47.3	10	23	ABB94538		CTF epitope HLA pe
13	25	45.5	7	23	AAU81553		Enterokinase recog
14	25	45.5	9	15	AAU77316		HLA-A1 HPV16.E5 an
15	25	45.5	9	20	AAU25502		Insulin like growt
16	25	45.5	9	22	AAU26670		Human Leukocyte An
17	25	45.5	9	22	AAU27003		Human Leukocyte An
18	25	45.5	10	15	AAU47315		HLA-A1 HPV16.E5 an
19	25	45.5	10	19	AAU65740		Fibronectin bindin
20	25	45.5	10	19	AAU65740		Fibronectin bindin
21	25	45.5	10	22	ABU20812		HIV A33 motif gag
22	25	45.5	10	22	ABU20812		HIV A33 motif gag
23	25	45.5	10	22	AAU99288		Potato patatin pro
24	24	43.6	7	20	AAU42578		Vpr-binding peptid
25	24	43.6	8	22	AAU89442		p53 DR supermotif
26	24	43.6	9	22	AAU26698		Human Leukocyte An
27	24	43.6	9	22	AAU27031		Human Leukocyte An
28	24	43.6	9	23	ABU12986		Human 125P5C8 epit
29	24	43.6	9	23	ABU12986		Human 125P5C8 epit
30	24	43.6	9	24	ABU21659		Human cancer-relat
31	24	43.6	10	18	AAU42711		Antigenic decapet
32	24	43.6	10	19	AAU42711		Beta (1 -> 4)-N-ac
33	24	43.6	10	19	AAU42711		Kojibiose phosphor
34	24	43.6	10	20	AAU46551		Immunogenic peptid
35	24	43.6	10	22	AAU95787		Human complementar
36	24	43.6	10	22	AAU95787		ErBB2-reactive VH
37	24	43.6	10	22	AAU95787		Humanised Fab vers
38	24	43.6	10	23	ABU14186		Human 125P5C8 epit
39	24	43.6	10	23	ABU14186		Human 125P5C8 epit
40	24	43.6	10	24	ABU47345		Staphylococcus aur
41	24	43.6	10	24	ABU21556		Human cancer relat
42	24	43.6	10	24	ABU22559		Human cancer relat
43	24	43.6	10	24	ABU22559		Human cancer relat
44	24	43.6	10	24	ABU22559		Human cancer relat
45	23	41.8	7	23	AAU81560		Enterokinase recog

#### ALIGNMENTS

RESULT 1  
AAB25910  
ID AAB25910 standard; Peptide: 10 AA  
XX  
AC AAB25910;  
XX  
XX 95-JAN-2003 (first entry)  
XX  
DE IgE Cys-glycin 2 domain surface exposed epitope peptide P4 SEQ ID NO:4  
XX  
XX Epitope: mimotope; Human; Immunoglobulin E; IgE; C-epsilon-2 domain;  
KW allergic disease; Immunoprophylaxis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.

OS Homo sapiens.  
XX  
XX WC3C0050460-A1.  
XX  
PD 31-AUG-2003.  
XX  
XX 22-FEB-2003; 2003WC EP01455.  
XX  
PR 25-FEB-1999; 99GB-C004425.  
PR 29-MAR-1999; 99GB-C007151.  
PR 07-MAY-1999; 99GB-C010537.  
PR 07-MAY-1999; 99GB-C010538.  
PR 07-AUG-1999; 99GB-C018594.  
PR 07-AUG-1999; 99GB-C018603.  
PR 07-SEP-1999; 99GB-C021046.  
PR 07-SEP-1999; 99GB-C021047.  
PR 29-OCT-1999; 99GB-C025613.



XX Claim 4: Page 9: 45pp; English.  
PS The present invention relates to conjugates suitable for use in vaccines.  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
XX  
XX  
SQ Sequence 10 AA:  
Query Match 100.0%; Score 55; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00687;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : GHTFEDSTKK 10  
DB : GHTFEDSTKK 10  
RESULT 4  
AA389420  
ID AA059420 standard; Peptide; 8 AA.  
XX  
AC AA059442;  
XX  
DT 11-SEP 2001 (first entry)  
XX  
DE p53 DR supermotif binding peptide core sequence #15.  
XX  
KW Human; p53, tumor suppressor; human leukocyte antigen; HLA; CTL;  
KW cytotoxic T lymphocyte; T cell; immune response; tumor; cancer;  
KW vaccine; epitope; cytostatic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2001/4789-A1.  
XX  
DT 14 JUN 2001.  
XX  
PF 11-DEC-2001; 2000W3-US33629.  
XX  
PR 10 DEC 1999; 99US-0458297.  
XX  
PA (EPIM-1) EPIMUNE INC.  
XX  
PI Fikes J, Satter A, Sidney J, Southwood S, Chiswick B, Levin E,  
PI Keosh E.  
XX  
WP1 2001-391493/40.  
XX  
PT Epitope based vaccines comprising p53 epitope having a short  
PT sequence, useful for treating and preventing cancer, the epitope  
PT peptide is useful as diagnostic agents and for evaluating immune  
PT response.  
XX  
PS Disclosure: Page 111, 138pp; English.  
XX  
CC The present invention describes isolated prepared epitopes and. Also  
CC described are: (i) a cytotoxic T lymphocyte (CTL) that is cultured  
CC in vivo and binds to a complex of (i); (2) a peptide (ii) comprising (i)  
CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
CC vaccine composition comprising (ii); a unit dose of a peptide with less  
CC than 50 contiguous amino acids with 100% identity to the native peptide  
CC sequence of p53; and a pharmaceutical excipient; (4) an isolated nucleic  
CC acid encoding (i); and (5) an isolated nucleic acid encoding (ii); (i)  
CC has cytostatic activity and can be used in vaccines. The vaccine  
CC composition is useful for treating or preventing cancer. (i) and (ii)  
CC are useful as diagnostic agents and for evaluating immune responses.  
CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
CC present in whole antigens can be avoided with the use of the vaccine  
CC composition of (i); the ability to combine selected epitopes and

CC further, to modify the composition of the epitopes enhances the  
CC immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigens, which might have their own  
CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
CC represent amino acid sequences used in the exemplification of the  
CC present invention.  
XX  
XX  
SQ Sequence 8 AA:  
Query Match 50.9%; Score 28; DB 22; Length 8;  
Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 HTFEDS ?  
DB 3 HTLEDS 8  
RESULT 5  
ABB94507  
ID ABB94507 standard; Peptide; 9 AA.  
XX  
AC ABB94507;  
XX  
DT 17-JUN 2002 (first entry)  
XX  
DE CTL epitope HLA peptide SEQ ID NO:36.  
XX  
KW Human; 158P1H4; chromosome 8q22q23; 158P1H4; chromosome 8q23; cancer;  
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
KW human leukocyte antigen; helper T lymphocyte; HTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2002/6598-A2.  
XX  
DT 28-FEB 2002.  
XX  
PF 22-AUG 2001; 2001W0-US26411.  
XX  
PR 22-AUG-2000; 2000US-227098P.  
PR 10-APR-2001; 2001US-282739P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chaitin-Eld PM, Hubert RS, Kaitaro AB, Afar DEH, Levin E,  
PI Faris M, Ge W, Jakubovits A;  
XX  
WP1 2002 269357/31.  
XX  
PT Monitoring 158P1H4 gene products in biological sample from patient who  
PT has or is suspected of having cancer, useful for treating cancer,  
PT comprises identifying presence of aberrant 158P1H4 gene products in  
PT biological sample  
XX  
PS Claim 64: Page 143; 209pp; English.  
XX  
CC The present invention describes a method for monitoring 158P1H4 gene  
CC products in a biological sample from a patient who has or is suspected  
CC of having cancer. The method comprises determining the status of 158P1H4  
CC gene products in a tissue sample from an individual, comparing the  
CC status to the status of 158P1H4 gene products in a normal sample, and  
CC identifying the presence of aberrant 158P1H4 gene products in the sample.  
CC 158P1H4 sequences have cytostatic activity and can be used in vaccine  
CC production. 158P1H4 polynucleotides may be used in monitoring genetic  
CC abnormalities. The 158P1H4 proteins may be used in assessing the status  
CC of 158P1H4 gene products in normal versus cancerous tissues and so  
CC elucidating the malignant phenotype, in generating and characterising  
CC domain-specific antibodies, for identifying agents or cellular factors  
CC that bind to 158P1H4 or its particular domain, and for generating  
CC cancer vaccines. Antibodies against 158P1H4 are useful in diagnostic  
CC and prognostic assays, in treating patients with cancer, in generating

CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158p1H4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158p1H4 gene has been  
 CC located to chromosome 8q22-q23, and the 158p1H4 gene also described in  
 CC the present invention has been located to chromosome 8q23. AB50429 to  
 CC AB50429 and AB594468 to AB595188 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 9 AA.

Query Match 49.18; Score 27; DP 13; Length 9;  
 Best Local Similarity 55.68; Pred. No. 9.3e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 :|||:  
 DB 1 NTFEDATKK 9

RESULT 6  
 AB594683  
 ID AB594683 standard; Peptide; 9 AA.  
 XX  
 AC AB594683;  
 DT 17 JUN 2002 (first entry);  
 DE CTL epitope HLA peptide SEQ ID NO:212.  
 XX Human; 158p1H4; chromosome 8q22q23, 158p1F4; chromosome 8q23; cancer;  
 XX Bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX Homo sapiens  
 CS Synthetic.  
 XX  
 TR WC2002:14598-A2.  
 XX  
 XX 28 FEB 2002.  
 XX  
 XX 27-AUG-2001; 2001WO-US26411.  
 XX  
 XX 22-AUG-2000; 2000US-227098P.  
 XX 10-APR-2001; 2001US-282739P.  
 XX  
 XX (AGEN: AGENSYS INC.  
 XX  
 XX Chaitin-Eld PM, Hubert RS, Raitano AB, Afari DEH, Levin E,  
 XX Faris M, Ge W, Jakobovits A;  
 XX WPI; 2002-269357/31.  
 XX  
 XX Monitoring 158p1H4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer,  
 XX comprises identifying presence of aberrant 158p1H4 gene products in  
 XX biological sample  
 XX  
 XX Claim 64, Page 149; 209pp; English.

PS The present invention describes a method for monitoring 158p1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158p1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158p1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158p1H4 gene products in the sample.  
 CC 158p1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158p1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158p1H4 proteins may be used in assessing the status  
 CC of 158p1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating agents or cellular factors  
 CC that bind to 158p1H4 or its particular domain, and for generating

CC cancer vaccines. Antibodies against 158p1H4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating  
 CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158p1H4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158p1H4 gene has been  
 CC located to chromosome 8q22-q23, and the 158p1H4 gene also described in  
 CC the present invention has been located to chromosome 8q23. AB50400 to  
 CC AB50429 and AB594469 to AB595189 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 9 AA.

Query Match 49.18; Score 27; DP 23; Length 9;  
 Best Local Similarity 55.68; Pred. No. 9.3e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 :|||:  
 DB 1 NTFEDATKK 9

RESULT 7  
 AB594777  
 ID AB594777 standard; Peptide; 9 AA.  
 XX  
 AC AB594777;  
 DT 17-JUN-2002 (first entry);  
 DE CTL epitope HLA peptide SEQ ID NO:106.  
 XX Human; 158p1H4; chromosome 8q22q23, 158p1F4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX Homo sapiens  
 CS Synthetic.  
 XX  
 XX WC2002:16598-A2.  
 XX  
 XX 28 FEB 2002.  
 XX  
 XX 22-AUG-2001; 2001WO-US26411.  
 XX  
 XX 22-AUG-2000; 2000US-227098P.  
 XX 10-APR-2001; 2001US-282739P.  
 XX  
 XX (AGEN: AGENSYS INC.  
 XX  
 XX Chaitin-Eld PM, Hubert RS, Raitano AB, Afari DEH, Levin E,  
 XX Faris M, Ge W, Jakobovits A;  
 XX WPI; 2002-269357/31.  
 XX  
 XX Monitoring 158p1H4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer,  
 XX comprises identifying presence of aberrant 158p1H4 gene products in  
 XX biological sample  
 XX  
 XX Claim 64; Page 152; 209pp; English.

PS The present invention describes a method for monitoring 158p1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158p1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158p1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158p1H4 gene products in the sample.  
 CC 158p1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158p1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158p1H4 proteins may be used in assessing the status  
 CC of 158p1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating agents or cellular factors  
 CC that bind to 158p1H4 or its particular domain, and for generating



CC domain specific antibodies, for identifying agents or cellular factors  
CC that bind to 158PIH4 or its particular domain, and for generating  
CC cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
CC and prognostic assays, in treating patients with cancer, in generating  
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
CC and as immunological reagents for detecting 158PIH4-expressing cells.  
CC The antibodies are particularly useful in bladder cancer diagnosis and  
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
CC located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
CC the present invention has been located to chromosome 8q23. ABL50420 to  
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 9 AA;

Query Match 49.1%; Score 27; DB 23; Length 3;  
Best Local Similarity 55.6%; Pred. No. 9.3e+06;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
: : : : :  
DB 1 NTFDIATKK 9

RESULT 8  
AAB94468  
ID ABB94466 standard; Peptide; 10 AA.  
XX  
AC ABB94466;  
XX  
DT 17 JUN-2002 (first entry)  
XX  
DE CTL epitope HLA peptide SEQ ID NO:395.  
XX  
KW Human; 158PIH4; chromosome 8q220q23, 158PIH4; chromosome 8q22, cancer;  
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL, HLA;  
KW human leukocyte antigen; helper T lymphocyte; HTL.  
XX  
CS Homo sapiens.  
CS Synthetic.  
XX  
FN WO200215598 A1.  
XX  
FD 28 FEB. 2002.  
XX  
PF 22-AUG-2001; 2001WO US26411.  
XX  
PE 22-AUG-2000; 2001US 221598P.  
PR 10-APR 2001; 2001US-282739P.  
XX  
PA (AGEN-1) AGENSYS INC.  
XX  
PI Chaitin-Rid PM, Hubert RS, Rattato AB, Atlas LBH, Lavin E,  
PI Faris M, Ge W, Jakobovits A.  
XX  
WP; 2002-269357/31.  
XX  
PT Monitoring 158PIH4 gene products in biological sample from patient who  
PT has or is suspected of having cancer, useful for treating cancer,  
PT comprises identifying presence of aberrant 158PIH4 gene products in  
PT biological sample -  
XX  
PS Claim 64; Page 155; 209pp; English  
XX  
CC The present invention describes a method for monitoring 158PIH4 gene  
CC products in a biological sample from a patient who has or is suspected  
CC of having cancer. The method comprises determining the status of 158PIH4  
CC gene products in a tissue sample from an individual, comparing the  
CC status to the status of 158PIH4 gene products in a normal sample, and  
CC identifying the presence of aberrant 158PIH4 gene products in the sample.  
CC 158PIH4 sequences have cytostatic activity and can be used in vaccine  
CC production. 158PIH4 polynucleotides may be used in "monitoring genetic  
CC abnormalities. The 158PIH4 proteins may be used in assessing the status

CC of 158PIH4 gene products in normal versus cancerous tissues and so  
CC elucidating the malignant phenotype, in generating and characterising  
CC domain-specific antibodies, for identifying agents or cellular factors  
CC that bind to 158PIH4 or its particular domain, and for generating  
CC cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
CC and prognostic assays, in treating patients with cancer, in generating  
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
CC and as immunological reagents for detecting 158PIH4-expressing cells.  
CC The antibodies are particularly useful in bladder cancer diagnosis and  
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
CC located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
CC the present invention has been located to chromosome 8q23. ABL50400 to  
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 10 AA;

Query Match 49.1%; Score 27; DB 23; Length 10;  
Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
: : : : :  
DB 2 NTFDIATKK 10

RESULT 9  
AAR27999  
ID AAR27999 standard; peptide; 6 AA.  
XX  
AC AAR27999;  
XX  
DT 25-MAR-2003 (updated);  
DT 17 MAR-1993 (first entry);  
XX  
DE Tryptic peptide fragment #17.  
XX  
KW Insulin receptor substrate-1; IRS 1; antibody; proteolytic cleavage;  
KW 1D-SDS PAGE.  
XX  
OS Rattus rattus.  
XX  
FN WO9211083 A1.  
XX  
PD 06-AUG-1992  
XX  
PF 17-JAN-1992; 92WO US00437.  
XX  
PR 18-JAN-1991; 91US-0643982.  
XX  
PA (JOSL-1) JOSLIN DIABETES CENT INC.  
XX  
PI Kahn CR, Rotherberg PL, White MF;  
XX  
WP; 1992-365881/44.  
XX  
PT Purified nucleic acid encoding Insulin Receptor Substrate - used  
PT to prepare IRS-1, for diagnosis and treatment of insulin related  
PT diseases and abnormal cellular proliferation  
XX  
PS Disclosure; Page 26; 128pp; English.  
XX  
CC The sequences given in AAR27983-8000 and AAR28044 are fragments from  
CC insulin receptor substrate-1 (IRS-1). These fragments were used to  
CC determine the sequence of IRS-1 and to distinguish it from proteins  
CC which are co-purified with it. Antibodies were raised against the  
CC IRS-1 proteins and were used to remove them from the reaction media.  
CC These peptides were formed by proteolytic cleavage of proteins  
CC isolated by 1D-SDS PAGE to be approx. 185 kD.  
CC (updated on 25-MAR 2001 to correct PN field.)  
XX  
SQ Sequence 8 AA;





XX CYTEC CYTEC CORP.  
 XX PA  
 XX PT Cells P. Grey HX. Kube RT. Sette A.  
 XX RP  
 XX WP1: 1994-065403/0A.  
 XX  
 XX Peptide which specifically binds selected MHC alleles, used to  
 XX induce an immune response for treatment or prevention of viral  
 XX infection or cancer, or for diagnosis  
 XX  
 XX Example 6: Page 51: 150pp: English  
 XX  
 XX The sequences given in AAR4304-13 and AAR4301-14 are immunoprecip-  
 XX ited peptides which have a HLA-A1.2, HLA-A1 or a HLA-A11 binding motif.  
 XX These peptides may be used in the composition of the invention  
 XX CC These peptides are capable of binding selected MHC molecules and  
 XX CC inducing an immune response. They can be used to treat and/or  
 XX CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,  
 XX CC hepatitis or AIDS. They can also be used to produce antibodies for  
 XX CC use as diagnostic or therapeutic agents. The peptides can also be  
 XX CC used as diagnostic agents.  
 XX CC (Updated on 25-MAR-2003 to correct EN field.)  
 XX CC (Updated on 14-MAR-2003 to correct ES field.)  
 XX  
 XX SQ Sequence 9 AA:  
 XX  
 XX Query Match 45.5%; Score 25; DB 15; Length 9;  
 XX Best Local Similarity 57.1%; Pred. No. 0.3e+05;  
 XX Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 4 FEDSTKK LC  
 XX II | | | | |  
 XX : FEDSTPP P  
 XX  
 XX PEARCE P  
 XX AAY5502  
 XX ID AAY5502 standard; peptide: 9 AA.  
 XX AC AAY255 4;  
 XX  
 XX DT 22-SEP-1999 (first entry)  
 XX  
 XX DE Insulin-like growth factor binding protein fragment 100.  
 XX  
 XX KW Insulin-like growth factor binding protein (IGF-binding protein-3) (IGFBP3)  
 XX KW antiproliferative, anti-inflammatory; glycoprotein; muscle relaxant;  
 XX KW shrinkage; wound-healing; osteoporosis; diabetes; myasthenia gravis;  
 XX KW neoplasia; inflammation; cancer; long-term disease; muscle wastage;  
 XX KW muscle, bone apparatus; wound healing; body building; gene therapy;  
 XX KW diabetes; nervous system; lymph glands; steroid administration.  
 XX  
 XX OS Unidentified.  
 XX  
 XX PN DEL3757250 A1.  
 XX  
 XX PO 01-JUL-1999.  
 XX  
 XX UF 22-DEC-1997; 94DE-1057250.  
 XX  
 XX UR 22-DEC-1997; 94DE-1057250.  
 XX  
 XX PA (FORS) FORSMANN W.  
 XX  
 XX PI Forstmann W, Kling L, Mostafaei H, Grendel H, Kling H,  
 XX PI Staendker L;  
 XX  
 XX CR WP1: 1999-372233/12.  
 XX  
 XX XX An insulin-like growth factor binding protein  
 XX Claim 12; Page 19, 26pp; German.

XX This invention describes a novel, insulin-like growth factor binding  
 XX protein (IBP) constructed using the formula R1-C-X1-PNC-X2-QC-X3-CWCV  
 XX X4-C-R2 where cyclic, glycosylated, phosphorylated, acetylated, amidated,  
 XX sulphated derivatives and fragments of these with the physiological  
 XX ability of IBP are included and R1NH2 - an amino acid or peptide with a  
 XX sequence of up to 41 amino acid residues, X1 = a peptide consisting of  
 XX 24-31 amino acids, X2 = a peptide consisting of 9 amino acids, X3 = a  
 XX peptide consisting of 10 amino acids, X4 = a peptide consisting of 18-24  
 XX amino acids, R2COOH = CONH2 or a peptide with up to 12 amino acids. The  
 XX products of the invention have immunoprotective, antiproliferative,  
 XX anti-inflammatory and cytostatic activity. The IBP peptides, complexes,  
 XX antibodies, inhibitors and antisense nucleic acids are all useful in  
 XX the treatment of muscle loss/shrinkage/wasting, osteoporosis, diabetes,  
 XX amyloid lateral sclerosis, peripheral and central neuropathies,  
 XX inflammatory processes, cancer, inflammatory and neoplastic diseases,  
 XX growth disturbances, diseases of the muscles, diseases of the bone  
 XX apparatus and wound or bone healing. The nucleic acids and antisense  
 XX oligonucleotides can be used in somatic or non-somatic gene therapy. The  
 XX peptides, etc., can be used in diagnosis of functional deficiencies in  
 XX bones, muscles, nervous systems, lymph glands, stomach/intestinal tracts,  
 XX immune systems, for diabetes, inflammatory and neoplastic processes and  
 XX also as a marker for cancer. This sequence represents a specific claimed  
 XX example of a peptide which can occupy the R2 position of the IBP of the  
 XX invention.  
 XX  
 XX SQ Sequence 9 AA:  
 XX  
 XX Query Match 45.5%; Score 25; DB 20; Length 9;  
 XX Best Local Similarity 56.7%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 2 HTFDS 7  
 XX II | | | | |  
 XX : HTFDS 6  
 XX  
 XX Search completed: November 5, 2003, 17:12:30  
 XX Job time : 34.3133 secs

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QX protein: protein search, using sw model

Run on: November 5, 2003, 17:14:46 / Search time 21 seconds  
(without alignments)  
81.79% Million cell of 11.08/sec

Title: US-09-914-088-4  
Perfect score: 55  
Sequence: 1 GHTFEDSTKK 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 644279 seqs, 171749284 residues

Total number of hits satisfying chosen parameters: 81026

Minimum DB seq length: 6  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.fpp\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCF\_NEW\_PUB.fpp\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.fpp\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.fpp\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.fpp\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCFUS\_PUBCOMB.fpp\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.fpp\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.fpp\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.fpp\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.fpp\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.fpp\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.fpp\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.fpp\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.fpp\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.fpp\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.fpp\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.fpp\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_PUBCOMB.fpp\*

Pred. No. is the number of results identified by the search engine  
score greater than or equal to the score of the best result printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	12	US-10-082-014-275
2	55	100.0	10	12	US-10-372-076-129
3	27	49.1	9	12	US-09-935-384-16
4	27	49.1	9	12	US-09-935-384-17
5	27	49.1	9	12	US-09-935-384-18
6	27	49.1	10	12	US-09-935-384-195
7	26	47.3	9	11	US-09-880-748-2354
8	26	47.3	10	12	US-09-935-384-17
9	25	45.5	7	10	US-09-884-767A-10
10	25	45.5	10	12	US-09-755-630A-222
11	24	43.6	7	11	US-09-281-495-18
12	24	43.6	10	11	US-09-572-434P-1981
13	24	43.6	10	15	US-10-268-561-7
14	23	41.8	7	10	US-09-884-767A-27
15	23	41.8	9	12	US-10-190-082-190

Query Match 100.0% Score 55; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00072;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV : GHTFEDSTKK 10  
| | | | |  
DB 1 GHTFEDSTKK 10

RESULT 2  
US-10-372-076-129  
; Sequence 129, Application US/10372076  
; Publication No. US20030198645A;  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

Sequence 9, Appl  
Sequence 45, Appl  
Sequence 497, Appl  
Sequence 1, Appl  
Sequence 147, Appl  
Sequence 216, Appl  
Sequence 38, Appl  
Sequence 2, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 146, Appl  
Sequence 1601, Ap  
Sequence 2303, Ap  
Sequence 12, Appl  
Sequence 95, Appl  
Sequence 253, Appl  
Sequence 361, Appl  
Sequence 138, Appl  
Sequence 100, Appl  
Sequence 219, Appl  
Sequence 63, Appl  
Sequence 757, Ap  
Sequence 1905, Ap  
Sequence 3735, Ap  
Sequence 2, Appl  
Sequence 3740, Ap  
Sequence 2, Appl  
Sequence 116, Appl  
Sequence 201, Appl

## ALIGNMENTS

RESULT 1  
US-10-082-014-275  
; Sequence 275, Application US/10082014  
; Publication No. US20030195858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birrett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N TERMINAL C  
; FILE REFERENCE: ICC-130.C 4564/85.24  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO: 275  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014 275

FILE REFERENCE: 4564/87179  
 CURRENT APPLICATION NUMBER: US/10/172,076  
 PRIOR FILING DATE: 2003-02-21  
 PRIOR APPLICATION NUMBER: 10/580,299  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/582,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 3.2  
 SEQ ID NO 129  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-172-076-129

Query Match 100.0% Score 35; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : GTFEDSTKK 10  
 |||||  
 DB 1 GTFEDSTKK 10

## RESULT 3

US-09-935-384-306  
 Sequence 36, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-00  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 36  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-306

Query Match 49.1% Score 27; DB 12; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.8e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB : NTFDIATKK 9

## RESULT 4

US-09-935-384-212  
 Sequence 212, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-00  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 36  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-306

APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-00  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 212  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-212

Query Match 49.1% Score 27; DB 12; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.8e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB : NTFDIATKK 9

## RESULT 5

US-09-935-384-306  
 Sequence 306, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-00  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 306  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-306

Query Match 49.1% Score 27; DB 12; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.8e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB : NTFDIATKK 9

## RESULT 6

US-09-935-384-395  
 Sequence 395, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-00  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 395  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-395

```

; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 159P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51159 2003.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 10
; TYPE: FRT
; ORGANISM: Homo sapiens
US 09-935-384-395

Query Match 49.1%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10
DB 2 HTFEDATKK 10

RESULT 7
US-09-880-748-2359
; Sequence 3959, Application US/09980748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Robert et al.
; TITLE OF INVENTION: Antibodies that Immunorecognize Fully and
; FILE REFERENCE: IF523
; CURRENT APPLICATION NUMBER: US/09/880,749
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2959
; LENGTH: 9
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-880-748-2359

Query Match 47.3%; Score 25; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTFEDS 7
DB 3 GHTFCS 9

RESULT 8
US-09-935-384-67
; Sequence 67, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA

```

```

; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 159P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51159 2003.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,096
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 10
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-935-384-67

Query Match 47.3%; Score 26; DB 12; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HTFEDSTKK 10
DB 1 HTFEDATKK 9

RESULT 9
US-09-884-767A-20
; Sequence 20, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Lureau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-312.1 US, DYX-012.1 ECT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,121
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 7
; TYPE: FRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-20

Query Match 45.5%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFED 6
DB 1 HTFSD 5

RESULT 10
US-09-755-130A-222
; Sequence 222, Application US/09755130A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, VIKTAKA K.
; APPLICANT: ASTWALO, JAMES D.

```

```

1 APPLICANT: SAMPSON, HUGH A.
2 APPLICANT: SCHWARTZ, CHARLES A.
3 TITLE OF INVENTION: PREPARATION OF DIALYZERIZED PROTEINS AND PEPTIDES
4 FILE REFERENCE: 11999-0217 NPS00 (MKT-17)
5 CURRENT APPLICATION NUMBER: US/09/766,630A
6 CURRENT FILING DATE: 2001-01-05
7 PRIOR APPLICATION NUMBER: US 60/174,669
8 PRIOR FILING DATE: 2000-01-04
9 NUMBER OF SEQ ID NOS: 293
10 SOFTWARE: Patent in version 3.0
11 SEQ ID NO: 222
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Synthetic polypeptide
17 US 09-755-632A-22

Query Match 45.5% Score 25; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.64e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 3 HTFEDSK 10
DB 2 TFEELKP 9

RESULT 11
US-09-751-495-18
1 Sequence 18, Application US/09281-495
2 Publication No. US2003009765A1
3 GENERAL INFORMATION:
4 APPLICANT: Pomeroy, Roger J
5 APPLICANT: Bouhadani, Mohamed
6 APPLICANT: Duang, Bora Xin
7 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING A PLASMA TO A
8 TITLE OF INVENTION: VIRION
9 FILE REFERENCE: 9801-2501
10 CURRENT APPLICATION NUMBER: US/09/281-495
11 PRIOR FILING DATE: 1999-03-30
12 EARLIER APPLICATION NUMBER: US 60/239,600
13 EARLIER FILING DATE: 1998-03-30
14 NUMBER OF SEQ ID NOS: 58
15 SOFTWARE: Patent in Ver. 2.1
16 SEQ ID NO: 18
17 LENGTH: 7
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificial Sequence: This is a synthetic peptide
22 OTHER INFORMATION: Polypeptide Building Blocks
23 US 09-281-495-18

Query Match 43.6% Score 24; DB 10; Length 10;
Best Local Similarity 66.1%; Pred. No. 8.84e+01;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 2 HTFEDS 7
DB 2 HSEFVS 7

RESULT 12
US-09-572-424B-1981
1 Sequence 1981, Application US/09572-424B
2 Publication No. US2003007837A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide binds to the human p50/p105
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572-424B
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 4203

```

```

10 SOFTWARE: ProtPatent version 1.0
11 SEQ ID NO 1981
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 FEATURE:
16 OTHER INFORMATION: Sequence located in CMKRL OR DEZ at 328-337 and may interact w
17 OTHER INFORMATION: Sequence 1982 in this patent.
18 US-09-572-424B 1981

Query Match 43.6% Score 24; DB 11; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

CY 1 HTFEDSK 9
DB 1 GETFPDKLR 9

RESULT 13
US-10-268-501-7
1 Sequence 7, Application US/10268501
2 Publication No. US2003008924A1
3 GENERAL INFORMATION:
4 APPLICANT: Silkowski, Mark X.
5 TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
6 FILE REFERENCE: P1467R2P1
7 CURRENT APPLICATION NUMBER: US/10/268-501
8 CURRENT FILING DATE: 2002-10-10
9 PRIOR APPLICATION NUMBER: US 09/602,812
10 PRIOR FILING DATE: 2000-06-23
11 PRIOR APPLICATION NUMBER: US 60/143,316
12 PRIOR FILING DATE: 1999-06-25
13 NUMBER OF SEQ ID NOS: 11
14 SEQ ID NO: 7
15 LENGTH: 10
16 TYPE: PRT
17 ORGANISM: Mus musculus
18 FEATURE:
19 NAME/KEY: unsure
20 LOCATION: 10
21 OTHER INFORMATION: unknown amino acid
22 US-10-268-501-7

Query Match 43.6% Score 24; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 HTFEDSK 8
DB 1 GETFPDKLR 8

RESULT 14
US-09-984-767A-27
1 Sequence 27, Application US/09884767A
2 Publication No. US2003192789A1
3 GENERAL INFORMATION:
4 APPLICANT: Dyax Corp.
5 APPLICANT: Lev, Arthur C.
6 APPLICANT: Lureau, Christopher J.
7 APPLICANT: Ladner, Robert C.
8 TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
9 FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
10 CURRENT APPLICATION NUMBER: US/09/884,767A
11 CURRENT FILING DATE: 2001-06-13
12 PRIOR APPLICATION NUMBER: US 09/597,321
13 PRIOR FILING DATE: 2000-06-19
14 NUMBER OF SEQ ID NOS: 217
15 SOFTWARE: Patent in version 3.0
16 SEQ ID NO: 27
17 LENGTH: 7
18 TYPE: PRT

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? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: synthetic enterotoxinase cleavage sequence
US-09-914-088-4

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Query Match: 41.8% Score 237 DB 100 Length 7
Best Local Similarity 57.1% Pred. No: 5.9e+05
Matches 4: Conservative 1: Mismatches 0: Gaps 0

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CY 1 GTFERS 7
DE 1 GTFERS 7

```

```

RESULT 15
US-10-190-082-1
? Sequence 180: Application US/1019008
? Publication No US20030148264A1
? GENERAL INFORMATION:
? APPLICANT: Lusk, Lawrence A.
? APPLICANT: Singh, Sachdev S.
? APPLICANT: Heid, Heike A.
? TITLE OF INVENTION: PHAGE DISPLAYED POZ DOMAIN LIGAND
? FILE REFERENCE: P1905P
? CURRENT APPLICATION NUMBER: US/10/190,082
? CURRENT FILING DATE: 2002-07-03
? PRIOR APPLICATION NUMBER: US 60/303,834
? PRIOR FILING DATE: 2001-07-06
? NUMBER OF SEQ ID NOS: 683
? SEQ ID NO 180
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: Synthetic
US-10-190-082-10

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```

Query Match: 41.8% Score 237 DB 100 Length 9
Best Local Similarity 57.1% Pred. No: 5.9e+05
Matches 4: Conservative 1: Mismatches 0: Gaps 0

```

```

CY 1 GTFERS 7
DE 1 GTFERS 7

```

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Search completed: November 5, 2003, 17:45:00
Job time 1.1 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2001 CorpuGen Ltd.

OV protein protein search, using sw model

Run on: November 5, 2003, 17:35:40 ; Search time 12.1133 seconds  
Without alignment  
14,104 Million cell updates/sec

Title: US 09 914 088-4  
Perfect score: 55  
Sequence: 1 GHTPDSSTKK 10

Scoring table: RASJMA-2  
Gapop 10.0 ; Gapext 0.5

Searched: 328717 seqs, 423:0858 residues

Total number of hits satisfying chosen parameters: 9,158

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA\*  
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2: /cgn2\_6/ptodata/1/aa/5S-COMB.pep\*  
3: /cgn2\_6/ptodata/1/aa/5A-COMB.pep\*  
4: /cgn2\_6/ptodata/1/aa/5B-COMB.pep\*  
5: /cgn2\_6/ptodata/1/aa/PTUS-COMB.pep\*  
6: /cgn2\_6/ptodata/1/aa/backfiles.pep\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	8	1	US-08-094-948A-21
2	26	47.3	8	5	PCT-US96/09119-21
3	25	45.5	9	3	US-08-159-339A-21
4	25	45.5	9	3	US-08-159-339A-104
5	25	45.5	10	3	US-08-159-339A-44
6	24	43.6	7	4	US-09-281-435-19
7	24	43.6	10	2	US-08-966-348-8
8	24	43.6	10	3	US-09-188-401-8
9	24	43.6	10	3	US-09-188-404-8
10	24	43.6	10	3	US-09-281-259-8
11	24	43.6	10	4	US-09-117-860-8
12	23	41.8	8	2	US-08-424-232-2
13	23	41.8	9	1	US-08-149-809-19
14	23	41.8	9	4	US-09-267-991-9
15	22	40.0	6	4	US-09-081-975-22
16	22	40.0	7	4	US-09-281-435-22
17	22	40.0	8	1	US-08-487-860-61
18	22	40.0	9	1	US-08-149-809-23
19	22	40.0	9	3	US-08-159-339A-282
20	22	40.0	9	3	US-08-159-339A-1196
21	22	40.0	9	4	US-09-238-924-31
22	22	40.0	10	1	US-08-235-946-51
23	22	40.0	10	1	US-08-487-860-61
24	22	40.0	10	6	5198347-23
25	21	38.2	5	4	US-09-187-859-1263
26	21	38.2	5	4	US-09-187-859-1265
27	21	38.2	5	4	US-09-187-859-3719

28	21	38.2	5	4	US-09-839-542B-1757	Sequence 1757, Ap
29	21	38.2	5	4	US-09-839-542B-1905	Sequence 1905, Ap
30	21	38.2	5	4	US-09-839-542B-3739	Sequence 3739, Ap
31	21	38.2	6	4	US-09-187-859-3740	Sequence 3740, Ap
32	21	38.2	6	4	US-08-982-285-2	Sequence 2, App.1
33	21	38.2	6	4	US-09-839-542B-3740	Sequence 3740, Ap
34	21	38.2	6	4	US-08-577-635-72	Sequence 72, App.1
35	21	38.2	6	5	PCT-US93-00136-8	Sequence 8, App.1
36	21	38.2	7	1	US-08-421-702A-12	Sequence 12, App.1
37	21	38.2	7	1	US-08-353-052A-8	Sequence 8, App.1
38	21	38.2	7	1	US-08-353-052A-12	Sequence 12, App.1
39	21	38.2	7	1	US-08-421-696A-12	Sequence 12, App.1
40	21	38.2	7	1	US-08-421-697A-12	Sequence 12, App.1
41	21	38.2	7	1	US-08-421-698A-12	Sequence 12, App.1
42	21	38.2	7	2	US-08-421-695A-12	Sequence 12, App.1
43	21	38.2	7	5	PCT-US95-04741-12	Sequence 12, App.1
44	21	38.2	8	1	US-08-346-455B-45	Sequence 45, App.1
45	21	38.2	8	2	US-08-686-599A-11	Sequence 11, App.1

## ALIGNMENTS

RESULT 1  
US-08-094-948A-21  
; Sequence 21, Application US/08094948A  
; Patent No. 5621875  
; GENERAL INFORMATION:  
; APPLICANT: Kahn, C. Ronald  
; APPLICANT: White, Morris F.  
; APPLICANT: Rothenberg, Paul Louis  
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cookfield  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/094,948A  
; FILING DATE: 21-JULY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/643,982  
; FILING DATE: 18-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis (PLM)  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: JDP-013DV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-094-948A-21

Query Match: 47.3%; Score 26; DB 1; Length 8;  
Best Local Similarity 62.5%; Pred. No. 2, Seq+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0;

QY 3 TREDSTKK 10

Db : TREDSTKK 8

```

1  RESULT 2
2  PCT US96-09419-A.1
3  Sequence 21, Application PC/TUS9609419
4  GENERAL INFORMATION:
5  APPLICANT: Kamm, C. Ronald
6  APPLICANT: White, Morris F.
7  APPLICANT: Rotherberg, Paul, Louis
8  TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
9  NUMBER OF SEQUENCES: 29
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Iahive & Cockfield
12 STREET: 60 State Street, Suite 510
13 CITY: Boston
14 STATE: Massachusetts
15 COUNTRY: U.S.A.
16 ZIP: 02109
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC Compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US96/09419
24 FILING DATE:
25 PRIORITY APPLICATION DATA:
26 APPLICATION NUMBER: US 08/094,948
27 FILING DATE: 21-JULY-1993
28 APPLICATION NUMBER: US 07/64,982
29 FILING DATE: 18-JAN-1993
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Myers, Louis (PLM)
32 REGISTRATION NUMBER: 35,965
33 REFERENCE/DOCKET NUMBER: JDP-0110V
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (617)227-7400
36 TELEFAX: (617)227-5941
37 INFORMATION FOR SEQ ID NO: 21:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8 amino acids
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: peptide
44 US-08-159-319A-B5
45 Query Match 47.1%, Score 20, DB 3, Length 8;
46 Best Local Similarity 62.5%, Pred. No. 2.5e+05,
47 Matches 5, Conservative 2, Mismatches 1, Gaps 0;
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49 QY 3 TFEOSTKK 10
50 DE 1 TFEOSTKK 8
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52 RESULT 3
53 US-08-159-319A-B5
54 Sequence 85, Application US/08:59339A
55 Patent No. 6037135
56 GENERAL INFORMATION:
57 APPLICANT: Kubo, Ralph T.
58 APPLICANT: Grey, Howard M.
59 APPLICANT: Sette, Alessandro
60 APPLICANT: Celis, Esteban
61 TITLE OF INVENTION: HLA Binding peptides and Their
62 NUMBER OF SEQUENCES: 1254
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Townsend and Townsend and Crew LLP
65 STREET: Two Embarcadero Center, Eighth Floor
66 CITY: San Francisco
67 STATE: CA
68 COUNTRY: USA
69 Zip: 94111-3834
70 COMPUTER READABLE FORM:
71 MEDIUM TYPE: Diskette
72 COMPUTER: IBM Compatible
73 OPERATING SYSTEM: DOS
74 SOFTWARE: FastSeq for Windows Version 2.0
75 CURRENT APPLICATION DATA:
76 APPLICATION NUMBER: US/08/159,339A
77 FILING DATE: 29 NOV-1993
78 CLASSIFICATION: 424
79 PRIOR APPLICATION DATA:
80 APPLICATION NUMBER: US 07/926,666

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1  ZIP: 94111-3834
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Diskette
4  COMPUTER: IBM Compatible
5  OPERATING SYSTEM: DOS
6  SOFTWARE: FastSeq for Windows Version 2.0
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/159,339A
9  FILING DATE: 29-NOV-1993
10 CLASSIFICATION: 424
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/926,666
13 FILING DATE: 07-AUG-1992
14 APPLICATION NUMBER: US 08/027,746
15 FILING DATE: 05-MAR-1993
16 APPLICATION NUMBER: US 08/103,396
17 FILING DATE: 06-AUG-1993
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Weber, Ellen Lauver
20 REGISTRATION NUMBER: 32,762
21 REFERENCE/DOCKET NUMBER: 019623-0050300US
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (415) 576-0200
24 TELEFAX: (415) 576-0300
25 TELEX:
26 INFORMATION FOR SEQ ID NO: 95:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 9 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 US-08-159-319A-B5
34 Query Match 45.5%, Score 25, DB 3, Length 9;
35 Best Local Similarity 57.1%, Pred. No. 2.5e+05,
36 Matches 4, Conservative 2, Mismatches 1, Indels 0; Gaps 0;
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38 QY 4 FFDSTKK 10
39 DE 1 FFDSTKK 7
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41 RESULT 4
42 US-08-159-319A-1004
43 Sequence 1004, Application US/08:59339A
44 Patent No. 6037135
45 GENERAL INFORMATION:
46 APPLICANT: Kubo, Ralph T.
47 APPLICANT: Grey, Howard M.
48 APPLICANT: Sette, Alessandro
49 APPLICANT: Celis, Esteban
50 TITLE OF INVENTION: HLA Binding peptides and Their
51 NUMBER OF SEQUENCES: 1254
52 CORRESPONDENCE ADDRESS:
53 ADDRESSEE: Townsend and Townsend and Crew LLP
54 STREET: Two Embarcadero Center, Eighth Floor
55 CITY: San Francisco
56 STATE: CA
57 COUNTRY: USA
58 Zip: 94111-3834
59 COMPUTER READABLE FORM:
60 MEDIUM TYPE: Diskette
61 COMPUTER: IBM Compatible
62 OPERATING SYSTEM: DOS
63 SOFTWARE: FastSeq for Windows Version 2.0
64 CURRENT APPLICATION DATA:
65 APPLICATION NUMBER: US/08/159,339A
66 FILING DATE: 29 NOV-1993
67 CLASSIFICATION: 424
68 PRIOR APPLICATION DATA:
69 APPLICATION NUMBER: US 07/926,666

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1 FILING DATE: 07-AUG-1992
2 APPLICATION NUMBER: US 08/027,746
3 FILING DATE: 05-MAR-1993
4 APPLICATION NUMBER: US 08/103,196
5 FILING DATE: 06-AUG-1993
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Weber, Ellen Lauver
8 REGISTRATION NUMBER: 32,762
9 REFERENCE/DOCKET NUMBER: 019623-005030US
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (415) 576-0200
12 TELEFAX: (415) 576-0300
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MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/98/966,464  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 311,235/1996  
 FILING DATE: 8-NOV-1996  
 PRIOR APPLICATION DATA: JP 61,716/97  
 FILING DATE: 3 MAR 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-966 388 8  
 Query Match: 43.6% Score 24; DB 3; Length 10;  
 Best Local Similarity 57.1%; Freq. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CQ 1 CHUFFED 7  
 DB 1 CHUFFED 7

RESULT 2  
 US-09-188-424-8  
 Sequence 8, Application US/09188404  
 Patent No. 6,454,877  
 GENERAL INFORMATION:  
 APPLICANT: TORIYUKI, NISHIMOTO  
 APPLICANT: MICHIO KUROTA  
 APPLICANT: HIROTO CHAEN  
 APPLICANT: TOSHIO MIYAKE  
 TITLE OF INVENTION: KJBILOSE PHOSPHORYLASE, ITS PREPARATION AND USES  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/188,464  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/966,388  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 61,716/97  
 FILING DATE: 3-MAR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-188-424-8  
 Query Match: 43.6% Score 24; DB 3; Length 10;  
 Best Local Similarity 57.1%; Freq. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CQ 1 CHUFFED 7  
 DB 1 CHUFFED 7

RESULT 9  
 US-09-188-424-8  
 Sequence 8, Application US/09188404  
 Patent No. 6,454,877  
 GENERAL INFORMATION:  
 APPLICANT: TORIYUKI, NISHIMOTO  
 APPLICANT: MICHIO KUROTA  
 APPLICANT: HIROTO CHAEN  
 APPLICANT: TOSHIO MIYAKE  
 TITLE OF INVENTION: KJBILOSE PHOSPHORYLASE, ITS PREPARATION AND USES  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/188,464  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/966,388  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 61,716/97  
 FILING DATE: 3-MAR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

US-09-188-404-8

Query Match 43.6% Score 24; DB 1; Length 10;

Best Local Similarity 57.1% Pred. No. 1.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTEFS 7

DB 1 GHTEFS 7

RESULT 10

US-09-281-259-8

Sequence 9, Application US/09281259

Patent No. 6204377

GENERAL INFORMATION:

APPLICANT: TOMOYUKI NISHIMOTO

APPLICANT: MICHIO KUBOTA

APPLICANT: HIROKO CHAEN

APPLICANT: TOSHIO MIYAKE

TITLE OF INVENTION: KOLIBRIOS PROSPORYLASE, ITS PREPARATION AND USES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 800

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.10

CURRENT APPLICATION DATA: US/09/281-259

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/966,388

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 61,710,797

FILING DATE: 3-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,518

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 528 5197

TELEFAX: 202 737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

US-09-281-259-8

Query Match 43.6% Score 24; DB 1; Length 10;

Best Local Similarity 57.1% Pred. No. 1.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTEFS 7

DB 1 GHTEFS 7

RESULT 11

US-09-117-860-8

Sequence 9, Application US/09117860A

Patent No. 6338955

GENERAL INFORMATION:

APPLICANT: OGURI, Suguru

APPLICANT: MINOWA, Mari

APPLICANT: YOSHIDA, Aritu

APPLICANT: TANIGUCHI, Naoyuki

APPLICANT: TAKEUCHI, Makoto

TITLE OF INVENTION: NOVEL 1, 4-N-ACTYLVISGLUCOSAMINYLTRANSFERASE AND GENE

FILE REFERENCE: 081356/0113

CURRENT APPLICATION NUMBER: US/09/117,860A

CURRENT FILING DATE: 1998-08-12

EARLIER APPLICATION NUMBER: WO 97/2697/04546

EARLIER FILING DATE: 1997-12-10

EARLIER FILING DATE: 1997-06-18

EARLIER APPLICATION NUMBER: JP 332411/1996

EARLIER FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO: 8

LENGTH: 10

TYPE: PRT

ORGANISM: Bovine

US-09-117-860-8

Query Match 43.6% Score 24; DB 4; Length 10;

Best Local Similarity 80.0% Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTEFS 5

DB 5 GHTEFS 9

RESULT 12

US-08-424-292-2

Sequence 2, Application US/08424292

Patent No. 5939273

GENERAL INFORMATION:

APPLICANT: Haurso, Stig

APPLICANT: Carlsson, John

APPLICANT: Kjelseter, Reid

APPLICANT: Gohansen, Tahir M.

APPLICANT: Larsen, Peter M.

APPLICANT: Gessen, Ulla A.

APPLICANT: Hey, Stephen J.

APPLICANT: Boutry, Marc

APPLICANT: Regard, Hervé

TITLE OF INVENTION: MARKERS FOR ORGAN REJECTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,292

FILING DATE: 18-APR-1995

CLASSIFICATION: 535

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1367-1-001

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5803  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 DESCRIPTION: Xaa at Position 1 is Gly or Leu; residue at Position 2 is Gly or Leu; residue at Position 3 is Gly or Leu; residue at Position 4 is Gly or Leu; residue at Position 5 is Gly or Leu; residue at Position 6 is Gly or Leu; residue at Position 7 is Gly or Leu; residue at Position 8 is Gly or Leu.  
 HYDROTHERMAL: NC

US-08-424-292-2  
 Query Match 41.8%; Score 23; DB 4; Length 8;  
 Best Local Similarity 80.0%; Pred No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHTFE 5  
 TL 2 GHTFE 5

RESULT 14  
 US-08-149-809-19  
 Sequence 19, Application US/08149809  
 Patent No. 549669  
 GENERAL INFORMATION:  
 APPLICANT: METCALFE, Dear D.  
 APPLICANT: MARLIN, Brian M.  
 APPLICANT: SAC, Pillars, V.S.  
 TITLE OF INVENTION: ICE-BINDING PEPTIDES OF A MALE  
 TITLE OF INVENTION: HEAT-STABLE CRUSTACEAN ALLERGEN DERIVED FROM SHRIMP  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/149,809  
 FILING DATE: 10 NOV 1993  
 CLASSIFICATION: 520  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A  
 REGISTRATION NUMBER: 29,769  
 REFERENCE/DOCKET NUMBER: 40399/183/NIHO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-149-809-19  
 Query Match 41.8%; Score 23; DB 4; Length 9;  
 Best Local Similarity 44.4%; Pred No. 2.5e-05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTFEDSTK 10  
 TL 1 HTFEDSTK 9

RESULT 14  
 US-09-267-993-9  
 Sequence 9, Application US/09267993  
 Patent No. 6349692  
 GENERAL INFORMATION:  
 APPLICANT: Jindal, Satish  
 APPLICANT: Regnier, Fred  
 APPLICANT: Evans, David  
 APPLICANT: Williams, Kevin  
 APPLICANT: Afevan, No. 634862tar  
 APPLICANT: Pallwal, Sandeep  
 APPLICANT: Pingali, Aruna  
 TITLE OF INVENTION: High Speed, automated, continuous flow,  
 FILE OF INVENTION: multi-dimensional molecular selection and analysis  
 FILE REFERENCE: SYP 101CN  
 CURRENT APPLICATION NUMBER: US/09/267,993  
 CURRENT FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 60/600,518  
 PRIOR FILING DATE: 1995-06-26  
 PRIOR APPLICATION NUMBER: 09/670,670  
 PRIOR FILING DATE: 1996-04-26  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 9  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 OTHER INFORMATION: peptide  
 US-09-267-993-5

Query Match 41.8%; Score 23; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHTFE 5  
 TL 4 GHTFE 8

RESULT 15  
 US-09-081-975-2  
 Sequence 2, Application US/09081975  
 Patent No. 6451975  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William  
 APPLICANT: Cost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 TITLE OF INVENTION: NRS 1, ANTIBODIES AND PROTEINS THEREOF, AND USES OF THE  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/946,207  
 FILING DATE: 12-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald

1 REGISTRATION NUMBER: 30,628  
 2 REFERENCE/DOCKET NUMBER: 47400  
 3 TELECOMMUNICATION INFORMATION:  
 4 TELEPHONE: 617-345-6054  
 5 TELEFAX: 617-345-1300  
 6 TELEX:  
 7 INFORMATION FOR SEQ ID NO: 2:  
 8 SEQUENCE CHARACTERISTICS:  
 9 LENGTH: 6 amino acids  
 10 TYPE: amino acid  
 11 STRANDEDNESS: single  
 12 TOPOLOGY: linear  
 13 US 09 081 975-2

Query Match: 40.0%; Score 22; DB 4; Ident 0;  
 Best Local Similarity: 100.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 3 TFE3 5  
 Db 1  
 1 TFE3 4

Search completed: November 5, 2003, 17:36:12  
 Job time: 13.333 secs



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OM protein: protein search, using sw model

Run on: November 5, 2003, 17:18:39 ; Search time 13.5 seconds  
(without alignments)  
56.999 Million cell updates/sec

Title: US-09-914-088-5

Perfect score: 51

Sequence: 1 GGGHFPPT 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 404

Minimum DB seq length: 0

Maximum DB seq length: 8

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	33.2	7	2 S42407	gramicidin S synth
2	18	35.3	5	2 C53284	T-cell receptor be
3	18	35.3	7	2 B61491	seed protein ws-5
4	18	35.3	8	2 PT0383	T-cell receptor be
5	16	31.4	6	2 PT0383	Ig heavy chain CRD
6	15	29.4	7	2 A61001	tryptophan, bas
7	15	29.4	8	2 PLO184	capid protein VP-
8	14	27.5	3	3 GKHU	growth-modulating
9	14	27.5	4	2 PLO140	carbon-monoxide de
10	14	27.5	4	2 I38898	GGT intrin 16 prot
11	14	27.5	5	2 B37928	acid prorelinase 1
12	14	27.5	6	2 A61429	sarcosine dehydrog
13	14	27.5	6	2 B56974	collagen alpha 1(I)
14	14	27.5	7	2 S71299	COL2 protein - Par
15	14	27.5	7	2 PT0383	Ig heavy chain CRD
16	14	27.5	8	2 S10596	adipokinetic hormo
17	14	27.5	8	2 B39745	endoglycosylseram
18	14	27.5	8	2 S16324	hypothetical prote
19	14	27.5	8	2 S21288	lectin - potato 1f
20	14	27.5	8	2 B47393	neuropeptide cala
21	14	27.5	8	2 S10793	myosin f - bovin
22	14	27.5	8	2 PT0559	T-cell receptor be
23	13	25.5	4	2 S53508	starvation-induced
24	13	25.5	6	2 GNC841	hepatyl dipeptida
25	13	25.5	6	2 A61049	halo-toxin - seed
26	13	25.5	6	2 A43129	neuropeptide GRPR
27	13	25.5	7	2 PH1408	Ig heavy chain V r
28	13	25.5	7	2 S58797	serine/threonine-s
29	13	25.5	8	2 A61348	red pigment-conde

## ALIGNMENTS

### RESULT 1

S42407

gramicidin S synthetase component II - Bacillus brevis (fragment)

C:Species: Bacillus brevis

C:Date: 20-Oct-1994 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996

C:Accession: S42407

R:Stein, T.; Vater, J.; Kruff, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc Dr

PEBS Lett. 340, 39-44, 1994

A:Title: Detection of 4'-phosphopantetheine at the thioester binding site for L-valin

A:Reference number: S42407; MUID:94164305; PMID:9119405

A:Accession: S42407

A:Molecule type: protein

A:Residues: 1-7 <STE>

Query Match 39.2%; Score 20; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGH 4

DB 2 GGH 4

### RESULT 2

C53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C:Accession: C53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 891-899, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity an

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: C53284

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <HAR>

A:Cross-references: DB:S60717; NID:g233916; PIDN:AA19519.1; PID:g233919

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60740)

C:Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

DB 3 GGG 5

### RESULT 3

E61491

seed protein ws-5 - winged bean (fragment)

C:Species: Psophocarpus tetragonolobus (winged bean)  
 C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
 C:Accession: E61491  
 R: Hirano, H.  
 A: Protein Chem. 8, 115-130, 1989  
 A>Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gels  
 A:Reference number: A61491; PMID:89351606; PMID:276119  
 A:Accession: E61491  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <R>  
 C:Keywords: glycoprotein; seed

Query Match 35.3%; Score 18; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3  
 ||  
 Db 5 GGG 7

#### RESULT 4

P10509  
 C:Cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 10-May-1997  
 C:Accession: P10509  
 J. Exp. Med. 174, 115-124, 1991  
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: P10509; PMID:91277601; PMID:711558  
 A:Accession: P10509  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <FE>  
 A:Experimental source: adult thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 35.3%; Score 18; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3  
 ||  
 Db 6 GGG 8

#### RESULT 5

P10280  
 Ig heavy chain CDR3 region (clone 4 918) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: P10280  
 R. Yamada, M., Wasserman, R., Reichard, B.A., Shann, S., Garton, A.J., Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J<sub>H</sub> gene segments in the CDR3 region of human IgG1 heavy chain CDR3  
 A:Reference number: P10280; PMID:91104337; PMID:1819102  
 A:Accession: P10280  
 A:Molecule type: DNA  
 A:Residues: 1-6 <YM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGHFP 6  
 ||  
 Db 1 GGGHFP 6

#### RESULT 6

A61081  
 tryptophyltin, basic - Rohde's leaf frog  
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
 C:Accession: A61081  
 R. Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.  
 Int. J. Pept. Protein Res. 33, 391-395, 1989  
 A>Title: Isolation, structure determination and synthesis of a novel tryptophan-containing peptide from the skin of *Phyllomedusa rohdei*  
 A:Reference number: A61081  
 A:Accession: A61081  
 A:Molecule type: protein  
 A:Residues: 1-7 <MON>  
 C:Comment: The biological activity of this peptide was not determined.  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hydroxyproline; skin  
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 29.4%; Score 15; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPT 8  
 ||  
 Db 2 PBS 4

#### RESULT 7

PL0184  
 capsid protein VP-1 - murine poliovirus (fragment)  
 C:Species: murine poliovirus, Theiler's encephalomyelitis virus  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995  
 C:Accession: PL0184  
 R. Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.  
 J. Exp. Med. 170, 2037-2049, 1989  
 A>Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogen specificity of murine poliovirus  
 A:Reference number: PL0184; PMID:90063468; PMID:2479706  
 A:Accession: PL0184  
 A:Molecule type: genomic RNA  
 A:Residues: 1-8 <ZUR>  
 C:Keywords: capsid protein

Query Match 29.4%; Score 15; DB 2; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 GGGHFP 6  
 ||  
 Db 2 GGGHFP 8

#### RESULT 8

GKHU  
 growth-modulating peptide - human  
 C:Species: Homo sapiens (man)  
 C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: A01421  
 R. Schlesinger, D.H.; Pickart, L.; Thaler, M.M.  
 Experientia 33, 324-325, 1977  
 A>Title: Growth modulating serum tripeptide is glycyl-histidyl-lysine.  
 A:Reference number: A01421; PMID:7752369; PMID:858356  
 A:Accession: A01421  
 A:Molecule type: protein  
 A:Residues: 1-3 <SCH>  
 A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth of others  
 C:Superfamily: unassigned animal peptides

Query Match 27.5%; Score 14; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
 ||  
 1 GH 2

RESULT 9  
 PL0140  
 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena  
 C:Species: Pseudomonas carboxydohydrogena  
 C:Date: 07-Sep-1990 #sequence\_revision: 07-Sep-1990 #text\_change: 28 Apr-1993  
 C:Accession: PL0140  
 R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
 Arch. Microbiol. 152, 335-341, 1989  
 A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrog  
 A:Reference number: PL0138; MUID:90056678; PMID:2618128  
 A:Accession: PL0140  
 A:Molecule type: protein  
 A:Residues: 1-4 <KRA>  
 C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me  
 C:Keywords: oxidoreductase

Query Match 27.5%; Score 14; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
 ||  
 2 GH 3

RESULT 10  
 I38888  
 COI intron 16 protein - Podospora anserina mitochondrion  
 C:Species: Mitochondrion Podospora anserina  
 C:Date: 03 Feb-1994 #sequence\_revision: 03-Feb-1994 #text\_change: 07-Dec-1999  
 C:Accession: I38888  
 R:Cummings, D.J.; Michel, F.; McNally, K.L.  
 Curr. Genet. 16, 381-406, 1989  
 A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I m  
 A:Reference number: A18327; MUID:90124722; PMID:2558803  
 A:Accession: I38888  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 <CUM>  
 A:Cross references: GB:X55026; GB:M12937; GB:M17134  
 C:GenetCS:  
 A:Genetic code: SQC3  
 C:Keywords: mitochondrion

Query Match 27.5%; Score 14; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
 ||  
 3 GH 4

RESULT 11  
 B37988  
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
 C:Species: Physarum polycephalum  
 C:Date: 28-Jun-1991 #sequence\_revision: 28-Jun-1991 #text\_change: 30-Sep-1993  
 C:Accession: B37988  
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, G.; Takeuchi, T.; Kitagaki-Og  
 J. Biol. Chem. 265, 19898-19903, 1990  
 A:Title: Purification and characterization of a novel intracellular acid proteinase from  
 A:Reference number: A37988; MUID:91060608; PMID:2246266  
 A:Accession: B37988  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <MUR>

Query Match 27.5%; Score 14; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 3 PP 4

RESULT 12  
 A61419  
 sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)  
 C:Species: Pseudomonas sp.  
 C:Date: 07-Oct-1994 #sequence\_revision: 07-Oct-1994 #text\_change: 07-May-1999  
 C:Accession: A61419  
 R:Pinto, J.T.; Frisell, W.R.  
 Arch. Biochem. Biophys. 169, 483-491, 1975  
 A:Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydro  
 A:Reference number: A61419; MUID:76038634; PMID:241294  
 A:Accession: A61419  
 A:Molecule type: protein  
 A:Residues: 1-6 <PIN>  
 C:Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein  
 C:Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
 ||  
 5 GH 6

RESULT 13  
 B56979  
 collagen alpha 1(II) chain - bovine (fragment)  
 N:Alternate names: collagen alpha 3(XI) chain  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 03-Oct-1995 #sequence\_revision: 03-Oct-1995 #text\_change: 03-Oct-1995  
 C:Accession: B56979  
 R:Wu, J.J.; Eyre, D.R.  
 J. Biol. Chem. 270, 18865-18870, 1995  
 A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. I  
 A:Reference number: A56978; MUID:95370194; PMID:7642541  
 A:Accession: B56979  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-6 <WJA>  
 A>Note: the residue designated "X" is modified lysine in collagen 1(II); some cross-link

Query Match 27.5%; Score 14; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
 ||  
 4 GH 5

RESULT 14  
 S71299  
 IC12 protein - Paramecium tetraurelia (fragment)  
 C:Species: Paramecium tetraurelia  
 C:Date: 11-Mar-1998 #sequence\_revision: 17-Apr-1998 #text\_change: 07-Dec-1999  
 C:Accession: S71299  
 R:Maddipati, L.; Klotz, C.; le Caer, J.P.; Beissson, J.  
 Eur. J. Biochem. 238, 121-128, 1996  
 A:Title: Characterization of centrin genes in Paramecium.  
 A:Reference number: S71298; MUID:96248429; PMID:8665928  
 A:Accession: S71299  
 A:Molecule type: protein

A;Residues: 1-7 <MAD>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGCS

Query Match 27.5%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7  
DB 3 pp 4

RESULT: 15  
PT0283  
IG heavy chain CDR3 region (clone 4-94B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Aug-1996  
C;Accession: PT0283  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Calton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; XUID:911C9337; PMID:1899102  
A;Accession: PT0283  
A;Molecule type: DNA  
A;Residues: 1-7 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7  
DB 6 pp 7

Search completed: November 5, 2003, 17:22:56  
Job time : 14.5 secs

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OM protein protein search, using sw model

Run on: November 5, 2003, 17:15:14 / Search time 9.5 Seconds  
(without alignment)  
39.601 Million cell updates/sec

Title: US-09 914-088-5  
Perfect score: 51  
Sequence: 1 GGSHFPPT 8

Scoring table: BL0SUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 8  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.4

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	33.3	8	1 LMT2_L0CM1	P22396 locusta mig
2	15	29.4	5	1 PAP2_PARMA	P81864 pardachirus
3	14	27.5	3	1 GRW1_HUMAN	P01157 homo sapien
4	14	27.5	4	1 DCM1_BSECH	P13216 pseudomonas
5	14	27.5	7	1 PARS_HIRVE	P42364 hirudo med
6	14	27.5	7	1 TPEY_PACDA	P41455 pachymedusa
7	14	27.5	7	1 UF04_MOUSE	P13642 mus musculu
8	14	27.5	7	1 UN06_PIRIS	P13678 pinus pinas
9	14	27.5	8	1 AKH1_LIGAL	P13478 libellula a
10	14	27.5	8	1 ALL5_CALNG	P11841 calliphora
11	14	27.5	8	1 BRK2_PERAM	P42394 periplaneta
12	14	27.5	8	1 UF06_MOUSE	P13644 mus musculu
13	13	25.5	6	1 FARP_MOUSE	P41966 oniezia ex
14	13	25.5	8	1 ALL6_CARMA	P41819 carcinus ma
15	13	25.5	8	1 ALL9_CARMA	P41812 carcinus ma
16	13	25.5	8	1 HTE1_PERAM	P42548 periplaneta
17	13	25.5	8	1 HTE1_TANXC	P25419 tenebrio mo
18	13	25.5	8	1 RPCH_PANBO	P08939 pandanus bo
19	12	23.5	5	1 PRCT_PERAM	P01373 periplaneta
20	12	23.5	6	1 TM0F_SARBU	P41495 sarcophaga
21	12	23.5	7	1 LANC_CARUI	P36960 carinobacter
22	12	23.5	8	1 ACI1_THUAL	P18691 thunnus alb
23	12	23.5	8	1 AKH1_TABAT	P14595 tabanus atr
24	12	23.5	8	1 HTE2_PERAM	P42549 periplaneta
25	12	23.5	8	1 LCK5_LEUMA	P19997 leucophaea
26	12	23.5	8	1 LPK1_LEUMA	P13049 leucophaea
27	12	23.5	8	1 NPB1_BOVIN	P15507 bos taurus
28	12	23.5	8	1 VGLG_HSV2B	P41783 herpes simp
29	12	23.5	8	1 WPI1_PERAT	P41125 perkinsus a
30	11	21.6	5	1 RE12_MITRU	P02073 litoria rub
31	11	21.6	6	1 E101_MITRU	P42396 litoria rub
32	11	21.6	8	1 ALL1_CYDPO	P42396 litoria rub
33	11	21.6	8	1 FARP_CALVE	P41894 calliphora

34	11	21.6	8	1 LCK8_LEUMA	P19990 leucophaea
35	11	21.6	8	1 PPK3_PERAM	P82618 periplaneta
36	10	19.6	8	1 AKH1_MELML	P25423 melolontha
37	10	19.6	8	1 FARI_PENMU	P83316 penaeus mor
38	10	19.6	8	1 FARI_PENMU	P43171 penaeus mor
39	10	19.6	8	1 FARI_PENMU	P43171 penaeus mor
40	10	19.6	8	1 FUS1_FUSO	P81010 fusarium so
41	9	17.6	4	1 UPAA_HUMAN	P30096 homo sapien
42	9	17.6	6	1 OCPI_OCTMI	P58648 octopus min
43	9	17.6	6	1 TRPI_PSEPU	P42985 leptonotars
44	9	17.6	7	1 E105_LITRU	P36414 pseudomonas
45	9	17.6	7	1 FARI_HELTI	P82101 litoria rub
					P41871 hellisoma tr

## ALIGNMENTS

RESULT 1  
LMT2\_L0CM1 L0CM1 STANDARD: PRT: 8 AA.  
ID P22396;  
AC P22396;  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locusta migratoria 2 (LOC-MT-2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE  
RC Tissue:Corpora cardiaca;  
RA Schoofs L., Holman G.X., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamigratorin II, an  
RT additional neuropeptide of Locusta migratoria. Member of the  
RT cephalomyotropic peptide family";  
RL Insect Biochem. 20:479-484(1990).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8  
FT SEQUENCE 8 AA; 934 KW; 2634177A9CAA87B CRC64;  
SQ

Query Match 33.3%; Score 17; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GHFP 7  
DB 2 GEFT 6

RESULT 2  
PAP2\_PARMA PARMA STANDARD: PRT: 5 AA.  
ID P81864;  
AC P81864;  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Pardaxin II (FXII) (Fragment).  
OS Pardachirus marmoratus (Red sea moose sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleoidei; Soleidae; Pardachirus.  
OX NCBI\_TaxID=31097;  
RN [1]  
RP SEQUENCE  
RC Tissue=Skin; Secretion;

```

RX MEDLINE=90055678; PubMed:2818128;
RA Kraut M., Hugedieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL carboxydorotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H2O C + acceptor = CO(2) + reduced
CC acceptor;
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PLC140; PLO140.
KW Oxidoreductase; Molybdenum-
FT NON TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E976F0000000 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
DB 2 GH 3

RESULT 5
FARS_HIRNE
ID FARS_HIRNE STANDARD; PRT; 7 AA.
AC P42564;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GGYWRF-amide.
OS Hirudo medicinalis (Medicina; leech).
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
CC Arynchobellida; Hirudiniformes; Hirudinidae; Hirudo.
CC NCBI_TaxID=6421;
RN [1] _SEQUENCE.
RP
RX MEDLINE=92195954; PubMed:1686933;
RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-909(1991).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; A-midation.
KW MOD RES 7
FT SEQUENCE 7 AA; 858 MW; 64D4068553387810 CRC64;
SQ

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHF 5
DB 1 3
GGKY 4

RESULT 6
TFPY_PACDA
ID TFPY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (PdT-1);
OS Pachymedusa daemnicolor (Giant mexican leaf frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
CC Phyllomedusinae; Pachymedusa.
CC NCBI_TaxID=75989;
RN [1]

```







RT the sheep tapeworm, *Moniezia expansa*;  
 RJ Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FAMFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: A43129; A43129.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C448100 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GHF 5  
 ||:  
 Db 1 GNP 3

## RESULT 14

ALL9 CARMA STANDARD; PRT; 8 AA.  
 ID A:16 CARMA  
 AC P81819;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostat 16.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCB:TaxID=6759;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jares P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*."  
 RJ Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 813 MW; 7C28E945A8476878 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GHF 5  
 ||:  
 Db 1 GNP 4

## RESULT 15

ALL9 CARMA STANDARD; PRT; 8 AA.  
 ID A:16 CARMA  
 AC P81812;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostat 9.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCB:TaxID=6759;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jares P.P.,

RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*."  
 RJ Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 781 MW; 7C2879C0CB476878 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GHF 5  
 ||:  
 Db 1 GNP 4

Search completed: November 5, 2003, 17:21:09  
 Job time : 10.5 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen, Inc.

OM protein: protein search, using sw model

Run on: November 5, 2003, 17:18:09 ; Search time 27.5 Seconds  
(without alignments)  
75,076 Million cell updates

Title: US-C9-914-088-5

Perfect score: 51

Sequence: : GGGTCTT 8

Scoring table: BLOSJM62

Learning rate: 0.0001  
Gap0 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total: number of hits satisfying chosen parameters: 452

Minimum DB seg length: 9

Max: num: D3 seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTKEMBL 23: \*

1: sp.archea.\*  
2: sp.bacteria.\*  
3: sp.fungi.\*  
4: sp.human.\*  
5: sp.invertebrate.\*  
6: sp.mammal.\*  
7: sp.mhc.\*  
8: sp.organelle.\*  
9: sp.phase.\*  
10: sp.plant.\*  
11: sp.rodent.\*  
12: sp.virus.\*  
13: sp.vertebrate.\*  
14: sp.unclassified.\*  
15: sp.rvms.\*  
16: sp.bacteriap.\*  
17: sp.atcbeap.\*

Pred. No. is the number of results predicted by the model to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	17	33.3	8	13	Q91098	Q91098	canonina mel
2	17	33.7	9	13	Q90498	Q90498	erythrura g
3	16	31.4	8	6	O02831	Q2881	erytholagus
4	15	29.4	8	6	Q9XSY1	Q9XSY1	canis fami
5	14	27.5	7	8	P92214	P92214	amblyopyrum
6	14	27.5	7	8	P92393	P92393	hordeum vul
7	14	27.5	7	8	P92403	P92403	leptopyrum
8	14	27.5	7	8	P92427	P92427	tridictyon
9	14	27.5	7	8	P92430	P92430	segilops ta
10	14	27.5	7	8	P92221	P92221	bromus iner
11	14	27.5	7	8	P92425	P92425	pseudoroegn
12	14	27.5	7	8	P92381	P92381	hordeum bra
13	14	27.5	7	8	P92387	P92387	renardia p
14	14	27.5	7	8	P92210	P92210	microcyron c
15	14	27.5	7	8	P92440	P92440	rhinopyru
16	14	27.5	7	8	P92218	P92218	astralopyr

## ALIGNMENTS

## RESULT 1

RESULT 1  
Q9:098  
ID Q91098  
PRELIMINARY:  
PRT: 8 AA.

AC	Q91098;
DT	01-NOV-1996 (TrEMBurel_01, Created)
DT	01-NOV-1996 (TrEMBurel_01, Last sequenced)
DT	01-NOV-1998 (TrEMBurel_08, Last annotated)
DE	Myoglobin (Fragment).
OS	Vandana melanocentra (Noisy miner)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archozoaria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina  
OS

NCBI TaxID=44314;

RN [1]

RP SEQUENCE FROM N.A.

## RESULT 2

Q90498 ID Q90498 PRELIMINARY PRT; 8 AA.

P92390 heteranther  
P92372 hainaldia v  
P92442 taeniathera  
P923226 chitropsis  
P923385 hordeum mar  
P93421 psathyrosta  
P92445 nicotiana t  
P91468 homo sapiens  
Q9375 leucopis  
Q91205 hepatis c  
Q90345 hepatis g  
Q90866 spinacia ol  
Q93480 rattus norv  
Q95184 rattus norv  
Q94517 clostridium  
Q159001 homo sapien  
Q94743 homo sapien  
Q20032 lytechinus  
P93688 periplaneta  
Q9785 leptospermu  
Q85b30 bacterioph  
Q89b31 bacterioph  
Q93v15 rattus sp.  
Q93p40 mus musculu  
Q94971 alfalfa mos  
Q8m76 taraxacum (



DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 CX NCBI\_TaxID=4513;  
 RV [1]\_  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77764; CAB01370.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 7

P92403  
 ID P92403 PRELIMINARY; PRT; 7 AA.  
 AC P92403;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Leptopyrum elongatum (Tall wheatgrass) (Aegilops elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Leptopyrum.  
 CX NCBI\_TaxID=458;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 8

P92427  
 ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Peridictyon.  
 CX NCBI\_TaxID=37683;  
 RV [1]\_  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 9

P92430  
 ID P92430 PRELIMINARY; PRT; 7 AA.  
 AC P92430;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Aegilops.  
 CX NCBI\_TaxID=37682;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6668; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77758; CAB01352.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 10

P92221  
 ID P92221 PRELIMINARY; PRT; 7 AA.

P02237;  
 AC 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Bromus inermis (Smooth brome grass).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Bromaeae; Bromus.  
 OC NCBI\_TaxID=15371;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277759; CAB01355.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 11  
 P02426  
 ID P02426 PRELIMINARY; PRT; 7 AA.  
 AC P02426;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Pseudoroegneria.  
 OC NCBI\_TaxID=4604;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277744; CAB01310.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 12  
 P02387;  
 ID P02387 PRELIMINARY; PRT; 7 AA.  
 AC P02387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=52712;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277761; CAB01361.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

P02387;  
 ID P02387 PRELIMINARY; PRT; 7 AA.  
 AC P02387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=52712;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277761; CAB01361.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 13  
 P02387;  
 ID P02387 PRELIMINARY; PRT; 7 AA.  
 AC P02387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=37679;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277748; CAB01322.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 14  
 P02387;  
 ID P02387 PRELIMINARY; PRT; 7 AA.  
 AC P02387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 CS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=37679;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 PL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277748; CAB01322.1; -.  
 KW Chloroplast.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

Search completed: November 5, 2003, 17:22:18  
Job time : 28.5 secs

P92210  
ID P92210 PRELIMINARY; PRT: 7 AA.  
AC P92210;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RS11.  
OS Agropyron cristatum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Agropyron.  
OX NCBI\_TaxID=4593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4349; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rps11  
sequence data."; Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77771; CAB01391.1; -.  
RW KW Chloroplast.  
FT NCN TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
Query Match 27.5%; Score 14; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 pp 7  
DB 1 pp 2

RESULT 15  
P92440  
ID P92440 PRELIMINARY; PRT: 7 AA.  
AC P92440;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RS11.  
OS Thiopyrum bessarabicum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Thiopyrum.  
OX NCBI\_TaxID=4601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6725; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rps11  
sequence data."; Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77769; CAB01385.1; -.  
RW KW Chloroplast.  
FT NCN TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
Query Match 27.5%; Score 14; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 pp 7  
DB 1 pp 2

GenCore version 5.1.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:14:39 ; Search time 33.5 Seconds  
(without alignments)  
37.905 Million cell updates/sec

Title: US-09-914-088-5

Perfect score: 51

Sequence: GCGHFFPT 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158724573 residues

Total number of hits satisfying chosen parameters: 102276

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:
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15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:
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20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:

Pred. No. is the number of results predicted by Chnco to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	8	AA25911	IgE C-epsilon-2 do
2	51	100.0	8	AA16636	Epitide: P5 deriv
3	51	100.0	8	AB20322	Human IgE immuno
4	40	78.4	6	AA25934	P5 epitope peptid
5	40	78.4	6	AA16659	Epitide: P5sh deriv
6	40	78.4	6	AB20323	Human IgE immuno
7	28	54.9	8	AA25950	Epitide: P5sh deriv
8	28	54.9	8	AA21874	Cyclic pseudostell
9	28	54.9	8	AA21876	Pseudostellatin F

10	27	52.9	7	12	AA25296	Metal binding effe
11	26	51.0	6	14	AA23652	Group II synthetic
12	26	51.0	7	14	AA23653	Group II synthetic
13	26	51.0	7	23	AB277672	Targetting peptide
14	26	51.0	8	14	AA236669	Group 4 synthetic
15	26	51.0	8	21	AA25873	n-myc mutant pep
16	26	51.0	8	22	AA200173	Human protein frag
17	25	49.0	7	14	AA235096	B. thuringiensis I
18	25	49.0	7	16	AA278212	B. thuringiensis e
19	25	49.0	8	14	AA235850	Hepatitis C virus
20	25	49.0	8	23	AB291830	Human antibody fra
21	25	49.0	8	23	AB278139	Human Fv molecule
22	25	49.0	8	24	AB209184	G-protein coupled
23	24	47.1	7	23	AB277584	Targetting peptide
24	24	47.1	7	23	AA247323	Dipeptide aminopep
25	24	47.1	8	22	AA202694	Hepatitis C virus
26	23	45.1	6	22	AA204163	Internal peptide f
27	23	45.1	7	20	AA211344	Amino acid sequenc
28	23	45.1	7	20	AA211338	Amino acid sequenc
29	23	45.1	8	13	AA224706	Sequence of an ant
30	23	45.1	8	14	AA235911	Hepatitis C virus
31	23	45.1	8	16	AA277959	Antigenic Tbp2 pep
32	23	45.1	8	18	AA246152	Predicted antigeni
33	23	45.1	8	19	AA254111	Tbp2 antigenic pep
34	23	45.1	8	21	AA251757	H. influenzae ant
35	23	45.1	8	21	AA280454	H. influenzae tran
36	23	45.1	8	22	AA202185	Hepatitis C virus
37	22	43.1	5	11	AA207581	Hypotensive polype
38	22	43.1	6	11	AA203369	Sequence and deriv
39	22	43.1	6	11	AA207582	Hypotensive polype
40	22	43.1	6	13	AA225996	Peptide 1. Zea ma
41	22	43.1	6	15	AA245392	Prolyl endopeptida
42	22	43.1	6	15	AA245394	Prolyl endopeptida
43	22	43.1	6	20	AA250289	Neutrophil-activat
44	22	43.1	7	22	AA208364	Antibody heavy cha
45	22	43.1	7	22	AA209152	Bacteriophage pept

## ALIGNMENTS

RESULT 1  
AA25911  
ID AA25911 standard; Peptide; 9 AA.  
XX  
XX AA25911,  
XX  
XX 05 JAN 2003 (first entry)  
XX  
XX IgE C-epsilon-2 domain surface exposed epitope peptide P5 SEQ ID NO:5.  
XX  
XX Epitope: mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
XX  
XX allergic disease; immunoprophylaxis; immunotherapy; antiallergic;  
XX  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX  
XX allergy; atopy.  
XX  
XX Homo sapiens.  
XX  
XX WO200050460-A1  
XX  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2000MO-EP01455.  
XX  
XX 25-FEB-1993; 99GB-0004405.  
XX  
XX 29-MAR-1993; 99GB-0007151.  
XX  
XX 07-MAY-1993; 99GB-C010537.  
XX  
XX 07-MAY-1993; 99GB-C010538.  
XX  
XX 07-AUG-1999; 99GB-C018594.  
XX  
XX 07-AUG-1999; 99GB-C018603.  
XX  
XX 07-SEP-1999; 99GB-0021046.  
XX  
XX 07-SEP-1999; 99GB-0021047.  
XX  
XX 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027698.  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT ) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Mason A, Mason S,  
 PI Randall R, Turnell WG, Van Meckelen WP, Vinals De Bassols YC;  
 XX WPI: 2003-52074/53.  
 DR  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 XX Claim 6: Page 5; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 CC immunogen (II) for treating allergy comprising (i); (2) a vaccine (III)  
 CC for treating allergies comprising (i); (3) a ligand (IV) capable of  
 CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of EI,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (I) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26039 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 51; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGHFPPT 8  
 DB 1 GGGHFPPT 8  
 |||||  
 |||||  
 RESULT 2  
 AAU16616  
 ID AAU16616 standard; Peptide; 8 AA.  
 XX  
 AC AAU16616;  
 XX  
 DT 07 NOV-2001 (first entry)  
 XX  
 DE Peptide P5 derived from Cepsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200145745-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 21-DEC-2000; 2003WO-GB04915.  
 XX  
 PR 21-DEC-1999; 99GB-0030233.  
 PR 22-FEB-2000; 2003GB-0004096.  
 PR 22-AUG-2000; 2003GB-0023707.  
 PR 22-AUG-2000; 2003GB-0023708.

XX (ACAM-) ACAMIS RES LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX  
 PI Flinn N, Johnson T;  
 XX WPI: 2001-521967/57.  
 DR  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases -  
 PT  
 XX Example 4: Page 21; 48pp; English.  
 PS  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 100.0%; Score 51; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGHFPPT 8  
 DB 1 GGGHFPPT 8  
 |||||  
 |||||  
 RESULT 3  
 ABUC0221  
 ID ABUC0221 standard; Peptide; 8 AA.  
 XX  
 AC ABUC0221;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 5.  
 XX  
 KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; anti-allergic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216409-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EPC9576.  
 XX  
 PR 22-AUG-2000; 2000GB 0020717.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
 XX WPI: 2002-489648/52.  
 DR  
 XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier -  
 PT



XX Claim 4; Page 9; 45pp; English.

PS The present invention relates to conjugates suitable for use in vaccines,

CC where the conjugate comprises a disulphide bridge cyclised peptide and an

CC immunogenic carrier. The vaccines can be used in the treatment of

CC allergies. The present sequence is a peptide immunogen derived from human

CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGHFFPT 8

DB 1 GGHFFPT 8

RESULT 4

ID AAB25934 standard; Peptide; 6 AA.

XX

AC AAB25934;

XX

DT 05-JAN-2001 (first entry)

XX

DE P5 mimotope peptide P5sh: SEQ ID NO:28.

XX

KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;

KW allergic disease; immunophylaxis; immunotherapy; antiallergic;

KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.

XX

OS Homo sapiens.

XX

PN WO20050460-A1.

XX

PD 31-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-EP0455.

XX

PK 25-FEB-1999; 99GB-0004405.

PR 29-MAY-1999; 99GB-0007151.

PR 07-MAY-1999; 99GB-0010537.

PR 07-MAY-1999; 99GB-0010538.

PR 27-AUG-1999; 99GB-0018594.

PR 07-AUG-1999; 99GB-0018603.

PR 07-SEP-1999; 99GB-0021046.

PR 07-SEP-1999; 99GB-0021047.

PR 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027698.

XX

PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

FA (PEPT) PEPTIDE THERAPEUTICS LTD.

XX

PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;

PI Randall R, Turnell WG, Van Mechelen XP, Vinals D, Bassols YC;

XX

WPI; 2000-572073/53.

XX

PT Peptides useful for treating, preventing and ameliorating allergic

PT diseases, comprising an isolated surface exposed group of a specific

PT domain from immunoglobulin E.

XX

PS Disclosure; Page 9; 129pp; English.

XX

CC The present invention describes a peptide (I) comprising an isolated

CC surface exposed group/epitope (EII) of C-epsilon-2 domain (D) of

CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an

CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)

CC for treating allergies comprising (II); (3) a ligand (IV) capable of

CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);

CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen

CC (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)

CC can have antiallergic and immunosuppressive activities, and can be used

CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are

CC useful in medicine and in the manufacture of medicaments for treating

CC and preventing allergies. (IV) is useful for identifying mimotopes of P,

CC in medicine and also in manufacturing medicaments for treating

CC allergies. (I) is useful in diagnostics and in the affinity purification

CC of circulating anti-IgE antibodies from blood. (I), (II) and (III) are

CC useful for treating a patient susceptible to or suffering from allergies.

CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent

CC peptide sequences which are used in the exemplification of the present

CC invention.

XX

SQ Sequence 6 AA;

Query Match 78.4%; Score 40; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFFP 7

DB 1 GGHFFP 6

RESULT 5

ID AAU16659 standard; Peptide; 6 AA.

XX

AC AAU16659;

XX

DT 07-NOV-2001 (first entry)

XX

DE Peptide P5sh derived as mimotope of Cepsilon2 region of human IgE.

XX

KW Human; linkage technology; conjugated compound; carrier vehicle;

KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;

KW IgE mediated disease; antibody response.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200145745-A2.

XX

PD 28-JUN-2001.

XX

PF 21-DEC-2000; 2000WO-GH04935.

XX

PR 21-DEC-1999; 99GB-0030233.

PR 22-FEB-2000; 2000GB-0004096.

PR 22-AUG-2000; 2000GB-0020707.

PR 22-AUG-2000; 2000GB-0020708.

XX

PA (ACAM) ACAMBIS RES LTD.

FA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI Flinn N, Johnson T;

XX

WPI; 2001-521967/57.

XX

PT A linkage comprising an immunogenic conjugate useful treatment of IgE

PT mediated diseases.

XX

PS Example 4; Page 21; 48pp; English.

XX

CC The present invention relates to linkage methodology for use in the

CC conjugation of compounds (e.g. peptides) to carrier vehicles

CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce

CC biological and immunological constructs. The invention provides a

CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a

CC protein) for use in a pharmaceutical composition or a vaccine. The

CC invention describes peptides derived from or mimotopes of the

CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE-mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU:6632 AAU:6913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

XX Sequence 6 AA;

Query Match 78.4%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 |||||  
 DB 1 GGHFPP 6

# RESULT 6

ABU00233  
 ID ABUC0233 standard; Peptide; 6 AA.

XX ARU00233;

XX 02-SEP-2002 (first entry)

XX Human IgE immunogenic peptide SEQ ID NO: 17.

XX Immunogen; human; IgE; immunoglobulin E; allergy; this ether linkage;  
 XX vaccine; antiallergic.

XX Homo sapiens.

XX WU200216489.A2.

XX 28-FEB-2002.

XX 17 AUG-2001; 2001WO-EP09576.

XX 22 AUG-2000; 2000GB-0026717.

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Friede M, Mason S, Turnell WG, Vinaly B, et al.

XX WPI, 2002 429648/52.

XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.

XX Claim 4; Page 9; 45pp; English.

CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Sequence 6 AA;

Query Match 78.4%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 |||||  
 DB 1 GGHFPP 6

# RESULT 7

AAR98050  
 ID AAR98050 standard; peptide; 8 AA.

XX AAR98050;

XX 01-AUG-1996 (first entry)

XX Pseudostellarin F, a cyclic octapeptide.

XX tyrosinase inhibitor; melanin; skin cosmetic.

XX Pseudostellaria heterophylla.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "not an N-terminal; this amino acid  
 FT condenses with the C-terminal to form  
 FT a cyclic peptide"

FT Modified-site 8

FT /note= "not a C-terminal; see above"

XX JPC7324095-A.

XX 12-DEC-1995.

XX 30-MAY-1994; 94JP-0116499.

XX 30-MAY-1994; 94JP-0116499.

XX (ITOG/) ITOGAWA H.

XX (HONS) YAKULT HONSHA KK.

XX WPI; 1996-065475/C7.

XX New cyclic peptide(s) designated pseudostellarin A-G - are tyrosinase  
 PT inhibitors and melanin formation inhibitors useful in skin cosmetics

XX Claim 6; Page 2; 13pp; Japanese.

XX The cyclic peptide is one component of the peptides designated  
 CC pseudostellarins A-G which have been extracted from *Taishijin* root.  
 CC These peptides are tyrosinase inhibitors and melanin formation  
 CC inhibitors which are useful in skin cosmetics. Pseudostellarins A,  
 CC B, C, D, E, F and G demonstrated tyrosinase inhibiting IC50 values of  
 CC 131, 187, 63, 100, 175, 50 and 75 microm resp., compared with a  
 CC value of 1.2 mM for arbutin.

XX Sequence 8 AA;

Query Match 54.9%; Score 28; DB 17; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 |||||  
 DB 1 GGVJPP 6

# RESULT 8

AAB11894  
 ID AAB11894 standard; peptide; 8 AA.

XX AAB11894;

XX 14-NOV-2000 (first entry)

XX Cyclic pseudostellarin F.

XX Split intein; peptide cyclisation; trans splicing; peptide library;  
 KW peptide screening; cyclic ester intermediate; Ssp DnaE C-intein;  
 KW plasmid pARCP-p; plasmid pARCB0-p; pseudostellarin F; cyclic.

OS Unidentified.  
 XX Key Location/Qualifiers  
 FH Modified site 1..8  
 FT /note= "The C-terminus condenses with the N terminus to  
 FT form a cyclic peptide"  
 XX  
 PN W0200036093-A2.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 18-DEC-1999; 99WO-US30162.  
 XX  
 PF 18-DEC-1998; 98US-0112723.  
 PR  
 PR 07 OCT-1999; 99US-0158077.  
 XX  
 PA (PENN ) PENN STATE RES FOUND.  
 XX  
 PI Benkovic SJ, Scott CP, Abel-Santos EV;  
 XX  
 DR WPI; 2000-43:582/37.  
 XX  
 PT Non-naturally occurring nucleic acid molecule encodes a target peptide  
 PT produced in a host system in a cyclized form or as a splicing  
 PT intermediate of the cyclized form -  
 XX  
 PS Examples; Page 44; 92pp; English.  
 XX  
 CC The invention relates to methods of producing cyclic peptides which  
 CC utilise the trans splicing ability of split inteins to catalyse  
 CC cyclisation of a peptide from a precursor peptide. The precursor peptide  
 CC has a target peptide interspersed between two portions of a split intein.  
 CC The interaction of the two portions of the split intein creates a  
 CC catalytically active intein, and also forces the target peptide into a  
 CC loop configuration that stabilises the ester isomer of the amino acid at  
 CC the junction between one of the intein portions and the target peptide.  
 CC A heteroatom from the other intein portion then reacts with the ester to  
 CC form a cyclic ester intermediate. The active intein catalyses the  
 CC formation of an aminosuccinimide that liberates a cyclised form of the  
 CC target peptide, which spontaneously rearranges to form the  
 CC thermodynamically favoured backbone cyclic peptide product. The invention  
 CC also discloses nucleic acids encoding the precursor peptide (i.e. the  
 CC target peptide flanked by the two portions of the split intein), the  
 CC expression vectors and host cells comprising the nucleic acid; the  
 CC cyclised peptide product or a splicing intermediate thereof (e.g., a  
 CC thioester or a lariat intermediate), methods of generating peptide  
 CC libraries, and methods of screening peptides. The nucleic acid molecules  
 CC of the invention are used for making cyclic peptides and peptide  
 CC splicing intermediates. The methods can be used for screening the cyclic  
 CC peptides, for identifying molecules that bind to the target peptides and  
 CC to detect the presence of a predetermined characteristic in a peptide  
 CC e.g., the ability to specifically bind a target molecule. The present  
 CC sequence represents cyclic pseudostellarin F which was generated  
 CC in the exemplifications of the invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 54.9%; Score 28; DB 21; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGHPFP 7  
 |||  
 Db 2 GGYLPP 7  
 |||  
 RESULT 9  
 AAR:1896  
 ID AAR:1896 standard; Protein; 8 AA.  
 XX AAR:1896;  
 AC  
 XX  
 DT 14-NOV-2000 (first entry)

XX Pseudostellarin F (linear).  
 DE  
 XX Split intein; peptide cyclisation; trans splicing; peptide library;  
 KW peptide screening; cyclic ester intermediate; Ssp DnaE C-intein;  
 KW plasmid PARCP-p; plasmid PARCBD-p; pseudostellarin F.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200036093-A2.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 18-DEC-1999; 99WO-US30162.  
 XX  
 PF 18-DEC-1998; 98US-0112723.  
 PR  
 PR 07-OCT-1999; 99US-0158077.  
 XX  
 PA (PENN-) PENN STATE RES FOUND.  
 XX  
 PI Benkovic SJ, Scott CP, Abel-Santos EV;  
 XX  
 DR WPI; 2000-43:582/37.  
 XX  
 DR N-PSDB; AAA61909.  
 XX  
 PT Non-naturally occurring nucleic acid molecule encodes a target peptide  
 PT produced in a host system in a cyclized form or as a splicing  
 PT intermediate of the cyclized form -  
 XX  
 PS Examples; Fig 3e; 92pp; English.  
 XX  
 CC The invention relates to methods of producing cyclic peptides which  
 CC utilise the trans splicing ability of split inteins to catalyse  
 CC cyclisation of a peptide from a precursor peptide. The precursor peptide  
 CC has a target peptide interspersed between two portions of a split intein.  
 CC The interaction of the two portions of the split intein creates a  
 CC catalytically active intein and also forces the target peptide into a  
 CC loop configuration that stabilises the ester isomer of the amino acid at  
 CC the junction between one of the intein portions and the target peptide.  
 CC A heteroatom from the other intein portion then reacts with the ester to  
 CC form a cyclic ester intermediate. The active intein catalyses the  
 CC formation of an aminosuccinimide that liberates a cyclised form of the  
 CC target peptide, which spontaneously rearranges to form the  
 CC thermodynamically favoured backbone cyclic peptide product. The  
 CC invention also discloses nucleic acids encoding the precursor peptide  
 CC (i.e. the target peptide flanked by the two portions of the split  
 CC intein), expression vectors and host cells comprising the nucleic acid,  
 CC the cyclised peptide product or a splicing intermediate thereof (e.g., a  
 CC thioester or a lariat intermediate), methods of generating peptide  
 CC libraries, and methods of screening peptides. The nucleic acid molecules  
 CC of the invention are used for making cyclic peptides and peptide  
 CC splicing intermediates. The methods can be used for screening the cyclic  
 CC peptides, for identifying molecules that bind to the target peptides and  
 CC to detect the presence of a predetermined characteristic in a peptide  
 CC e.g., the ability to specifically bind a target molecule. The present  
 CC sequence represents pseudostellarin F in its linear form. Plasmids  
 CC PARCP-p and PARCBD p encode pseudostellarin F. Expression of these  
 CC plasmids generates cyclic pseudostellarin F (AAB11894).  
 XX  
 SQ Sequence 8 AA;  
 Query Match 54.9%; Score 28; DB 21; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGHPFP 7  
 |||  
 Db 2 GGYLPP 7  
 |||  
 RESULT 10  
 AAR:5296  
 ID AAR:5296 standard; Protein; 7 AA.

XX AAR15286;  
 XX 17 FEB-1992 (first entry)  
 XX DE Metal binding effector domain (15)  
 XX KW Molecular recognition unit; MRU; platelet function receptor; effector domain;  
 XX OS Synthetic.  
 XX UN KC911713-A  
 XX PE 14-NOV-1991  
 XX EF 01-MAY-1991; 91WO-US01116.  
 XX PR 07-MAY-1990; 90US-0519702.  
 XX PA (CYTOC) CYTOGEN CORP.  
 XX PI Podwall JD, McKeern TJ, Alvarez VL, Radcliffe SB;  
 XX DS WPI; 1991 353714/48.  
 XX New conjugates of molecular recognition units - having first binding domain for desired target site and second effector domain; useful in medicine, agriculture, waste management etc.  
 XX Claim 8; Page 63; 74pp; English.  
 XX A conjugate of an MRU comprises a fusion peptide having a first binding domain (e.g. having the sequence represented in AAR15286-91) which is an MRU having binding specificity and affinity for an activated platelet fibronogen receptor and a second effector domain (e.g. having the sequence represented in AAR15292-97) which has the ability to bind iron. The amino or carboxy terminus of the peptide can be blocked.  
 XX See also AAR15193-97.  
 XX Sequence 7 AA;  
 Query Match 52.9%; Score 27; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGH 4  
 DB 1 GGH 4  
 RESULT 11  
 AAR36652  
 ID AAR36652 standard; peptide; 6 AA.  
 XX AC AAR36652;  
 XX DT 07 SEP 1993 (first entry)  
 XX DE Group II synthetic peptide 185.  
 XX KW Thiol-active cysteine; antibody; complex; rheumatoid arthritis; therapy; IgA-alpha-antitrypsin.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified site 6 /note= "amidated"  
 XX GN GB2261665 A.  
 XX PD 26-MAY-1993.  
 XX PF 25-NOV-1992; 92GB-0024684.  
 XX PR 25-NOV-1991; 91GB-0025024.  
 XX PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.  
 XX PI Kirby J, Lewin JV, Nayyar S, Stanworth DR;  
 XX CR WPI; 1993 169522/21.  
 XX New synthetic peptide(s) - cause dissociation or prevent formation of IgA alpha-antitrypsin complex, useful for treating

XX 25-NOV-1992; 92GB-0024684.  
 XX PR 25-NOV-1991; 91GB-0025024.  
 XX PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.  
 XX PI Kirby J, Lewin JV, Nayyar S, Stanworth DR;  
 XX DR WPI; 1993 169522/21.  
 XX New synthetic peptide(s) - cause dissociation or prevent formation of IgA-alpha-antitrypsin complex, useful for treating and preventing rheumatoid arthritis  
 XX Claim 1; Page 25; 38pp; English.  
 XX The peptide is an example of a synthetic peptide contg. a thiol-active cysteine residue and at least two positively charged amino acid residues situated at the N and/or C terminal sides of the thiol-active cysteine. The peptide is pref. amidated at the C-terminus. The peptide may be used in conjunction with an antibody complex comprising a domain specific for an antigenic determinant of a complex of human IgA and alpha-1-antitrypsin, for use in therapy of rheumatoid arthritis. Admin. is oral or parenteral.  
 XX See also AAR36613-74.  
 XX Sequence 6 AA;  
 Query Match 51.0%; Score 26; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGH 4  
 DB 2 GGH 5  
 RESULT 12  
 AAR36653  
 ID AAR36653 standard; peptide; 7 AA.  
 XX AC AAR36653;  
 XX DT 07 SEP 1993 (first entry)  
 XX DE Group II synthetic peptide 184.  
 XX KW Thiol-active cysteine; antibody; complex; rheumatoid arthritis; therapy; IgA-alpha antitrypsin.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 7 /note= "amidated"  
 XX GN GB2261665 A.  
 XX PD 26-MAY-1993.  
 XX PF 25-NOV-1992; 92GB-0024684.  
 XX PR 25-NOV-1991; 91GB-0025024.  
 XX PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.  
 XX PI Kirby J, Lewin JV, Nayyar S, Stanworth DR;  
 XX CR WPI; 1993 169522/21.  
 XX New synthetic peptide(s) - cause dissociation or prevent formation of IgA alpha-antitrypsin complex, useful for treating

PT and preventing rheumatoid arthritis  
PS Claim 1; Page 25; 38pp; English.

XX The peptide is an example of a synthetic peptide contg. a thiol-  
CC active cysteine residue and at least two positively charged amino  
CC acid residues situated at the the N and/or C terminal sides of the  
CC thiol-active cysteine. The peptide is pref. amidated at the C  
CC terminus. The peptides may be used in conjunction with an antibody  
CC complex comprising a domain specific for an antigenic determinant of  
CC a complex of human IgA and alpha-1-antitrypsin, for use in therapy of  
CC rheumatoid arthritis. Admin. is oral or parenteral.  
CC See also AAR36613-74.

XX Sequence 7 AA;

Query Match 51.0%; Score 26; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
|  
|  
|  
|  
DB 3 GGGH 6

RESULT 13

AB577672  
ID ABG77672 standard; Peptide; 7 AA.

AC ABG77672;

XX 05-NOV-2002 (first entry)

DE Targetting peptide selective for human organ, tissue or cell type #205.

XX Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
XX arthritis; diabetes; inflammatory disease; atherosclerosis;  
XX autoimmune disease; bacterial infection; viral infection;  
KW cardiovascular disease; degenerative disease.

XX Homo sapiens.

XX WC26C20723-A2.

XX 14-MAR 2002.

XX 07-SEP-2001; 2001WC-US28044.

XX 08-SEP-2003; 2003US-231266P.

XX 17-JAN-2001; 2001US-0765101.

XX TEXA; UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;

XX WPI; 2002-599247/64.

XX New targeting peptides identified by phage display, useful for treating  
PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
PT cardiovascular disease

PS Claim 16; Fig 2B; 269pp; English.

XX The invention describes an isolated peptide of 100 amino acids or less  
CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
CC disease, bacterial infection, viral infection, cardiovascular disease  
CC or degenerative disease. This sequence represents a human targeting  
CC peptide selective for human organs, tissues or cell types.

XX Sequence 7 AA;

Query Match 51.0%; Score 26; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGH 5  
|  
|  
|  
|  
DB 1 GGGH 4

RESULT 14

AAR36669

ID AAR36669 standard; peptide; 8 AA.

XX AAR36669;

XX 07-SEP-1993 (first entry)

DE Group 4 synthetic peptide 117.

XX Thiol-active cysteine; antibody; complex; rheumatoid arthritis;  
KW therapy; IgA-alpha-antitrypsin.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 8 /note= "amidated"

XX GB226:665-A.

XX 26-MAY-1993.

XX 25-NOV-1992; 92GB-0024684.

XX 25-NOV-1991; 91GB-0025024.

XX (BRITE-) BRITISH TECHNOLOGY GROUP LTD.

XX Kirby J, Lewin IV, Nayyar S, Stanworth DR;

XX WPI; 1993-169522/21.

XX New synthetic peptide(s) - cause dissociation or prevent  
PT formation of IgA-alpha-antitrypsin complex, useful for treating  
PT and preventing rheumatoid arthritis

XX Claim 1; Page 27; 38pp; English.

XX The peptide is an example of a synthetic peptide contg. a thiol-  
CC active cysteine residue and at least two positively charged amino  
CC acid residues situated at the the N and/or C terminal sides of the  
CC thiol-active cysteine. The peptide is pref. amidated at the C-  
CC terminus. The peptides may be used in conjunction with an antibody  
CC complex comprising a domain specific for an antigenic determinant of  
CC a complex of human IgA and alpha-1-antitrypsin, for use in therapy of  
CC rheumatoid arthritis. Admin. is oral or parenteral.  
CC See also AAR36613-74 and AAR37353-74.

XX Sequence 8 AA;

Query Match 51.0%; Score 26; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
|  
|  
|  
|  
DB 2 GGGH 5

RESULT 15

AAY65873

ID AAY65873 standard; Peptide; 8 AA.

XX AAY65873;  
 AC  
 XX 10-FEB-2000 (first entry)  
 DT  
 XX  
 DE R-myc mutant peptide 2.  
 DE  
 XX Human; frameshift mutant; T cell response; tumour; treatment; cancer;  
 KW mutatin.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 XX  
 XX W09958552.A2.  
 XX  
 XX 18 NOV 1999.  
 XX  
 XX 03-MAY-1999; 99WO-N000143.  
 EF  
 XX 08-MAY-1998; 98NC-0002097.  
 PR  
 XX (NH2 ) NCRRK HYDRO AS.  
 PA  
 XX Gaudernack G, Eriksen JA, Moller M, Steensen MK, Sæverdal I;  
 P:  
 XX WPI; 2000-099064/03.  
 DP  
 XX  
 XX New peptides derived from genes with frameshift mutations, used to  
 PT develop products for the treatment and prophylaxis of cancers .  
 PT  
 XX  
 XX Claim 13; Page 29; 166pp; English  
 ES  
 XX  
 XX Peptides AAY6584 Y6642 are fragments of mutant proteins arising from a  
 CC frameshift mutation in a gene from a cancer cell. The peptides are  
 CC characterised in that they:  
 CC (i) are at least 8 amino acids long and a fragment of a mutant protein  
 CC arising from a frameshift mutation in a gene of a cancer cell;  
 CC (ii) consist of at least one amino acid of the mutant part of a protein  
 CC sequence encoded by the gene;  
 CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal  
 CC part of the protein sequence preceding the amino terminus of the mutant  
 CC sequence and may further extend to the carboxyl terminus of the mutant  
 CC part of the protein as determined by a new stop codon generated by the  
 CC frameshift mutation; and  
 CC (iv) induce, either in their full length or after processing by an  
 CC antigen presenting cell (APC), T cell responses.  
 CC The genes that the peptides are derived from are said to be as  
 CC susceptible to frameshift mutation by having a 100 nucleotide base  
 CC repeat sequence of at least 5 residues, made up of nucleotide base repeat  
 CC sequence of at least 4 dinucleoside base units. The peptides are  
 CC created by the addition or deletion of 1 or 2 nucleotide base residues  
 CC from the repeat sequence. The novel peptides can elicit T cell responses  
 CC and toxicity against tumours and cancer cells carrying genes with  
 CC frameshift mutations. The novel peptides and DNA sequences can be used  
 CC for the preparation of a composition for the treatment or prophylaxis of  
 CC cancer.  
 XX  
 XX Sequence A AY:  
 SC  
 Query Match 51.0%; Score 26; DB 21; Length 47  
 Best local Similarity 100.0%; Posi No. 1; 100%  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGH 4  
 Rn 1 GGGH 4

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OM protein - protein: search, using sw model

Run on: November 5, 2003, 17:22:25 ; Search time 22 seconds  
(without alignments)  
62.454 Million cell updates/sec

Title: US-09-914-088-5  
Perfect score: 51  
Sequence: 1 GGGHFPPT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 42162

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*  
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16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	51	100.0	8	12	US-10-082-014-276
2	51	100.0	8	12	US-10-372-076-130
3	26	51.0	4	15	US-10-058-636-7
4	26	51.0	7	12	US-10-080-2632-32
5	25	49.0	6	11	US-08-774-639-225
6	25	49.0	6	11	US-09-969-710-321
7	25	49.0	8	15	US-10-012-035A-32
8	24	47.1	5	12	US-10-301-499A-36
9	23	45.1	7	11	US-09-229-751A-25
10	23	45.1	7	11	US-09-229-751A-31
11	23	45.1	8	15	US-10-043-344-75
12	22	43.1	7	11	US-09-791-151A-20
13	22	43.1	7	12	US-10-223-033-19
14	22	43.1	8	15	US-10-043-344-146
15	22	43.1	8	15	US-10-226-007-1336

16	22	43.1	8	15	US-10-226-007-1336	Sequence 1336, Ap
17	22	43.1	8	15	US-10-226-007-1349	Sequence 1349, Ap
18	21	41.2	6	9	US-09-062-113-1	Sequence 1, Appli
19	21	41.2	6	11	US-09-994-595-89	Sequence 89, Appli
20	21	41.2	6	12	US-10-232-858-1	Sequence 1, Appli
21	21	41.2	6	15	US-10-209-323-6	Sequence 6, Appli
22	21	41.2	7	9	US-09-205-658-296	Sequence 296, App
23	21	41.2	7	9	US-09-182-650-1	Sequence 1, Appli
24	21	41.2	7	9	US-09-731-242A-24	Sequence 24, Appli
25	21	41.2	7	9	US-09-845-667-12	Sequence 12, Appli
26	21	41.2	7	11	US-09-910-582B-2	Sequence 2, Appli
27	21	41.2	7	11	US-09-281-495-9	Sequence 9, Appli
28	21	41.2	7	11	US-09-940-727B-60	Sequence 60, Appli
29	21	41.2	7	11	US-09-940-727B-63	Sequence 63, Appli
30	21	41.2	7	11	US-09-940-727B-66	Sequence 66, Appli
31	21	41.2	7	11	US-09-940-727B-78	Sequence 78, Appli
32	21	41.2	7	12	US-09-963-693-296	Sequence 296, App
33	21	41.2	8	12	US-10-073-333A-17	Sequence 17, Appli
34	21	41.2	8	14	US-10-011-436-10	Sequence 10, Appli
35	21	41.2	8	15	US-10-140-164-18	Sequence 18, Appli
36	21	41.2	8	15	US-10-140-164-47	Sequence 47, Appli
37	20	39.2	3	10	US-09-898-376-2	Sequence 2, Appli
38	20	39.2	3	10	US-09-988-127-2	Sequence 2, Appli
39	20	39.2	3	10	US-09-986-897-2	Sequence 2, Appli
40	20	39.2	3	11	US-09-852-910-167	Sequence 167, App
41	20	39.2	4	12	US-09-800-187-64	Sequence 64, Appli
42	20	39.2	4	12	US-09-800-187-65	Sequence 65, Appli
43	20	39.2	4	12	US-09-800-187-66	Sequence 66, Appli
44	20	39.2	4	12	US-09-800-187-67	Sequence 67, Appli
45	20	39.2	4	12	US-09-800-187-68	Sequence 68, Appli

ALIGNMENTS

RESULT 1

US-10-082-014-276  
; Sequence 276, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR FILING DATE: 2001-C8-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 276  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-276

Query Match	100.0%	Score 51	DB 12	Length 8
Best Local Similarity	100.0%	Pred. No. 5.8e-05	Indels 0	Gaps 0
Matches	8	Conservative 0	Mismatches 0	
Qv	1	GGGHFPPT 8		
Db	1	GGGHFPPT 8		
RESULT 2				
US-10-372-076-130				
; Sequence 130, Application US/10372076				
; Publication No. US20030198645A1				
; GENERAL INFORMATION:				
; APPLICANT: Friede, Mark				
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR				
; TITLE OF INVENTION: CHRONIC HEPATITIS				

```

; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/086,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-076-130

```

```

Query Match          100.0%; Score 51; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGCHFPPT 8
    |||||
Db 1 GGCHFPPT 8

```

```

RESULT 3
US-10-058-636-7
; Sequence 7, Application US/10058636
; Publication No. US20030049270A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakatuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and its uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/10/058,636
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/212,960
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/038,891
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/272,960
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linker between
US-10-058-636-7

```

```

Query Match          51.0%; Score 26; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGCH 4
    |||
Db 1 GGCH 4

```

```

RESULT 4
US-10-080-263C-32
; Sequence 32, Application US/10080263C
; Publication No. US20030143670A1
; GENERAL INFORMATION:
; APPLICANT: Sonini, James A.
; APPLICANT: Huang, Ling-Yan
; APPLICANT: Wilson, Amy
; TITLE OF INVENTION: DNA ENCODING SW-6344 SECRETOR
; FILE REFERENCE: 1795/59370-A/CPW/ADM/ANX

```

```

; CURRENT APPLICATION NUMBER: US/10/090,263C
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-263C-32

```

```

Query Match          51.0%; Score 26; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 GGHF 5
    ||||
Db 2 GGHF 5

```

```

RESULT 5
US-09-774-639-225
; Sequence 225, Application US/09774639
; Publication No. US2003003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-225

```

```

Query Match          49.0%; Score 25; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 FPPT 8
    |||
Db 3 FPPT 6

```

```

RESULT 6
US-09-969-730-321
; Sequence 321, Application US/09969730
; Publication No. US20030054443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364

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; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,733
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 32:
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US 09 969 730-321

Query Match 49.0%; Score 25; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 GHFP 9
Db 3 GHFP 6

RESULT 7
US-10-012-035A-12
; Sequence 32, Application US/10012035A
; Publication No. US20030004103A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel
; TITLE OF INVENTION: MODULATORS OF ACTIVITY OF
; TITLE OF INVENTION: G-PROTEIN-COUPLED RECEPTOR KINASES
; FILE REFERENCE: BEN-SASSON2C
; CURRENT APPLICATION NUMBER: US/10/012-035A
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 09/735,274
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/10314
; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Myr:styl:styl at position 1
US-10-012-035A-32

Query Match 49.0%; Score 25; DB 15; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GHFP 6
Db 1 GHFP 5

RESULT 8
US-10-301-499A-36
; Sequence 36, Application US/10301499A
; Publication No. US20030148932A1
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Berezov, Alan
; APPLICANT: Murali, Mamachandran
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME
; FILE REFERENCE: 4040/1K999-US1
; CURRENT APPLICATION NUMBER: US/10/301,499A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/331,935
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic peptide
US 10-301-499A-36

Query Match 47.1%; Score 24; DB 12; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 3 GHFP 6
Db 2 GHFP 5

RESULT 9
US-09-229-751A-25
; Sequence 25, Application US/09229751A
; Publication No. US20030044838A1
; GENERAL INFORMATION:
; APPLICANT: Turnbough, Charles K
; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES
; OF BACTERIAL CELLS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glenna Hendricks
; STREET: P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: USA
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,751A  
FILING DATE: 14-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna M  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: turn  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-8405  
TELEFAX: (703) 425-8406  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-229-751A-25

Query Match 45.1%; Score 23; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HFPPT 8  
|||  
Db 2 HFLPT 6

RESULT 10  
US-09-229-751A-21  
Sequence 11, Application US/0922379A  
Publication No. US20030644838A1  
GENERAL INFORMATION:  
APPLICANT: Turnbough, Charles E  
TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
OF BACTERIAL CELLS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glenna Hendricks  
STREET: P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: USA  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,751A  
FILING DATE: 14-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna M  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: turn  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-8405  
TELEFAX: (703) 425-8406  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-229-751A-31

Query Match 45.1%; Score 23; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HFPPT 8  
|||  
Db 2 HFLPT 6

RESULT 11  
US-10-043-344-75  
Sequence 75, Application US/10043344  
Publication No. US2003088986A1  
GENERAL INFORMATION:  
APPLICANT: Loomore, Sheena M.  
APPLICANT: Harkness, Robin E.  
APPLICANT: Schryvers, Anthony B.  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Mordin, Andrew D.  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES  
FILE REFERENCE: 1038-1221 MIS  
CURRENT APPLICATION NUMBER: US/10/043,344  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: 08/649,518  
PRIOR FILING DATE: 1996-05-17  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 75  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Haemophilus influenzae  
US-10-043-344-75

Query Match 45.1%; Score 23; DB 15; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCHF 5  
|||  
Db 3 GGCSF 7

RESULT 12  
US-09-791-153A-20  
Sequence 20, Application US/09791153A  
Publication No. US20030103978A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Hitz, Anna  
APPLICANT: Boyle, William  
APPLICANT: Sullivan, John  
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN  
FILE REFERENCE: A-633A  
CURRENT APPLICATION NUMBER: US/09/791,153A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: 09/511,139  
PRIOR FILING DATE: 2000-02-23  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 7  
TYPE: PPT  
ORGANISM: Homo sapiens  
US-09-791-153A-20  
Query Match 43.1%; Score 22; DB 11; Length 7;

Best Local Similarity 80.0%; Pred. No. 5.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGHF 5  
|||  
Db 1 GGGGF 5

RESULT 13  
US-10-220-033-18  
; Sequence 18, Application US/10220033  
; Publication No. US20030186906A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene  
; TITLE OF INVENTION: and a molecule binding to an expression product of that  
; TITLE OF INVENTION: gene  
; FILE REFERENCE: P68119US0  
; CURRENT APPLICATION NUMBER: US/10/220,033  
; PRIOR FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: PCT/EP01/02694  
; PRIOR FILING DATE: 2001-03-10  
; PRIOR APPLICATION NUMBER: EP00105190.3  
; PRIOR FILING DATE: 2000-03-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: obtained by screening randomly synthesized  
; OTHER INFORMATION: peptides  
US-10-220-033-18

Query Match 43.1%; Score 22; DB 12; Length 7;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPPP 7  
|||  
Db 3 HPP 6

RESULT 14  
US-10-043-344-146  
; Sequence 146, Application US/10043344  
; Publication No. US2003008086A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Harkness, Robin E.  
; APPLICANT: Schuyvers, Anthony B.  
; APPLICANT: Cheng, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Mordin, Andrew L.  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES  
; FILE REFERENCE: 1038-1221 MIS  
; CURRENT APPLICATION NUMBER: US/10/043,344  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 08/649,519  
; PRIOR FILING DATE: 1996-05-17  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 146  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Haemophilus influenzae  
US-10-043-344-146

Query Match 43.1%; Score 22; DB 15; Length 8;

Best Local Similarity 66.7%; Pred. No. 5.8e+05; Mismatches 2; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHFP 7  
|||  
Db 3 GFFGP 8

RESULT 15  
US-10-226-007-1323  
; Sequence 1323, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1323  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 7  
US-10-226-007-1323

Query Match 43.1%; Score 22; DB 15; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPPP 7  
|||  
Db 1 HPP 4

Search completed: November 5, 2003, 17:30:36  
Job time : 23 secs

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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:19:19 Search time 14 seconds  
(without alignments)  
24,158 Million cell updates/sec

Title: US-09-914-088-5  
Perfect score: 51  
Sequence: 1 GGHFPT 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	27	52.9	7	5196510-10	Patent No. 5196510
2	26	51.0	4	3	Sequence 5, Appl
3	26	51.0	4	4	Sequence 4, Appl
4	26	51.0	6	2	Sequence 41, Appl
5	26	51.0	7	2	Sequence 42, Appl
6	26	51.0	8	2	Sequence 58, Appl
7	25	49.0	7	1	Sequence 65, Appl
8	25	49.0	8	3	Sequence 334, Appl
9	23	45.1	4	1	Sequence 43, Appl
10	23	45.1	6	3	Sequence 2, Appl
11	23	45.1	8	1	Sequence 31, Appl
12	23	45.1	8	1	Sequence 35, Appl
13	23	45.1	8	2	Sequence 75, Appl
14	23	45.1	8	2	Sequence 75, Appl
15	23	45.1	8	2	Sequence 75, Appl
16	23	45.1	8	2	Sequence 75, Appl
17	23	45.1	8	3	Sequence 75, Appl
18	23	45.1	8	3	Sequence 75, Appl
19	23	45.1	8	3	Sequence 75, Appl
20	23	45.1	8	3	Sequence 75, Appl
21	23	45.1	8	4	Sequence 75, Appl
22	23	45.1	8	4	Sequence 75, Appl
23	22	43.1	7	1	Sequence 14, Appl
24	22	43.1	8	1	Sequence 17, Appl
25	22	43.1	8	1	Sequence 4, Appl
26	22	43.1	8	1	Sequence 3, Appl
27	22	43.1	8	1	Sequence 146, Appl

28	22	43.1	8	2	US-08-636-176-4	Sequence 4, Appl
29	22	43.1	8	2	US-08-478-435-146	Sequence 146, Appl
30	22	43.1	8	2	US-08-337-483-146	Sequence 146, Appl
31	22	43.1	8	2	US-08-478-373-146	Sequence 146, Appl
32	22	43.1	8	3	US-08-474-671-146	Sequence 146, Appl
33	22	43.1	8	3	US-08-483-577A-146	Sequence 146, Appl
34	22	43.1	8	3	US-08-946-329A-16	Sequence 16, Appl
35	22	43.1	8	3	US-08-567-357A-16	Sequence 16, Appl
36	22	43.1	8	3	US-08-729-743A-16	Sequence 16, Appl
37	22	43.1	8	3	US-08-997-438-146	Sequence 146, Appl
38	22	43.1	8	3	US-08-349-498-16	Sequence 16, Appl
39	22	43.1	8	4	US-08-637-654-146	Sequence 146, Appl
40	22	43.1	8	4	US-08-649-518-146	Sequence 146, Appl
41	22	43.1	8	5	PCT-US94-05355-3	Sequence 3, Appl
42	22	43.1	8	5	PCT-US95-01618-4	Sequence 4, Appl
43	22	43.1	8	5	PCT-US95-15463-16	Sequence 16, Appl
44	22	43.1	8	5	PCT-US95-15923-16	Sequence 16, Appl
45	21	41.2	4	2	US-08-667-001-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
5196510-10  
; Patent No. 5196510  
; APPLICANT: RODWELL, JOHN D.; MCKEARN, THOMAS J.; ALVAREZ,  
; VERNON, L.; RADCLIFFE, ROBERT D.  
; TITLE OF INVENTION: MOLECULAR RECOGNITION UNITS  
; NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/519,702  
; FILING DATE: 07-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 291,730  
; FILING DATE: 29-DEC-1988  
; SEQ ID NO:10:  
; LENGTH: 7  
5196510-10

Query Match 52.9%, Score 27; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GHFP 6  
DB 1 GHFP 4

RESULT 2  
US-08-660-697A-5  
; Sequence 5, Application US/08660697A  
; Patent No. 6027711  
; GENERAL INFORMATION:  
; APPLICANT: Sharma, Shubh D.  
; TITLE OF INVENTION: STRUCTURALLY DETERMINED  
; METALLO-CONSTRUCTS AND APPLICATIONS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM PC/XT/AT, IBM PS/2 or  
; COMPATIBLE: compatibles  
; OPERATING SYSTEM: PC-DOS or MS-DOS  
; SOFTWARE: Wordperfect 6.1 for Windows  
; CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/08/660,697A  
 ? FILING DATE: 05-JUN-1996  
 ? CLASSIFICATION: 424  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/476,652  
 ? FILING DATE: 07-JUN-1995  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: ADEA C. GOGORIS  
 ? REGISTRATION NUMBER: 29,714  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (212) 527-7700  
 ? TELEFAX: (212) 753-6237  
 ? INFORMATION FOR SEQ ID NO: 5:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 4 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: Peptide  
 ? HYPOTHEICAL: NO  
 ? ANTI-SENSE: NO  
 ?  
 ? US-08-660-697A-5

Query Match 51.0%, Score 26; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 1 GGGH 4

## RESULT 3

? US-09-464-358-4  
 ? Sequence 41, Application US/09464358  
 ? Patent No. 5837686

? GENERAL INFORMATION:  
 ? APPLICANT: Pharmed Incorporated  
 ? TITLE OF INVENTION: Structurally Determined Cyclic Peptide Constructs and  
 ? FILE REFERENCE: Cyclic Peptide Divisional  
 ? CURRENT APPLICATION NUMBER: US/09/464,358  
 ? CURRENT FILING DATE: 1999-12-15  
 ? PRIOR APPLICATION NUMBER: 08/476,652  
 ? PRIOR FILING DATE: 1996-06-05  
 ? PRIOR APPLICATION NUMBER: 08/476,652  
 ? PRIOR FILING DATE: 1995-06-07  
 ? NUMBER OF SEQ ID NOS: 5  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO: 4  
 ? LENGTH: 4  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURES:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Protein  
 ?  
 ? US-09-464-358-4

Query Match 51.0%, Score 26; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 1 GGGH 4

## RESULT 4

? US-08-244-496-4  
 ? Sequence 41, Application US/08244496  
 ? Patent No. 5837686

? GENERAL INFORMATION:  
 ? APPLICANT:  
 ? TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
 ? NUMBER OF SEQUENCES: 85  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ? CURRENT APPLICATION DATA: US/08/244,496  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: GB 9125024.1  
 ? FILING DATE: 25-NOV-1991  
 ? INFORMATION FOR SEQ ID NO: 42:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? FEATURE:  
 ? NAME/KEY: Modified-site  
 ? LOCATION: 7  
 ? OTHER INFORMATION: /product= "OTHER"  
 ? OTHER INFORMATION: /note= "AMIDATED"  
 ?  
 ? US-08-244-496-42

Query Match 51.0%, Score 26; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

? TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
 ? TITLE OF INVENTION: RHEUMATOID ARTHRITIS  
 ? NUMBER OF SEQUENCES: 85  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ? CURRENT APPLICATION DATA: US/08/244,496  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: GB 9125024.1  
 ? FILING DATE: 25-NOV-1991  
 ? INFORMATION FOR SEQ ID NO: 41:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 6 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? FEATURE:  
 ? NAME/KEY: Modified-site  
 ? LOCATION: 6  
 ? OTHER INFORMATION: /product= "OTHER"  
 ? OTHER INFORMATION: /note= "AMIDATED"  
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 ? US-08-244-496-41

Query Match 51.0%, Score 26; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 2 GGGH 5

## RESULT 5

? US-08-244-496-42  
 ? Sequence 42, Application US/08244496  
 ? Patent No. 5837686  
 ? GENERAL INFORMATION:  
 ? APPLICANT:  
 ? TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
 ? NUMBER OF SEQUENCES: 95  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ? CURRENT APPLICATION DATA: US/08/244,496  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: GB 9125024.1  
 ? FILING DATE: 25-NOV-1991  
 ? INFORMATION FOR SEQ ID NO: 42:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? FEATURE:  
 ? NAME/KEY: Modified-site  
 ? LOCATION: 7  
 ? OTHER INFORMATION: /product= "OTHER"  
 ? OTHER INFORMATION: /note= "AMIDATED"  
 ?  
 ? US-08-244-496-42

Query Match 51.0%, Score 26; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GGCH 4
      1111
Db      3 GGCH 6

RESULT 6
US-08-244 496-58
: Sequence 58, Application US/08244456
: Patent No. 5837686
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR THE TREATMENT OF
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS
: NUMBER OF SEQUENCES: 85
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.10 (10/91)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/244,456
: PRIOR APPLICATION NUMBER: GR 912524.1
: FILING DATE: 25 NOV-1991
: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURES:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: /product: "OTHER"
: OTHER INFORMATION: /note: "AMITATED"
US 08-244-496-58

Query Match 51.0%; Score 26; FR 21, 100% E. N.
Best Local Similarity 100.0%; Pred. No. 2, 100-0%;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      1 GGCH 4
      1111
Db      2 GGCH 6

RESULT 7
US-07-968 781A-65
: Sequence 65, Application US/07968781A
: Patent No. 5430177
: GENERAL INFORMATION:
: APPLICANT: Gaertner, Frank H.
: APPLICANT: Sick, August J.
: APPLICANT: Thompson, Mark
: APPLICANT: Schneft, H. Ernest
: APPLICANT: Schwab, George E.
: APPLICANT: Narva, Kenneth E.
: TITLE OF INVENTION: Probes for the Identification of : Bacteria
: NUMBER OF SEQUENCES: 89
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.10

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/968, 781A
: FILING DATE: 1992-03-0
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: MA44.FWCC1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 354-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-968-781A-65

Query Match 49.0%; Score 25; FR 1, Length 7;
Best Local Similarity 80.0%; Pred. No. 1, 50-0%;
Matches 4; Conservative 0; Mismatches 1; Gaps 0;

QY      4 HFFPT 8
      1111
Db      3 HFFPT 7

RESULT 8
US-08 444-618-334
: Sequence 334, Application US/084444818
: Patent No. 6150097
: GENERAL INFORMATION:
: APPLICANT: Chien, David Y.
: APPLICANT: Ruster, William J.
: TITLE OF INVENTION: NANO Diagnostics and Vaccines
: NUMBER OF SEQUENCES: 777
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Chiron Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,618
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/06/403,540
: FILING DATE: 14 MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Harbin, Alisa A.
: REGISTRATION NUMBER: 31,895
: REFERENCE/DOCKET NUMBER: 0110.002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (508)359-3876
: TELEFAX: (508)359-3885
: INFORMATION FOR SEQ ID NO: 334:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08 444-618-334

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Query Match 49.0% Score 25; DB 3; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Gaps 0;  
QY 4 HFPF 7  
DB 5 HYPF 8  
RESULT 9  
US-08-159-340A-43  
; Sequence 43, Application US/08159340A  
; Patent No. 5565352  
; GENERAL INFORMATION:  
; APPLICANT: Hochstrasser, Mark  
; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS  
; TITLE OF INVENTION: AND METHODS  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159.340A  
; FILING DATE: 24 NOV-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: APCD:112/HYL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-340A-43  
Query Match 45.1% Score 23; DB 17; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Gaps 0;  
QY 2 GGHF 5  
DB 1 GGHY 4  
RESULT 10  
US-08-570-761-2  
; Sequence 2, Application US/08570761  
; Patent No. 6009190  
; GENERAL INFORMATION:  
; APPLICANT: Meade, Thomas J.  
; APPLICANT: Takeuchi, Toshihiro  
; APPLICANT: Gray, Harry B.  
; APPLICANT: Simon, Melvin  
; APPLICANT: Louis, Angeleique Y.  
; TITLE OF INVENTION: COBALT SCHIFF BASE COMPOUNDS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570.761  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-62630/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-570-761-2  
Query Match 45.1% Score 23; DB 3; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Gaps 0;  
QY 2 GGHF 6  
DB 1 GGGF 5  
RESULT 11  
US-08-159-340A-31  
; Sequence 31, Application US/08159340A  
; Patent No. 5565352  
; GENERAL INFORMATION:  
; APPLICANT: Hochstrasser, Mark  
; APPLICANT: Papa, Ferioz  
; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS  
; TITLE OF INVENTION: AND METHODS  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159.340A  
; FILING DATE: 24-NOV-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: APCD:112/HYL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-340A-31

Query Match 45.1%; Score 23; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHF 5
   |||
Db 1 GGHY 4

RESULT 12
US-08-159-340A-35
Sequence 35, Application US/08159340A
Patent No. 5565352
GENERAL INFORMATION:
APPLICANT: Hochstrasser, Mark
APPLICANT: Papa, Peroz
TITLE OF INVENTION: DEBICQUINATING ENZYME COMPOSITIONS
NUMBER OF SEQUENCES: 44
TITLE OF INVENTION: AND METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Duke
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,340A
FILING DATE: 24 NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-340A-35

Query Match 45.1%; Score 23; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHF 5
   |||
Db 1 GGHY 4

RESULT 13
US-08-487-890A-75
Sequence 75, Application US/08487890A
```

```
Patent No. 5769149
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS.jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-75

Query Match 45.1%; Score 23; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGHF 5
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Db 3 GGSF 7

RESULT 14
US-08-478-435-75
Sequence 75, Application US/08478435
Patent No. 592323
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
```



CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/337,483  
 FILING DATE: 08 NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/134,116  
 FILING DATE: 29-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/144,948  
 FILING DATE: 09-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-410 MIS:JD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 75:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-478-435-75

Query Match: 45.1%; Score 23; DB 2; Length 8;  
 Best Local Similarity: 80.0%; Pred. No. 2.5e+05;  
 Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 GCGHF 5  
 DB 3 GCGSF 7

RESULT 1:  
 US-08-437-483-75  
 Sequence 75: Application US/08337483  
 Patent No. 5925662  
 GENERAL INFORMATION:  
 APPLICANT: Cosmore, Sheena  
 APPLICANT: Hartness, Robin  
 APPLICANT: Schuyvers, Anthony  
 APPLICANT: Cheng, Pele  
 APPLICANT: Gray-Owen, Scott  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Mardin, Andrew  
 APPLICANT: Klein, Michel  
 TITLE OF INVENTION: Transferrin Receptor Gene  
 NUMBER OF SEQUENCES: 147  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/337,483  
 FILING DATE: 08-NOV-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-410 MIS:JD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 75:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-337-483-75

Query Match: 45.1%; Score 23; DB 2; Length 8;  
 Best Local Similarity: 80.0%; Pred. No. 2.5e+05;  
 Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 GCGHF 5  
 DB 3 GCGSF 7

Search completed: November 5, 2003, 17:23:36  
 Job time: 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run On: November 5, 2003, 17:44:56 : Search time 21 Seconds  
(without alignments)  
27.477 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32

Sequence: 1 PGTIN1 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 293308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	50.0	6	A61049	halo-toxin - Pseudomonas syringae pv. mori
2	14	43.8	5	A61049	halo-toxin - Pseudomonas syringae pv. mori
3	13	40.6	4	A44624	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
4	13	40.6	4	A44624	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
5	13	40.6	5	PT0274	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
6	13	40.6	5	PT0274	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
7	13	40.6	6	PT0274	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
8	13	40.6	6	A35039	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
9	11	34.4	4	PT0566	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
10	11	34.4	5	F22565	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
11	11	34.4	5	S51027	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
12	11	34.4	5	S51027	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
13	11	34.4	5	PT0725	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
14	11	34.4	5	PT0725	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
15	11	34.4	6	165545	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
16	11	34.4	6	PT0531	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
17	11	34.4	6	PT0531	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
18	11	34.4	6	PT0568	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
19	11	34.4	6	PT0568	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
20	11	34.4	6	PT0725	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
21	10	31.2	4	PT0565	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
22	10	31.2	4	PT0291	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
23	10	31.2	5	S62963	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
24	10	31.2	5	G44817	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
25	10	31.2	5	I44817	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
26	10	31.2	5	E44917	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
27	10	31.2	5	C44917	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
28	10	31.2	5	A44917	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken
29	9	28.1	4	A37843	hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken

## ALIGNMENTS

### RESULT 1

A61049

halo-toxin - Pseudomonas syringae pv. mori

C:Species: Pseudomonas syringae pv. mori

A:Note: Host mulberry tree

C:Date: 10-Mar-1994 #sequence\_revision: 10-Mar-1994 #text\_change 21-Jan-1997

C:Accession: A61049

R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, I.

Chem. Lett. 00, 679-680, 1989

A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas sp;

A:Reference number: A61049

A:Accession: A61049

A:Molecule type: protein

A:Residues: 1-6 <KAJ>

A:Note: sequence confirmed by synthesis

C:Comment: This toxin is one of the etiological agents of halo bright disease in mulb-

C:Keywords: toxin

Query Match 50.0%; Score 16; DB 2; Length 6;

Best Local Similarity 75.0%; Pred No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGT 4

DB 1 PGT 6

### RESULT 2

S53595

hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Jul-1995 #sequence\_revision: 01-Sep-1995 #text\_change 07-May-1999

C:Accession: S53595

R:Calhoun, C.F.; Bouman, P.R.C.; Snippe, L.; Ab, G.

Nucleic Acids Res. 22, 5540-5547, 1994

A:Title: Translation start site multiplicity of the CCAAT/enhancer binding protein al;

A:Reference number: S53595; MJID:95140613; PMID:7838705

A:Accession: S53595

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <CAJ>

A:Cross-references: EXBL:X66844

Query Match 43.8%; Score 14; DB 2; Length 5;

Best Local Similarity 50.0%; Pred No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGT 4

DB 2 PGT 5

```

RESULT 3
A34626
R:CH-related neuroepitope - ferruginous spindle
C:Species: Ruminans ferrugineus (ferruginous spindle)
C>Date: 30-Jul-1992 #sequence_revision 36-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, T.; Fujisawa, Y.; Ikeda, T.; Minamitake, Y.;
Hocher, Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuroepitope related to the crustacean hormone, RPH.
A:Reference number: A34626; MUID:90174762; PMID:2311394
A:Accession: A34626
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuroepitope

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 4
P70240
C: heavy chain CRD3 region (clone 2 100H; human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16 Aug-1996
C:Accession: P70240
R:Yarada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Gatten, A.C.; Povera, G.
C: Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: P70222; MUID:91108337; PMID:1899102
A:Accession: P70240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 5
P70714
T-cell receptor beta chain V-D-J region (165-31) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10 May-1997
C:Accession: P70714
R:Feeney, A.J.
C: Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70714
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 6
P70715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C: Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 7
P70715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C: Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 8
A35039
Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R:Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: GB:M33382; NID:9211043
A:Note: this ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative trans
C:Keywords: alternative splicing; cartilage

Query Match 40.6%; Score 13; DB 4; Length 6;

```

```

Db 4 PG 5

RESULT 6
S69237
surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C>Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peterson, J.; Nitsch, M.; Kuenhmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Eng
J. Mol. Biol. 245, 385-401, 1995
A:Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of uni
A:Reference number: S69237; MUID:951139068; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <PET>
A:Experimental source: strain Fl, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 40.6%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4
DB 1 GTL 3

RESULT 7
P70715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C: Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 8
A35039
Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R:Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: GB:M33382; NID:9211043
A:Note: this ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative trans
C:Keywords: alternative splicing; cartilage

Query Match 40.6%; Score 13; DB 4; Length 6;

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2  
||  
Db 5 PG 6

## RESULT 9

PT0566  
T-cell receptor beta chain V-D-J region (141-10H) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30 May 1997  
C:Accession: PT0566  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0566  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <PEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 3 GT 4

## RESULT 10

P22565  
R-phycerythrin gamma A chain - red alga (Gastrodiclonium confertii) (fragment)  
C:Species: Gastrodiclonium confertii  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: P22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the Bilin attachment sites in R-phycerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:1946644  
A:Accession: P22565  
A:Molecule type: protein  
A:Residues: 1-5 <KIQ>

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 1 GT 2

## RESULT 11

S51077  
alpha-amylase - rice  
C:Species: Oryza sativa (rice)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 01-Sep-1995  
C:Accession: S51077  
R:Terashima, M.; Kubo, A.; Suzawa, M.; Itoh, Y.; Katoh, S.  
Eur. J. Biochem. 226, 249-254, 1994  
A:Title: The roles of the N-linked carbohydrate chain of rice alpha-amylase in thermostability.  
A:Reference number: S51077; MUID:95045597; PMID:17957236  
A:Accession: S51077  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <TER>

Query Match 34.4%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 3 GT 4

## RESULT 12

C53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: C53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: C53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <HAR>  
A:Cross-references: GB:S60737; MUID:g233916; PIDN:AAB19519.1; PID:g233919  
A>Note: sequence extracted from NCBI backbone (NCBI:60737, NCBIP:60740)  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 1 GT 2

## RESULT 13

PT0525  
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0525  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0525  
A:Molecule type: mRNA  
A:Residues: 1-5 <FHE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 4 GT 5

## RESULT 14

PT0701  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0658; PT0701  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0658  
A>Status: translation not shown

A/Molecule type: mRNA  
 A/Residues: 1-5 <FE2>  
 A/Experimental source: day 4 postnatal thymus, strain BALB/c, 121-3E  
 A/Accession: P10701  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-5 <FE2>  
 A/Experimental source: newborn thymus, strain BALB/c, 161-2E  
 C/Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
 ||  
 DB 4 GT 5

RESULT 15  
 I65546  
 MHC H2-L antigen - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02 Aug-1996 #sequence\_revision 02-Aug-1996 #text change 65-Nov-1999  
 C/Accession: I65546  
 R/Kimura, A.; Israel, A.; Le Bail, G.; Kourilsky, P.  
 Cell 44, 261-272, 1986  
 A/Title: Detailed analysis of the mouse H 2Kb promoter: Enhancer-like sequences and their  
 A/Reference number: 152778; MIMD:86105202; PNU:13510743  
 A/Accession: I65546  
 A/Status: preliminary; translated from CP/EMBL/DBP  
 A/Molecule type: DNA  
 A/Residues: 1-6 <RES>  
 A/Cross-references: GB:M12483; NID:0193565; P1EN:AAA190001.1; P1D:9554214

Query Match 34.4%; Score 11; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PCTL 4  
 |||  
 DB 3 PCTL 6

Search completed: November 5, 2003, 1:14:40.  
 Job time: 22 sec

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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:16:16 / Search time 10 seconds  
(without alignments)  
28.216 Million cells updates/sec

Title: US-09-914-088-6  
Perfect score: 32  
Sequence: ; PGTIN: 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 2.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	28.3	9	28.3	5 1 EI04_LITRU	P42103 Litoria rub
2	8	25.0	6 1 TM0F_SARBU	P41495 sarcophaga	
3	8	25.0	6 1 UN06_CLOPA	P13011 clostridium	
4	7	21.9	3 1 THYL_PIG	P11151 sus scrofa	
5	7	21.9	4 1 DCMV_PSETH	P19916 pseudomonas	
6	7	21.9	4 1 E051_HUMAN	P27731 homo sapien	
7	7	21.9	4 1 OCPI_GCTV	P26649 octopus min	
8	7	21.9	4 1 RMCI_YEAST	P45515 saccharomyc	
9	7	21.9	4 1 TUFT_HUMAN	P01858 homo sapien	
10	7	21.9	5 1 BPP7_POTIN	P10435 bothriops in	
11	7	21.9	5 1 EIC3_LITRU	P82039 litoria rub	
12	7	21.9	5 1 PAP2_PASMA	P81864 pardachirus	
13	7	21.9	5 1 PRCT_PERAM	P01373 periplaneta	
14	7	21.9	5 1 SUGA_ACHDO	P19931 acheta dome	
15	7	21.9	6 1 CIP1_MYTED	P13736 mytilus edu	
16	7	21.9	6 1 CIP2_MYTED	P13737 mytilus edu	
17	7	21.9	6 1 EIC1_LITRU	P82036 litoria rub	
18	7	21.9	6 1 OVM_LEPDE	P42985 leptonotars	
19	7	21.9	6 1 TRP1_PSEPU	P36414 pseudomonas	
20	7	21.9	6 1 VP19_HSVK	P23212 herpes simp	
21	6	18.8	3 1 GRWV_HUMAN	P01157 homo sapien	
22	6	18.8	4 1 ACHI_ACHFU	P59004 achina fu	
23	6	18.8	4 1 FLR1_ANCEU	P58767 achtopleura	
24	6	18.8	4 1 OCPI_OCTMI	P58648 octopus min	
25	6	18.8	5 1 AL14_CARMA	P81817 carcinus ma	
26	6	18.8	5 1 R312_LITRU	P82073 litoria rub	
27	6	18.8	5 1 TP15_CANFA	P34714 canis fami	
28	6	18.8	5 1 TRM3_ECOL	P13973 escherichia	
29	6	18.8	5 1 UF01_MOUSE	P38639 mus musculu	
30	6	18.8	5 1 UXA4_CHLTR	P38005 chlamydia t	
31	6	18.8	6 1 ASP2_LACSN	P92655 lactobacilli	
32	6	18.8	6 1 FARP_MONEX	P41966 manniezia ex	
33	6	18.9	6 1 LOK1_LOONI	P41491 locusta mig	

RESULT 1  
EI04\_LITRU STANDARD; PRT; 5 AA.  
ID EI04\_LITRU  
AC P82100;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electric 4.

OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]

SEQUENCE.  
RP TISSUE=Skin secretion;  
RC Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RA "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litori electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 5 5  
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TIN 5  
DB 3 TVH 5

RESULT 2  
TM0F\_SARBU STANDARD; PRT; 6 AA.  
ID TM0F\_SARBU  
AC P41495;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Trypsin-modulating oostatic factor (TMOF).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]

SEQUENCE, AND SYNTHESIS.  
RP TISSUE=Ovary;  
RC MEDLINE=94211930; PubMed=8159807;  
RA Bylerans D., Bcrowsky D., Shabanowitz J., Grauwels L.,  
de Locf A.;  
RT "Sequencing and characterization of trypsin modulating oostatic

RT factor (TM01) from the ovaries of the grey fleshfly, *Neobellieria*  
 RT (*Sarcophaga bullata*).  
 RL Regul. Rept. 50:61-72(1994).  
 CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE  
 CC DEVELOPMENT.  
 CC -2- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72451E7642200 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 6;  
 Best Local Similarity 20.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PUTIN 5  
 Db 2 PPNLH 6

## RESULT 3

INRE\_CLOPA STANDARD; PRT; 6 AA.  
 ID UNK06\_CLOPA  
 AC P81351;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 6 from 2D-page (fragment).  
 OS Clostridium pasteurianum.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 CC NCBI TaxID=1501;  
 RN 1;  
 RP SEQUENCE.  
 RC STRAIN=WS;  
 RX MEDLINE=98291870; Pubmed=9699919;  
 RA Fergusson R., Skjeldal L.;  
 RT "Two dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5.1";  
 FL Electrophoresis 19:802-806(1998).  
 CC 1 MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa  
 FT NCM TER 6  
 SQ SEQUENCE 6 AA; 657 MW; 606P171A5A4176 09 144

Query Match 25.0%; Score 8; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.0e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TIM 6  
 Db 3 TAVL 6

## RESULT 4

THYL\_PIG STANDARD; PRT; 3 AA.  
 ID THYL\_PIG  
 AC P01157;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thyroliberin (thyrotropin releasing hormone) (THL) (Protein).  
 OS Sus scrofa (pig),  
 OS Sus aries (sheep),  
 OS Ovis aries (sheep),  
 OS Bombina orientalis (Oriental fire-bellied toad), and  
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus  
 CC NCBI TaxID=9923; 9940, 8346, 8316;  
 RN 1;  
 RP SEQUENCE.  
 RC SPECIES=Pig; TISSUE:Hypothalamus;

RX MEDLINE=70136150; Pubmed=4984938;  
 RA Nair R.M.G., Barrett C.F., Bowers C.Y., Schally A.V.;  
 RT "Structure of porcine thyrotropin releasing hormone.";  
 RL Biochemistry 9:1103-1106(1970).  
 RN 2;  
 RP SYNTHESIS.  
 RC SPECIES=Pig;  
 RX MEDLINE=70039904; Pubmed=4982117;  
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
 RT "The identity of chemical and hormonal properties of the thyrotropin  
 RT releasing hormone and pyroglutamyl-histidyl-proline amide.";  
 RL Biochem. Biophys. Res. Commun. 37:735-710(1969).  
 RN 3;  
 RP SEQUENCE.  
 RC SPECIES=Sheep; TISSUE:Hypothalamus;  
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.;  
 RA Ward D.N.;  
 RT "The elucidation of the primary structure of the hypothalamic thyroid  
 RT stimulating hormone releasing factor of ovine origin by means of mass  
 RT spectrometry.";  
 RL Orig. Mass Spectrom. 5:221-228(1971).  
 RN 4;  
 RP SYNTHESIS.  
 RC SPECIES=Sheep;  
 RX MEDLINE=70163386; Pubmed=4985794;  
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
 RA Guillemin R.;  
 RT "Characterization of ovine hypothalamic hypophysiotropic  
 RT TSH-releasing factor.";  
 RL Nature 226:321-325(1970).  
 RN 5;  
 RP SEQUENCE.  
 RC SPECIES=B. orientalis; TISSUE=Skin;  
 RX MEDLINE=76138399; Pubmed=815011;  
 RA Yasuhara T., Nakajima T.;  
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
 RL Chem. Pharm. Bull. 23:330-3303(1975).  
 RN 6;  
 RP SEQUENCE.  
 RC SPECIES=N. viridescens;  
 RX MEDLINE=75035605; Pubmed=4214528;  
 RA Grimm-Jorgensen Y., McKelvy J.F.;  
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
 RT viridescens) brain in vitro. Isolation and characterization of  
 RT thyrotropin releasing factor.";  
 RL J. Neurochem. 23:471-478(1974).  
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH  
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
 CC PIR; A90919; RHDTTO.  
 DR PIR; A92971; A92971.  
 DR PIR; A93750; RHSH.  
 KW Amidation; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 3 3 AMIDATION.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 P 1  
 Db 3 P 3

## RESULT 5

DCML\_PSECH STANDARD; PRT; 4 AA.  
 ID DCML\_PSECH  
 AC P19516;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
 DN dehydrogenase subunit L) (CO-BL 5) (Fragment).

GN CUTL.  
 CS Pseudomonas carboxydohydrogena.  
 GC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer C.;  
 PT "Homology and distribution of CO dehydrogenase structural genes in  
 R: carboxydohydrophobic bacteria.";   
 RL Arch. Microbiol. 152:335-341(1999).  
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC -!- CATALYTIC ACTIVITY: CO + H<sub>2</sub>O + acceptor = CO(2) + reduced  
 CC acceptor.  
 CC -!- COFACTOR: Molybdenum (molybdopterin).  
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR; P01440; P0140.  
 KW Oxidoreductase; Molybdenum.  
 FT NON TER 4  
 FT MOD RES 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761876FC0000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1

DB 4 P 4

RESULT 6

EOSI\_HUMAN  
 ID EOSI\_HUMAN STANDARD; PRT; 4 AA.  
 AC P02731;  
 DT 21-JUL-1996 (Rel. 01, Created)  
 DT 21-JUL-1996 (Rel. 01, Last sequence update)  
 DT 21-JUL-1996 (Rel. 01, Last annotation update)  
 DE Eosinophilic cell peptides.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Chumata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartida; Hominoidea; Hominidae;  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060393;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilic cell peptides of  
 RT human lung tissue: identification as eosinophilic chemotactic factor of  
 RT anaphylaxis";   
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG  
 CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.  
 DR GO; GO:0030105; P:anaphylaxis; IDA.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 FT VARIANT 1 1  
 FT VARS A (IN OTHER PEPTIDES).  
 FT /FTID=VAR\_005201.  
 SQ SEQUENCE 4 AA; 390 MW; 6B05B962AC0000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Q1 3

DB 2 GS 3

RESULT 7

OCP3\_OCTM;  
 ID OCP3\_OCTM1 STANDARD; PRT; 4 AA.  
 AC P58649;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 DE Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RP TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10976044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";   
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
 CC active than Ocp-3.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD RES 2 2  
 FT D-SERINE (IN OCP-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3

DB 1 GS 2

RESULT 8

RM01\_YEAST  
 ID RM01\_YEAST STANDARD; PRT; 4 AA.  
 AC P36515;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).  
 GN MRP1.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=91285106; PubMed=2060626;  
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,  
 RA Kitakawa M.;  
 RT "Extended N-terminal sequencing of proteins of the large ribosomal  
 RT subunit from yeast mitochondria";   
 RL FEBS Lett. 284:51-56(1991).  
 DR PIR; S17255; S17255.  
 DR SGD; L0002881; MRP1.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON TER 4 4  
 FT SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1



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Db 4 P 4

RESULT 9
TUFT_HUMAN STANDARD; PRT; 4 AA.
ID TUFT_HUMAN AC P01968;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (tuftsin).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCB1_TaxID=9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=412769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Nijjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN 12;
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Nijjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophagic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392(1967).
CC 1; MISCELLANEOUS: AN IGS CALLED LEUCOKININ BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR XMM; 191150.
DR GO; GO:0001823; Antigen binding activity; NAS.
DR GO; GO:0006309; Phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74196321C0C0C000 CRC64.

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
DB 3 F 3

RESULT 10
SPPT_BOTIN STANDARD; PRT; 5 AA.
ID SPPT_BOTIN AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin converting
enzyme inhibitor).
OS Bothrops insularis (Island Jaracaca) (Quimada Jaracaca).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
CC Viperidae; Crotalinae; Bothrops.
CX NCB1_TaxID=8723;
RN 1;
RP SEQUENCE.
RX MEDLINE=90351557; PubMed=2386619;
RA Gupta A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990)

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CC 1; FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B0C000 CRC64;

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Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 P 1
DB 5 P 5

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RESULT 11
E103_LITRU STANDARD; PRT; 5 AA.
ID E103_LITRU AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
CC Pelodyadinae; Litoria.
CX NCB1_TaxID=104895;
RN 1;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella."
RL Aust. J. Chem. 52:619-645(1999).
CC 1; SUBCELLULAR LOCATION: Secreted.
CC 1; TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 569761F2C9A0C000 CRC64;

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Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 P 1
DB 4 P 4

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RESULT 12
PAP2_PARMA STANDARD; PRT; 5 AA.
ID PAP2_PARMA AC P82864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus ramaratus (Red sea roses sole).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
CC Soleidae; Soleidae; Pardachirus.
CX NCB1_TaxID=31087;
RN 1;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=7057359; PubMed=3782138;
RA Lazarevic P., Primot N., Loew E.M.;

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RT "purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the Red sea moses sole (Paradichirus  
 RT tamaratus).";  
 RT J. Biol. Chem. 261:16704-16713(1986).  
 CC !- FUNCTION: Exhibits unusual, shark repellent and surfactant  
 CC properties. Forms voltage-dependent, ion-permeable channels  
 CC in membranes. At high concentration causes cell membrane lysis.  
 CC !- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC !- SUBCELLULAR LOCATION: Secreted.  
 CC !- SIMILARITY: BELONGS TO THE PARADAXIN FAMILY.  
 KW Toxin.  
 FT NON TER 5 5  
 SQ SEQUENCE 5 AA: 614 MW; 7769C9C8100000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 5 P 5

RESULT 11  
 PRCT\_PERAM  
 ID PRCT\_PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach).  
 CS Limulus polypherrus (Atlantic horseshoe crab), and  
 CS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;  
 CC Blattidae; Periplaneta.  
 CC NCBI\_TaxID=6978, 6850, 6759;  
 RN [1].  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starbuck A.N., Brown B.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron."  
 RT in insects.";  
 RL Life Sci. 17:1251-1256(1976).  
 RN [2].  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=8:225865; PubMed=6113590;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron."  
 RL Science 213:567-569(1981).  
 RN [3].  
 RP SEQUENCE.  
 RC SPECIES=L.polyphemus;  
 RX MEDLINE=90284800; PubMed=2356151;  
 RA Groomer J.R., Tillinghast E.K., Townley M.A., Vertovs A.,  
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus.";  
 RL Peptides 11:205-211(1990).  
 RN [4].  
 RP SEQUENCE.  
 RC SPECIES=C.maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus.";  
 RL Peptides 7:167-172(1986).  
 CC !- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

CC !- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC THE CRAB PERICARDIAL ORGANS.  
 CC PIR; A01644; HORCHA.  
 CC PIR; A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA: 649 MW; 71B7671B44600000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 4 P 4

RESULT 14  
 SUGA\_ACHDO  
 ID SUGA\_ACHDO STANDARD; PRT; 5 AA.  
 AC P1991;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Subesophageal ganglion pentapeptide.  
 OS Acheta domesticus (House cricket).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 CC Acheta.  
 CC NCBI\_TaxID=6997;  
 RN [1].  
 RP SEQUENCE.  
 RA Wicker C., Wicker C.;  
 RT "Isolation and structure of a peptide isolated from the  
 RT subesophageal ganglion of Acheta domesticus (orthoptera).";  
 RL Comp. Biochem. Physiol. 88C:185-187(1987).  
 CC !- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
 CC GANGLIA.  
 CC PIR; JS0319; JS0319.  
 SQ SEQUENCE 5 AA: 476 MW; 69D76DDDD8000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 4 P 4

RESULT 15  
 CIFI\_MYTED  
 ID CIFI\_MYTED STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).  
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 CC Mytiloidea; Mytilidae; Mytilus.  
 CC NCBI\_TaxID=6550;  
 RN [1].  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Munesaka Y.;  
 RA "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC !- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC !- SIMILARITY: TO MIP II.  
 CC PIR; A27696; A27696.  
 KW Hormone; Amidation.

PT MOD PES 6 6 AMINATION  
SQ SEQUENCE 6 AA: 637 MW: 720906875881900 ORC+4;  
Query Match 21.94; Score 7; DB 1; Length 6;  
Res. Local Similarity 50.01; Pred. No. 1.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CY 2 GT 1  
Et 1  
GS 2

Search completed: November 5, 2003, 17:47:23  
Job time : 11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:44:11 : Search time 33 seconds  
(without alignment's)  
46.919 Million cell updates/sec

Title: US-09-914-088-6  
Perfect score: 32  
Sequence: 1 PGTINI 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

```

1: SP_TREMBL_23.*
2: SP_Archea.*
3: SP_Bacteria.*
4: SP_Fungi.*
5: SP_Invertebrate.*
6: SP_Mammal.*
7: SP_Misc.*
8: SP_Organelle.*
9: SP_Phage.*
10: SP_Plant.*
11: SP_Todent.*
12: SP_Virus.*
13: SP_Vertebrate.*
14: SP_Unclassified.*
15: SP_Xvirus.*
16: SP_Bacteriap.*
17: SP_Archeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	28.1	4	11 Q08433	Q08433 Rattus sp.
2	7	21.9	5	13 P83308	P83308 Gallus gall
3	6	18.8	5	10 Q99007	Q99007 Hordeum vul
4	5	15.6	5	2 P83073	P83073 Bacillus ce
5	5	15.6	6	10 P82181	P82181 Spinacia ol
6	5	15.6	6	10 P82541	P82541 Spinacia ol
7	5	15.6	6	10 P82152	P82152 Spinacia ol

#### ALIGNMENTS

RESULT 1  
Q08433  
ID Q08433 PRELIMINARY; PRT; 4 AA.  
AC Q08433;

DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gunn;  
RX MEDLINE=91282758; PubMed=1840486;  
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";  
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).  
DR EMBL; S38636; AAB19259.1; -;  
KW Transferase.  
FT NON\_TER  
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 28.1%; Score 9; DB 11; Length 4;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NI 6  
DB 1 NV 2

#### RESULT 2

P83308  
ID P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE FMRamide-like neuropeptide (LPRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RX PubMed=6137771;  
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by antibodies to FMRamide.";  
RL Nature 305:329-330 (1983).  
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE) FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 21.9%; Score 7; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
DB 2 P 2

#### RESULT 3

Q99007  
ID Q99007 PRELIMINARY; PRT; 5 AA.  
AC Q99007;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)



```

RESULT 7
P21182
ID P82182 PRELIMINARY; PRI: 6 AA.
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
E1 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
E2 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
CS Spinacia oleracea (Spinach).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID:3562;
RN 11;
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yanaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC 1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC 1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC 1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC 1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC 1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10.
DR InterPro: IPR002363; Ribosomal_L10cub.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA: 63213415E05DB300 CRC64.

Query Match 15.6%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
DB 5 1 5

Search completed: November 5, 2003, 10:49 AM
Job time : 33 secs

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GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:45:26 : Search time 40 seconds  
(without alignment)  
23,409 Million cell updates/sec

Title: US 09-914-088-6

Perfect score: 32

Sequence: 1 PGTIN1 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1:07563 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 50962

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	6	21	IGF C epsilon-2 do
2	32	100.0	6	22	Peptide p6 derived
3	32	100.0	6	23	Human IGE immunoge
4	22	68.8	6	23	Campothecin pepti
5	22	68.8	6	23	Campothecin pepti
6	20	62.5	6	15	IGF-1 analogue N-t
7	20	62.5	6	23	Human CD66 family
8	19	59.4	6	21	Ad5 HSV5 loop frag
9	18	56.2	3	21	T cell antigen rec

10	18	56.2	4	24	AA533660	Human BCA3 SH2-dom
11	18	56.2	5	19	AA214493	Human neuroendocri
12	18	56.2	5	23	ABG93533	Human P-glycoprote
13	18	56.2	6	14	AA382334	Alzheimer paired h
14	18	56.2	6	14	AA337553	Phosphorylated tau
15	18	56.2	6	19	AA445755	Apoptotic protease
16	18	56.2	6	20	AA235110	V beta 6 clone fou
17	18	56.2	6	21	AA95785	LPXIG motif of er
18	18	56.2	6	22	AA205491	Synthetic hexapept
19	18	56.2	6	23	AA205559	Soybean diverged d
20	17	53.1	5	18	AAW31287	Bovine beta casein
21	17	53.1	5	23	ABP67559	Human CD66 family
22	17	53.1	6	16	AA70280	Soluble laminin (L
23	17	53.1	6	17	AA95608	Diabetogenic hexap
24	17	53.1	6	20	AA914090	Affinity ligand fo
25	17	53.1	6	21	AA93404	WT3 immunogenic p
26	17	53.1	6	22	AA859293	Peptide encoded by
27	17	53.1	6	23	ABP67549	Human CD66 family
28	17	53.1	6	24	ABU57841	Soluble laminin ce
29	16	50.0	4	19	AA79576	Peptide 1, from LK
30	16	50.0	4	23	ABP67571	Human CD66 family
31	16	50.0	4	23	ABP67582	Human CD66 family
32	16	50.0	5	10	AA95653	Sequence of varian
33	16	50.0	5	19	AAW31288	Bovine beta casein
34	16	50.0	5	19	AAW87388	Peptide determined
35	16	50.0	5	23	ABP67560	Human CD66 family
36	16	50.0	5	23	ABP67561	Human CD66 family
37	16	50.0	6	10	AA93345	Portion of myc var
38	16	50.0	6	14	AA44419	rBPI-IgG fusion N-
39	16	50.0	6	18	AAW45377	Peptide antagonist
40	16	50.0	6	19	AAW87396	Peptide determined
41	16	50.0	6	19	AAW75368	Hexapeptide #8 bin
42	16	50.0	6	19	AAW75300	Hexapeptide #8 bin
43	16	50.0	6	21	AA49376	Beta-casomorphin d
44	16	50.0	6	22	AAE09360	rBPI(1-199) Ig fus
45	16	50.0	6	22	AA891590	Opioid peptide SEQ

#### ALIGNMENTS

#### RESULT 1

AA825912  
ID AA825912 standard; Peptide: 6 AA.

XX AC AA825912.

XX DT 05 JAN-2001 (first entry)

XX DE IGE C-epsilon-2 domain surface exposed epitope peptide P6 SEQ ID NO:6.

XX XX Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;

KW allergic disease; immunophylaxis; immunotherapy; anti-allergic;

KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.

XX OS Homo sapiens.

XX PN WO200005460-A1.

XX PD 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-BP01455.

XX PR 25-FEB-1999; 99GB-0004405.

XX PR 29-MAR-1999; 99GB-0007152.

XX PR 07-MAY-1999; 99GB-0010537.

XX PR 07-MAY-1999; 99GB-0010538.

XX PR 07-AUG-1999; 99GB-0018594.

XX PR 07-AUG-1999; 99GB-0018663.

XX PR 07-SEP-1999; 99GB-0021046.

XX PR 07-SEP-1999; 99GB-0021047.

XX PR 29-OCT-1999; 99GB-0025619.





XX Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 32; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGTINI 6  
 DB 1 PGTINI 6

RESULT 4  
 ABP53525  
 ID ABP53525 standard; peptide; 6 AA.

AC ABP53525;

DT 12-DEC-2002 (first entry);

DE Carptothecin peptide conjugate II.21.

KW Carptothecin peptide conjugate; cytostatic; glycoconjugate; tumour;  
 KW specifically cleavable peptidic linking unit; cancer.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with 20-O-"

FT Modified-site 6 /note= "C-terminally modified with camptothecin TFA"

PN EPI219305 AL.

XX 03-JUL-2002.

PF 27-DEC-2000; 2000EP-0128402.

PR 27 DEC-2000; 2002EP-0128402.

PA (FARB ) BAYER AG.

PI Lerchen H, Baumgarten J, Lockhoff O;

DR WPI; 2002 629644/68.

PT Cytostatic-glycoconjugates useful for treating cancer have specifically  
 PT cleavable peptide linking units so as to deliver drug to tumor only  
 PS Example; Page 17; 46pp; English.

XX The present invention describes a conjugate (I) and its salts. (I) has  
 CC the formula C<sub>1</sub>-Li-Sp<sub>2</sub>-K; where: C<sub>1</sub> = cytotoxic radical or radical of  
 CC a cytostatic derivative optionally also carrying a CH<sub>3</sub>, C<sub>2</sub>H<sub>5</sub> or NH<sub>2</sub> group;  
 CC Li = linker comprising 5 to 8 amino acids each optionally carrying  
 CC protecting groups; Sp<sub>1</sub> = absent, CO or CS; Sp<sub>2</sub> = optionally substituted  
 CC arylene or alkylene; and K = unsubstituted or regioselectively modified  
 CC carbohydrate radical. Also described: (1) a process for preparation of  
 CC the conjugate; (2) a medicament comprising the conjugate; (1) has  
 CC cytostatic activity. The conjugates are useful for treating cancer.  
 CC The conjugate is cleaved by enzymes found especially in tumor tissue  
 CC to release the cytotoxic drug. As the drug is not active until after  
 CC cleavage it will not cause harm to non-tumor proliferating cells.  
 CC therefore reducing the side-effects associated with the use of such

CC drugs. The present sequence represents a camptothecin peptide conjugate,  
 CC which is used in an example from the present invention.

XX Sequence 6 AA;

Query Match 68.8%; Score 22; DB 23; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGTINI 6  
 DB 1 PGGLNV 6

RESULT 5

ABG31530

ID ABG31530 standard; Peptide; 6 AA.

AC ABG31530;

XX 05-NOV-2002 (first entry);

XX Camptothecin peptide conjugate #19.

KW Camptothecin; integrin receptor antagonist; cytostatic agent;  
 KW tumour cell; metallo matrix protease; MMP; carcinomatous disorder;  
 KW integrin alpha\_vbeta\_3 receptor antagonist; tumour growth inhibitor;  
 KW tumour; integrin; camptothecin-bis-trifluoroacetate.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 6 /label= OTHER

FT /note= "Bound to Camptothecin bis-trifluoroacetate  
 at position 20-O"

PN EPI219305-AL.

XX 03-JUL-2002.

XX 27-DEC-2000; 2000EP-0128401.

XX 27-DEC-2000; 2000EP-0128401.

XX (FARB ) BAYER AG.

XX Lerchen H, Baumgarten J, Lockhoff O, Albers M, Schoop A;

XX WPI; 2002-576993/62.

XX New conjugates of integrin receptor antagonist and a cytostatic agent  
 XX with specific cleavable linking unit useful in the treatment of cancer

XX Examples; Page 61; 127pp; English.

XX This invention relates to conjugates of integrin receptor antagonist and  
 CC a cytostatic agent with cleavable linking unit that are selectively  
 CC cleaved by tumour cell metallo matrix proteases (MMPs). The  
 CC conjugates of the invention may have cytostatic activity and may be  
 CC used as an integrin alpha\_vbeta\_3 receptor antagonist or a tumour  
 CC growth inhibitor. The conjugates of the invention may be used in the  
 CC production of a medicament for the treatment of carcinomatous disorders.  
 CC Compounds of the invention containing the conjugates of the invention  
 CC exhibit a selective and tumour-specific action as a result of linkage to  
 CC alpha\_vbeta\_3 integrin antagonists via linking units which can be  
 CC selectively cleaved by enzymes such as metallo matrix proteases, i.e.  
 CC enzymes found in tumour tissue. The linking units can also maintain the  
 CC serum stability of the conjugate of cytostatic and alpha\_vbeta\_3  
 CC integrin antagonist, and at the same time, show the desired  
 CC intracellular action within tumour cells as a result of its specific  
 CC enzymatic and hydrolytic cleavability with release of the cytostatic.

CC The present sequence represents a captothecin-bis-trifluoroacetate  
 CC conjugated peptide used in an example of the method of the invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 68.8%; Score 22; DB 23; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PGTH 6  
 DB 1 PGTHV 6

RESULT 6  
 AAR51446  
 ID AAR51446 standard; peptide; 6 AA.

XX AAR51446;  
 AC AAR51446;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 27-OCT-1994 (first entry)  
 XX  
 XX IGF-1 analogue N-terminal.  
 DE  
 XX Insulin-like growth factor; IGF-1; IGF 2; birds: chickens; IGF-1  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; DR3 IGF-1.  
 XX  
 XX Homo sapiens.  
 CS  
 XX WO9426445-A1.  
 PN  
 XX 31-MAR-1994.  
 PD  
 XX 02-SEP-1993; 93WO-US08279.  
 PF  
 XX 17 SEP-1994; 92US-0947035.  
 PR  
 XX (EMPR-) EMPREX INC.  
 PA (GROUP-) GROPEP PTY LTD.  
 PA (USDA ) US SEC OF AGRIC.  
 PI Ballard RJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 DR WPI/ 1994 118144/14.  
 XX

XX Increasing growth of birds with insulin like growth factor  
 PT delivered to the egg before hatching exp. for the resulting egg gain  
 PT in chickens.  
 XX  
 PS Claim 6; Page 37; 45pp; English.  
 XX  
 CC Growth of birds is increased by (a) adding to the bird, in ovo,  
 CC insulin-like growth factor (IGF-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in AAR51439-49.  
 CC IGF 2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF 2 analogue pref.  
 CC comprises the N-terminal given in AAR51450-53  
 CC esp. long R3 IGF-1, given in AAR51454 is used. It is the full human  
 CC IGF 1 sequence with Arg replacing Glu(3) and a 13 amino acid  
 CC N-terminal extension.  
 CC (updated on 25-MAR-2003 to correct in field.)  
 XX

Sequence 6 AA;

Query Match 62.5%; Score 20; DB 15; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PGTH 4  
 DB 2 PGTH 5

RESULT 7  
 ABP67550  
 ID ABP67550 standard; Peptide; 6 AA.

XX AC ABP67550;  
 XX  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human CD66 family modulating peptide SEQ ID NO 421.  
 XX  
 XX Human; CD66; CEACAM; cytostatic; antiinflammatory; immunomodulator;  
 KW antibacterial; virucide; gene therapy; vaccine; neutrophil;  
 KW immune system; autoimmune disease; cancer; infection; bacterial; virus;  
 KW inflammatory disease; transplantation; immunisation.  
 XX

OS Homo sapiens.

XX WO200269601-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 27-FEB-2002; 2002WO-US05720.  
 PF  
 XX 28-FEB 2001; 2001US-272113P.  
 PR  
 XX (SKUB/) SKUBITZ K M.  
 PA (SKUB/) SKUBITZ A P N.

XX Skubitz KV, Skubitz APN;

XX WPI/ 2002-70698/76.

XX New peptide from a surface exposed region of a CD66 family member,  
 PT useful for modulating the function of CD66 family members, e.g.  
 PT activation of neutrophils, for treating or diagnosing autoimmune  
 PT diseases or cancer, and as a vaccine -  
 XX  
 PS Claim 2; Page 27; 96pp; English.

XX The invention relates to an isolated peptide (I) from a surface exposed  
 CC region of a CD66 family member (ABP6713C ABP67990). The peptide  
 CC modulates:  
 CC (a) activation of neutrophils;  
 CC (b) activation or inhibition of T-cells, B-cells, NK cells, LAK cells,  
 CC dendritic cells or other immune system cells;  
 CC (c) proliferation and/or differentiation of the above cells, including  
 CC epithelial cells;  
 CC (d) homotypic and/or heterotypic adhesion among CD66 family members;  
 CC and  
 CC (e) adhesion of CD66 family members to other ligands. The peptide is  
 CC useful in modulating the function of CD66 family members and/or their  
 CC ligands, such as activation of neutrophils and activation, inhibition,  
 CC proliferation and/or differentiation of the immune cells. The peptides  
 CC may also be used in treating or diagnosing autoimmune diseases, cancer,  
 CC infections (e.g. bacterial or viral) or inflammatory diseases, in  
 CC transplantation therapies and for immunisation.  
 XX

SQ Sequence 6 AA;

Query Match 62.5%; Score 20; DB 23; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PGTH 6

DB 1 PCT:LNW 6

RESULT 8  
ID AAY90183 standard; peptide; 6 AA.

XX AAY90183;  
DT 21 SEP-2000 (first entry);  
DE Ad5 HVR5 loop fragment.  
KW Ligand epitope; UPAR; utokinasase-type plasminogen activator receptor;  
KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;  
KW recombinant adenovirus vector; tumor; restenosis; gene therapy; asthma;  
KW smooth muscle cell proliferation inhibitor; coronary artery disease;  
KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
KW thrombosis; diabetes; tropism-modified virus.

XX Adenovirus sp.  
XX WC220012738-A1.  
XX 09-MAR-2000.  
XX 27 AUG-1999; 99MO-IB01524.  
XX 27-AUG 1998; 98US-0098028.  
XX (AVET) AVENTIS PHARMA SA.

PI Vigne E, Delieu J, Latta M, Yeh P, Perricaudet M;  
XX MPI; 2000 256653/22.  
XX Urokinase-type plasminogen activator receptor (UPAR)-targeted  
PT adenovirus vectors having modified hexon HVR5 and HI loops and modified  
PT fiber proteins useful for targeted gene therapy to treat cancer or  
PT restenosis.

PS Example 1; Page 32; 128pp; English.  
XX This sequence is a fragment of the adenovirus Ab5 loop, containing the  
CC HVR5 loop. The invention relates to an adenovirus from which at  
CC least a part of the hexon HVR5 or HI loop is replaced with a binding  
CC peptide, or targeting sequence, flanked by activating domain and spacers,  
CC to functionally display its binding specificity at the capsid surface.  
CC The invention also relates to a recombinant adenovirus vector where a  
CC binding peptide, or targeting sequence, is connected to the C-terminus of  
CC the fiber by a connecting spacer, or linker, so as to functionally  
CC display its binding specificity at the capsid surface. The adenovirus or  
CC recombinant adenovirus vector can be used to preferentially express a  
CC gene in a target cell, especially a cell that expresses a UPAR. The  
CC targeted adenovirus vector preferably comprises a heterologous gene  
CC encoding a gene for treatment of a tumor or restenosis. The targeted  
CC adenovirus vector is useful for gene therapy treatment of a disease, and  
CC for manufacturing a medicine used in gene therapy treatment of a disease.  
CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,  
CC thrombosis, and diabetes. The viruses are particularly targeted against a  
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
CC are tropism-modified without adversely affecting infectivity of the  
CC vectors.

XX Sequence 6 AA;

Query Match 59.4%; Score 19; DB 21; Length 6;  
Best local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TINI 6  
DB 3 TINI 6

RESULT 9  
ID AAY66968 standard; peptide; 3 AA.

XX AAY66968;  
DT 11-APR-2000 (first entry)  
DE T cell antigen receptor Vbeta chain CDR3 peptide.  
KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;  
KW Vbeta chain; autoantigen; immunological tolerance.

XX Homo sapiens.  
XX MO9963084-A1.  
XX 09-DEC-1999.  
XX 28-MAY-1999; 99MO-JP02814.  
XX 29-MAY-1998; 98JP-0149855.  
XX 14-OCT-1998; 98JP-0328761.  
XX (TORI) TORII PHARM CO LTD.  
XX Nishiooka K, Yoshino S;  
XX MPI; 2000-086978/97.

XX T-cell antigen receptor V-beta chain CDR3 region sequences accumulated  
PT in synovial membranes of rheumatoid arthritis patients -  
XX Claim 4; Page 15; 136pp; Japanese.

XX The invention relates to peptide sequences present in the synovial fluid  
CC and membranes of rheumatoid arthritis patients, arising from the CDR  
CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.  
CC Compositions which contain autoantigenic peptides binding specifically  
CC to T cells expressing receptors containing the peptide sequences, which  
CC include antigen-specific immunological tolerance to rheumatoid arthritis  
CC can be used for the treatment and prevention of rheumatoid arthritis.  
CC The invention can be used for the diagnosis, treatment and prevention  
CC of rheumatoid arthritis. Sequences AAY66959-977 represent peptides from  
CC the CDR3 region of various Vbeta chains of T cell antigen receptor.

XX Sequence 3 AA;

Query Match 56.2%; Score 18; DB 21; Length 3;  
Best local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3  
DB 1 PGT 3

RESULT 10  
ID AAE33660 standard; peptide; 4 AA.

XX AAE33660;  
DT 16-APR-2003 (first entry)

XX Human BCA3 SH2 domain binding site #5.  
DE Human; breast cancer-associated gene; BCA-related disorder; lymphoma;  
KW Human; breast cancer-associated gene; BCA-related disorder; lymphoma;

KW infectious disease; eating disorder; cancer; Ewing's tumor; allergy;  
 KW tumor; polycythemia vera; forensic biology; gene therapy; leukaemia;  
 KW bone disease; sarcoma; vaccine.

XX Homo sapiens.

OS W020287507-A2.

XX 07-NOV-2002.

XX 29-APR-2002; 2002WO-US:3484.

XX 27-APR-2001; 2001US-28710P.

XX (SUNN-) SUNNYBROOK & WOMEN'S COLLEGE HEALTH SCI

XX Seth A;

XX WPI; 2003 120443/11.

XX New breast cancer-associated (BCA) genes and polypeptides, useful for  
 preventing, treating, diagnosing or staging breast cancer, or other  
 BCA-related disorders, e.g. prostate cancer, sarcoma, Ewing's tumor,  
 leukemia or lymphomas

XX Claim 17; Page 146; 195pp; English.

XX The invention relates to human breast cancer associated (BCA) genes and  
 polypeptides. BCA sequences are useful for preventing or treating breast  
 cancer. Other BCA-related disorders that may be treated include allergy,  
 bone disease, eating disorder, infectious disease, ovarian cancer,  
 prostate cancer, skin cancer or brain cancer, malignant or non-malignant  
 tumours, sarcoma, Ewing's tumor, leukaemia, lymphomas, or polycythemia  
 vera. BCA sequences are also useful in forensic biology, diagnostic  
 assays, prognostic assays or pharmacogenomics or for monitoring clinical  
 trials. The invention is useful in gene therapy and as vaccines. The  
 present sequence is human BCA SR2-domain binding site.

XX Sequence 4 AA;

Query Match 56.28; Score 18; DB 24; Length 4;

Best Local Similarity 100.00; Pred. No. 9.3e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 PGT 3

DB 2 PGT 4

RESULT 11

AAV21493

XX AAV21493 standard; Protein; 5 AA

AC AAV21493;

XX 22 JUL 1999 (first entry)

XX Human neuroendocrine-specific protein NSP-A mutant treatment 43.

XX Human; beta-amyloid precursor protein; beta APL; diagnosis; cancer;  
 KW transfection mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament; neurofilament-M;  
 KW neurofilament-F; presenilin 1; presenilin 11; cellular tumor antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGB 1; NSF A;  
 KW high mobility group protein C; neuroendocrine specific protein A.

XX Synthetic.

OS Homo sapiens.

XX EF1223514 A1.

PN W09845322-A2.

XX 15-OCT-1998.

XX 02-APR 1998; 98WO-IB0705.

XX 10-APR-1997; 97US-0043163.

XX (JVCU-) RICKSUN-V UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PI Butbach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI; 1998-609901/51.

XX N-PSCB; AAX75770.

XX Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also  
 PT for treatment and prevention with specific ribozymes or wild-type  
 RNA

XX Disclosure; Figure 19; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin 1, presenilin 11, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumor antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP C) and neuroendocrine specific protein A.

XX Sequence 5 AA;

Query Match 56.28; Score 18; DB 19; Length 5;

Best Local Similarity 100.00; Pred. No. 9.3e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 PGT 3

DB 2 PGT 4

RESULT 12

ABG33533

XX ABG33533 standard; Peptide; 5 AA.

AC ABG33533;

XX 25-NOV-2002 (first entry)

XX Human P-glycoprotein tryptic peptide #53.

XX Human; P-glycoprotein; tryptic digest; proteolytic cleavage product;  
 KW diabetes; Parkinson's disease; Alzheimer's disease; malaria; cholera;  
 KW human immunodeficiency virus infection; influenza; rabies; diphtheria;  
 KW cancer; multi drug resistance; MDR.

XX Homo sapiens.

OS Homo sapiens.

XX EF1223514 A1.



XX Homo sapiens.  
 XX EP544342-A1.  
 XX C9-JUN-1993.  
 XX 06-DEC-1991; 9:EP-CL20974.  
 XX 06-DEC-1991; 9:EP-CL20974.  
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX Biernat J, Drewes G, Lichtenberg-Kraag B, Winkl-Kow EM, Steinert B;  
 XX WPT; 1993 183841/23.  
 XX Phosphorylated tau protein epitope associated with Alzheimer's  
 XX disease - is used as protein kinase inhibitor for treatment and  
 XX diagnosis  
 XX Claim 4; Page 16; 34pp; English.  
 XX The sequence is that of an epitope of tau protein which specifically  
 XX occurs in a phosphorylated state in tau protein from Alzheimer's  
 XX paired helical fragments. It may be used as part of a method for the  
 XX in vitro diagnosis and/or monitoring of Alzheimer disease. It may  
 XX also be used in an in vitro model for the study of the generation of  
 XX the Alzheimer state of proteins and the testing of substances which  
 XX prevent the conversion of normal to Alzheimer tau protein. The  
 XX epitope occurs at residues 202-205 of human tau protein.  
 XX (Updated on 25-MAR-2003 to correct PW field.)  
 XX Sequence 6 AA:  
 XX Query Match 56.2%; Score 18; DB 14; Length 6;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 PGT 3  
 XX 1 1 1  
 XX 4 PGT 6  
 XX RESULT 14  
 XX AA045755  
 XX ID AA045755 standard; peptide; 6 AA  
 XX AC AA045755;  
 XX XX 19 JUN-1998 (first entry)  
 XX DE Apoptotic protease activating factor 2 tryptic peptide #4.  
 XX XX  
 XX XX Cytochrome c tryptic peptide; Apaf-2; Hela cell S-100; apoptosis;  
 XX XX apoptotic protease activating factor 2; cytosolic antitumor  
 XX XX  
 XX Homo sapiens.  
 XX XX W09802579 A1.  
 XX XX 22-JAN-1999.  
 XX XX  
 XX XX 11 JUL-1997; 97WO-US2090.  
 XX XX 12 JUL-1996; 96US-002269.  
 XX XX (UNIV) UNIV EMORY.  
 XX XX Liu X, Wang X.  
 XX XX WPT; 1998 110623/10.  
 XX XX

PT Cell-free assay to identify compositions that regulate apoptosis  
 PT from their effect on e.g. cytosolic cytochrome c levels in cellular  
 PT extracts, particularly to identify antitumor agents  
 XX Example 8; Page 22; 42pp; English.  
 XX This sequence represents an apoptotic protease activating factor-2  
 CC (Apaf-2) tryptic peptide which corresponds to residues 40-53 of  
 CC human cytochrome c. The invention relates to an in vitro model for  
 CC studying the regulation of apoptosis. Compositions are assayed in vitro  
 CC for regulation of apoptosis by (a) preparing a 100000 g supernatant  
 CC extract (A) from cells, not committed to apoptosis, from a multicellular  
 CC eukaryote; (b) adding test composition to (A); (c) preparing control  
 CC assays comprising (A) and a known inhibitor or known inducer of  
 CC apoptosis, or a compound known to have no effect on apoptosis; (d)  
 CC assessing either (i) activation of apoptosis from an increase in  
 CC cytosolic cytochrome c; CPP32 protease activity or ability to fragment  
 CC genomic DNA, relative to system without added test compounds or (ii)  
 CC inhibition of apoptosis by a reduction in these quantities in a  
 CC mixture containing a known inducer, relative to control without test  
 CC compound. The test is performed on mammalian cells, specifically HeLa  
 CC cells. Cytochrome c is determined by immunoassay and CPP32 by adding  
 CC radiolabelled polyadenosine diphosphate-ribose (SRPP), and then detecting  
 CC fragments of these compounds by sodium dodecylsulphate-polyacrylamide gel  
 CC electrophoresis (SDS-PAGE). DNA fragmentation is determined by adding  
 CC intact mammalian cell nuclei, incubating, extracting genomic DNA and  
 CC analysing its size distribution. The extract contains enough dATP and/or  
 CC corresponding diphosphate (dNTP) to allow induction of an apoptotic  
 CC response. dATP and soluble cytochrome c are required for initiation of  
 CC apoptosis in the cell-free system. The method is especially used to  
 CC identify chemotherapeutic agents that can induce apoptosis in tumor  
 CC cells even when these express the Bcl-2 protein associated with  
 CC resistance to chemotherapy. Compounds identified this way may also (a)  
 CC improve the effect of apoptosis-inducing chemotherapeutic agents or (b)  
 CC antagonise decyadenosine triphosphate (dATP) in the cytosol of patients  
 CC with adenosine deaminase deficiency (severe combined immune  
 CC deficiency), as a potential treatment for this condition. Unlike known  
 CC methods, this process does not use cells in which the apoptotic pathway  
 CC has already been induced, i.e. it is not subject to interference from  
 CC other apoptosis-inducing factors or other conditions.  
 XX Sequence 6 AA:  
 XX Query Match 56.2%; Score 18; DB 19; Length 6;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 PGT 3  
 XX 1 1 1  
 XX 3 PGT 5  
 XX DB  
 XX Search completed: November 5, 2003, 17:47:00  
 XX Job time : 41 secs

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OX protein - protein search, using sw model  
Run on: November 5, 2003, 17:48:12 : Search time 28 Seconds  
(withour alignment)  
36,803 Million cell updates/sec

Title: US-09-914-088-6  
Perfect score: 32  
Sequence: 1 PGTINI 6  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 644079 seqs, 171749292 residues  
Total number of hits satisfying chosen parameters: 1688  
Minimum DB seq length: 0  
Maximum DB seq length: 6  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications, AA:  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by Clustal to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	32	100.0	6	12	US-10-082-014-277
2	32	100.0	6	12	US-10-372-076-131
3	19	59.4	6	12	US-09-791-524-57
4	18	56.2	4	11	US-09-812-444-12
5	18	56.2	5	10	US-09-982-172-55
6	18	56.2	6	8	US-09-891-525-4
7	18	56.2	6	12	US-10-256-126-3
8	18	56.2	5	15	US-10-198-530-4
9	16	50.0	6	15	US-10-206-699-228
10	16	50.0	6	10	US-09-817-193A-9
11	16	50.0	6	11	US-09-851-257-4
12	16	50.0	6	12	US-10-280-811-1
13	16	50.0	6	14	US-10-156-820-69
14	15	46.9	5	11	US-09-789-006-142
15	15	46.9	5	11	US-09-789-006-143

16	15	46.9	5	11	US-09-788-006-144	Sequence 144, App
17	15	46.9	5	15	US-10-006-869-451	Sequence 451, App
18	15	46.9	5	15	US-10-006-869-1031	Sequence 1031, App
19	15	46.9	5	15	US-10-206-699-182	Sequence 182, App
20	15	46.9	6	9	US-09-997-900-7	Sequence 7, Appl
21	15	46.9	6	9	US-09-484-704-10	Sequence 10, Appl
22	15	46.9	6	10	US-09-818-656A-15	Sequence 15, Appl
23	15	46.9	6	10	US-09-947-387-141	Sequence 141, App
24	15	46.9	6	11	US-09-507-362-122	Sequence 122, App
25	15	46.9	6	12	US-10-187-049-7	Sequence 7, Appl
26	15	46.9	6	12	US-10-357-467-11	Sequence 11, Appl
27	15	46.9	6	15	US-10-006-869-452	Sequence 452, App
28	15	46.9	6	15	US-10-006-869-454	Sequence 454, App
29	15	46.9	6	15	US-10-006-869-1032	Sequence 1032, App
30	15	46.9	6	15	US-10-006-869-1034	Sequence 1034, App
31	14	43.8	4	10	US-09-768-155-8	Sequence 8, Appl
32	14	43.8	5	9	US-09-817-661-33	Sequence 33, Appl
33	14	43.8	5	15	US-10-206-699-181	Sequence 181, App
34	14	43.8	6	9	US-09-741-148A-17	Sequence 17, Appl
35	14	43.8	6	10	US-09-865-018-22	Sequence 22, Appl
36	14	43.8	6	10	US-09-990-762-39	Sequence 39, Appl
37	14	43.8	6	11	US-09-974-879-421	Sequence 421, App
38	14	43.8	6	11	US-09-858-852A-39	Sequence 39, Appl
39	14	43.8	6	11	US-09-305-736-421	Sequence 421, App
40	14	43.8	6	12	US-10-262-435-10	Sequence 10, Appl
41	14	43.8	6	12	US-10-348-232-94	Sequence 94, Appl
42	14	43.8	6	12	US-10-020-354-102	Sequence 102, App
43	14	43.8	6	12	US-10-086-208-10	Sequence 10, Appl
44	14	43.8	6	14	US-10-011-436-12	Sequence 12, Appl
45	14	43.8	6	14	US-10-156-820-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1  
US-10-082-014-277  
; Sequence 277, Application US/0092014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-09-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 277  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-277

Query Match 100.0% Score 32; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 PGTINI 6  
Db 1 PGTINI 6  
  
RESULT 2  
US-10-372-076-131  
; Sequence 131, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/172,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/380,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/092,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 131  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10-372 076-131

Query Match 100.0% Score 32; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGTNI 6  
Db 1 PGTNI 6

RESULT 3  
US-09-791-524-57  
Sequence 57, Application US/09791524  
Publication No. US20030143209A1  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharmaceuticals Products Inc.  
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery of Heterologous Genes  
FILE REFERENCE: A319A  
CURRENT APPLICATION NUMBER: US/09/791,524  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/03828  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 57  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Adenovirus  
US 09-791 524-57

Query Match 59.4% Score 19; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TINI 6  
Db 3 TINI 6

RESULT 4  
US-09 932-464 12  
Sequence 12, Application US/09832464  
Publication No. US20030096953A1  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHOD FOR SCREENING ANTIMICROBIALS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 120  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/832,464  
FILING DATE: 11-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/184,826  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Cartoli, Peter G.  
REGISTRATION NUMBER: 12,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: No US20030096953A1 Relevant  
TOPOLOGY: No US20030096953A1 Relevant  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-832-464-12

Query Match 56.2% Score 18; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3  
Db 1 PGT 3

RESULT 5  
US-09-982-172-53  
Sequence 53, Application US/09982172  
Patent No. US20020137119A1  
GENERAL INFORMATION:  
APPLICANT: Emli Israel Katz  
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING SUCH PEPTIDES  
TITLE OF INVENTION: UTILIZING EACH  
FILE REFERENCE: 01/22283  
CURRENT APPLICATION NUMBER: US/09/982,172  
CURRENT FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 253  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 53  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-53

Query Match 56.2% Score 18; DB 10; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TINI 6  
Db 1 TINI 4

RESULT 6  
US-08-921 525-4  
Sequence 4, Application US/08991525  
Publication No. US20020081643A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xiaohong  
APPLICANT: Liu, Xuesong



TITLE OF INVENTION: Regulation of Apoptosis and In Vitro  
TITLE OF INVENTION: Model for Studies Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,525  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/021,248  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 45-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8090  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-891-525-4

Query Match 56.2%; Score 18; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Cy 1 PGT 3  
Db 3 PGT 5

RESULT 7  
US-10-256-326 3  
Sequence 3, Application US/10256326  
Publication No. US20030186326A1  
GENERAL INFORMATION:  
APPLICANT: PURDUE RESEARCH FOUNDATION  
TITLE OF INVENTION: MATERIALS AND METHODS FOR CONTROLLING ISOTOPE EFFECTS DURING  
TITLE OF INVENTION: FRACTIONATION OF ANALYTES  
FILE REFERENCE: 290.00230101  
CURRENT APPLICATION NUMBER: US/10/256,326  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: US 60/325,335  
PRIOR FILING DATE: 2001-09-27  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PR7  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: test peptide  
US-10-256-326-3

Query Match 56.2%; Score 18; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 1 PGT 3  
Db 3 PGT 5  
RESULT 8  
US-10-198-590-4  
Sequence 4, Application US/10198590  
Publication No. US20030032045A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xiaodong  
TITLE OF INVENTION: Regulation of Apoptosis and In Vitro  
MODEL for Studies Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/198,590  
FILING DATE: 18-JUL-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/891,525  
FILING DATE: 11-JUL-1997  
APPLICATION NUMBER: US 60/021,268  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Vogt-Warren, Heela  
REGISTRATION NUMBER: 45,495  
REFERENCE/DOCKET NUMBER: 45-96A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-198-590-4

Query Match 56.2%; Score 18; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 PGT 3  
Db 3 PGT 5

RESULT 9  
US-10-256-699-228  
Sequence 228, Application US/10206699  
Publication No. US20030102510A1  
GENERAL INFORMATION:  
APPLICANT: Sundata-Oorthy, N.

```
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: YHRH 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/352,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 65/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,954
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 228
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-228

Query Match
Best Local Similarity 50.0%; Score 16; DB 15; Length 5;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTIN 5
Db 2 GTIN 5

RESULT 10
US-09-917-199A.9
; Sequence 9, Application US/69817199A
; Patent No. US2002042390A1
; GENERAL INFORMATION:
; APPLICANT: SHAG, Wei, et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLOC1187
; CURRENT APPLICATION NUMBER: US/09/817,199A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-199A.9

Query Match
Best Local Similarity 50.0%; Score 16; DB 15; Length 6;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 3 PGAV 6

RESULT 11
US-09-853-257-4
; Sequence 4, Application US/09853257
; Publication No. US20030021032A1
; GENERAL INFORMATION:
; APPLICANT: Bonnie L. Bassler
; APPLICANT: Brendan N. Lilley
; TITLE OF INVENTION: LUXO-SIGMAS4 INTERACTIONS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: PCT/US02A
; CURRENT APPLICATION NUMBER: US/09/853,257
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/202,999
; PRIOR FILING DATE: 2000-05-10
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
; NAME/KEY: VARIANT
; LOCATION: 11.....16;
; OTHER INFORMATION: Aaa = Tip of Phe
US-09-853-257-4

Query Match
Best Local Similarity 50.0%; Score 16; DB 11; Length 6;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 3 PGNV 6

RESULT 12
US-10-280-833-1
; Sequence 1, Application US/10280833
; Publication No. US2003019515CA1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Charles Eric
; APPLICANT: Dashper, Stuart Geoffrey
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Talbot, Gert Hoy
; APPLICANT: Malkoski, Marina
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: BOMP-CC1CON
; CURRENT APPLICATION NUMBER: US/10/280,833
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/554,997
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PP 0514
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: bovine
US-10-280-833-1

Query Match
Best Local Similarity 50.0%; Score 16; DB 12; Length 6;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 1 PGP: 4

RESULT 13
US-10-156-820-69
; Sequence 69, Application US/10156820
; Publication No. US2002015058A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/C-005
; PRIOR FILING DATE: 1997-01-30
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; PRIOR APPLICATION NUMBER: FR 97/11166  
 ; PRIOR FILING DATE: 1997-09-09  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 69  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Phagotope  
 US-10-156-820-69

Query Match 50.0%; Score 16; DB 14; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTI 4  
 DB 3 PNTI 6

## RESULT 14

US-09-788-006-142  
 ; Sequence 142, Application US/09788006  
 ; Publication No. US2003003603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; TITLE OF INVENTION: Polypeptide Tertiary Structures  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 142  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-142

Query Match 46.9%; Score 15; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4  
 DB 3 GTI 5

## RESULT 15

US-09-788-006-143  
 ; Sequence 143, Application US/09788006  
 ; Publication No. US2003003603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; TITLE OF INVENTION: Polypeptide Tertiary Structures  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 143  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-143

Query Match 46.9%; Score 15; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4  
 DB 2 GTI 4

Search completed: November 5, 2003, 17:53:22  
 Job time : 29 secs

GenCore version 5.1.6  
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OX protein - protein search, using sw model

Run on: November 5, 2003, 17:46:11 ; Search time 22 Seconds  
(without alignments)  
11,539 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32

Sequence: 1 PGTNI 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 37639

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep\*  
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5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	62.5	6	1	US-07-947-035-10
2	20	62.5	6	1	US-08-321-585A-9
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4	18	56.2	4	3	US-09-184-826-12
5	18	56.2	5	1	US-07-989-962-1
6	19	56.2	5	1	US-07-989-962-4
7	18	56.2	5	1	US-08-213-422-3
8	18	56.2	5	1	US-08-213-422-4
9	18	56.2	5	1	US-08-459-888-4
10	18	56.2	5	1	US-08-459-888-4
11	19	56.2	5	2	US-08-460-452-3
12	18	56.2	5	2	US-08-460-452-4
13	18	56.2	5	2	US-08-459-557-3
14	18	56.2	5	2	US-08-459-557-4
15	18	56.2	5	2	US-08-459-209-3
16	18	56.2	5	2	US-08-459-209-4
17	18	56.2	5	3	US-09-174-642-21
18	18	56.2	5	4	US-09-292-089-3
19	19	56.2	5	4	US-09-282-089-4
20	18	56.2	6	1	US-07-989-962-1
21	18	56.2	6	1	US-07-989-962-13
22	18	56.2	6	1	US-07-989-962-19
23	18	56.2	6	1	US-08-213-422-3
24	18	56.2	6	1	US-08-213-422-12
25	18	56.2	6	1	US-08-213-422-19
26	18	56.2	6	1	US-08-459-888-4
27	18	56.2	6	1	US-08-459-888-18

28	18	56.2	6	1	US-08-459-888-19
29	18	56.2	6	2	US-08-460-452-5
30	18	56.2	6	2	US-08-460-452-18
31	18	56.2	6	2	US-08-460-452-19
32	18	56.2	6	2	US-08-459-557-5
33	18	56.2	6	2	US-08-459-557-18
34	18	56.2	6	2	US-08-459-557-19
35	18	56.2	6	2	US-08-637-759B-476
36	18	56.2	6	2	US-08-459-209-5
37	18	56.2	6	2	US-08-459-209-18
38	18	56.2	6	2	US-08-459-209-19
39	18	56.2	6	2	US-08-724-354D-23
40	18	56.2	6	3	US-08-871-355A-476
41	18	56.2	6	3	US-09-270-984A-23
42	18	56.2	6	3	US-09-274-642-22
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ALIGNMENTS

RESULT 1  
US-07-947-035-10  
; Sequence 10, Application US/07947035  
; Patent No. 5444045  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Geoffrey L.  
; APPLICANT: Walton, Paul E.  
; APPLICANT: Ballard, Francis J.  
; APPLICANT: McMurty, John P.  
; APPLICANT: Phelps, Patricia V.  
; TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,  
; TITLE OF INVENTION: and Analogs Thereof to Birds  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5444045th Carolina  
; COUNTRY: US  
; ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/947,035  
FILING DATE: 17-SEP-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5175-59  
TELEPHONE: (919) 881-3140  
TELEFAX: (919) 881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL: NO  
US 07-947-035-10

Query Match 62.5% Score 20; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 4  
Db 2 PGT 5

RESULT 2  
US-08-321-585A-8  
Sequence 9, Application US/08321585A  
Patent No. 5679731  
GENERAL INFORMATION:  
APPLICANT: Ballard, Francis  
APPLICANT: Read, Leanna  
TITLE OF INVENTION: METHOD FOR TREATING INTESTINAL DISEASES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchants, Gould, Smith, Edell, Weller & Schmidt  
STREET: 3100 No. 5679771 West Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,585A  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/854,983  
FILING DATE: 28-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 6159-245USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-321-585A-8

Query Match 62.5%; Score 20; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 0;

Qy 1 PGT: 4  
Db 2 PGT 5

RESULT 3  
US-08-651-818A-12  
Sequence 12, Application US/08651818A  
Patent No. 5948889  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
APPLICANT: Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING  
TELECOMMUNICATION INFORMATION:

NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,818A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-651-818A-12

Query Match 56.2%; Score 18; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 1 PGT 3  
Db 1 PGT 3

RESULT 4  
US-09-184-826-12  
Sequence 12, Application US/99184826  
Patent No. 6248543  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
APPLICANT: Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING  
TELECOMMUNICATION INFORMATION:  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/184,826  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-09 184-826-12

Query Match 56.2%; Score 18; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3  
DB 1 PGT 3

RESULT 5  
US-07-989-962-3  
Sequence 3, Application US/07989962  
Patent No. 5324820  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert  
TITLE OF INVENTION: ACID-LABILE SUBUNIT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,962  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/646,779  
FILING DATE:  
APPLICATION NUMBER: PCT/AU89/60299  
NAME: 14-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P03350/89  
NAME: 23-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P19314/88  
NAME: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 521p1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-07 989-962-3

Query Match 56.2%; Score 18; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PGT 3  
DB 3 PGT 5

RESULT 6  
US-07-989-962-4  
Sequence 4, Application US/07989962  
Patent No. 5324820  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert  
TITLE OF INVENTION: ACID-LABILE SUBUNIT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,962  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/646,779  
FILING DATE:  
APPLICATION NUMBER: PCT/AU89/60299  
NAME: 14-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P03350/89  
NAME: 23-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P19314/88  
NAME: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 521p1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-07-989-962-4

Query Match 56.2%; Score 18; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3  
DB 3 PGT 5

RESULT 7  
US-08-213-402-3  
Sequence 3, Application US/08213402  
Patent No. 5561046  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert



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; APPLICATION NUMBER: 08/213422
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PIC1D3
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-459-888-3

Query Match 56.2%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3
Db 3 PGT 5

RESULT 1:
US-08-460-452-3
; Sequence 3, Application US/08460452
; Patent No. 5849687
; GENERAL INFORMATION:
; APPLICANT: Baxter, Robert
; TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF INSULIN-LIKE-GROWTH FACTOR (IGF)
; TITLE OF INVENTION: BINDING PROTEIN COMPLEX
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,452
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213402
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PIC1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-452-3

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3
Db 3 PGT 5

US-09-914-088-4
; Sequence 4, Application US/08459888
; Patent No. 573651;
; GENERAL INFORMATION:
; APPLICANT: Baxter, Robert
; TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
; TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,888
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213402
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PIC1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-914-088-6

Query Match 56.2%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3
Db 3 PGT 5
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RESULT 12
US-08-460-452-4
: Sequence 4, Application US/08460452
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF INSULIN-LIKE-GROWTH FACTOR (IGF)
: TITLE OF INVENTION: BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460-452
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989962
: FILING DATE: 11-DEC-1992
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-460-452-4

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3
Db 3 PGT 5

RESULT 13
US-08-459-557-3
: Sequence 3, Application US/08459557
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
: TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459-557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989962
: FILING DATE: 11-DEC-1992
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-460-452-4

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3
Db 3 PGT 5

RESULT 14
US-08-459-557-4
: Sequence 4, Application US/08459557
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
: TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459-557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
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: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459-557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989962
: FILING DATE: 11-DEC-1992
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-459-557-3

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3
Db 3 PGT 5

RESULT 14
US-08-459-557-4
: Sequence 4, Application US/08459557
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
: TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459-557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/989962
? FILING DATE: 11-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/646779
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 521P1C1D3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-459-557-4

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3
Db 3 PGT 5

Search completed: November 5, 2003, 17:49:17
Job time : 23 secs

? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-459-209-3

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3
Db 3 PGT 5

Search completed: November 5, 2003, 17:49:17
Job time : 23 secs

RESULT 15
US 08-459-209-3
? Sequence 3, Application US/084592C3
? Patent No. 5936064
? GENERAL INFORMATION:
? APPLICANT: Baxter, Robert
? TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
? TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
? NUMBER OF SEQUENCES: 28
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.50 inch, 1 mb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS DOS
? SOFTWARE: FatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,209
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/213402
? FILING DATE: 14-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/989962
? FILING DATE: 11-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/646779
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 521P1C1D3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 3:
```

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:52:48 ; Search time 21 Seconds  
(without alignments)  
22.897 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FTPT 5

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283309 seqs, 96168602 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: PIR.76:\*
- 2: PIR1:\*
- 3: PIR3:\*
- 4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	53.3	5	2	ribulose-bisphosph
2	14	46.7	5	2	acid proteinase li
3	12	40.0	3	3	tyrosine protein k
4	12	40.0	4	2	stativ: sh-induced
5	12	40.0	4	2	ribosomal protein
6	12	40.0	5	1	musclelin - Americ
7	12	40.0	5	2	proctolin - Atlant
8	11	36.7	4	2	phagocytosis-stimu
9	11	36.7	5	2	T-cell receptor be
10	9	30.0	5	2	flagellar protein
11	9	30.0	5	2	major protein anti
12	8	26.7	5	2	copper resistance
13	8	26.7	5	2	ribosomal protein
14	8	26.7	5	2	ribosomal protein
15	8	26.7	5	2	bradykinin-potenti
16	8	26.7	5	2	T-cell receptor be
17	8	26.7	5	2	phospholipase A2
18	8	26.7	5	3	thyrotropin-releas
19	7	23.3	3	3	thyrotropin-releas
20	7	23.3	3	3	TRH-like tripeptid
21	7	23.3	3	3	tyrosine-melanocyt
22	7	23.3	3	3	carbon monoxide de
23	7	23.3	3	3	RPCV-related neuro
24	7	23.3	4	2	metallothionein-A
25	7	23.3	4	2	ig heavy chain CRD
26	7	23.3	4	2	
27	7	23.3	4	2	
28	7	23.3	4	2	
29	7	23.3	4	2	

30	7	23.3	4	2	IS4357
31	7	23.3	4	2	PT0675
32	7	23.3	4	2	A60521
33	7	23.3	5	2	JN0862
34	7	23.3	5	2	JN0860
35	7	23.3	5	2	C41225
36	7	23.3	5	2	B60274
37	7	23.3	5	2	B22565
38	7	23.3	5	2	PQ0009
39	7	23.3	5	2	JS0119
40	7	23.3	5	2	S53595
41	7	23.3	5	2	S11127
42	7	23.3	5	2	PT0267
43	7	23.3	5	2	JT0520
44	7	23.3	5	2	PT0669
45	6	20.0	3	3	S68328

## ALIGNMENTS

### RESULT 1

PS0324  
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998  
C:Accession: PS0324  
R:Tsugita, A.  
submitted to JIPID, April 1993  
A:Reference number: PS0206  
A:Accession: PS0324  
A:Molecule type: protein  
A:Residues: 1-5 <TSU>  
A:Experimental source: leaf, chlorophyll

Query Match: 53.3% Score 16; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTPT 5  
| | |  
Db 1 FQAPT 5

### RESULT 2

B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C:Accession: B37988  
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase f  
A:Reference number: A37988; MUID:9106C608; PMID:2246266  
A:Accession: B37988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MUR>

Query Match: 46.7% Score 14; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4  
| | |  
Db 3 PP 4

### RESULT 3

I78890  
tyrosine protein kinase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: 176890  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 01-Aug-1994 #sequence\_revision 01-Sep-1995 #text\_change 07 May 1999  
 C:Accession: S83508  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <RES>  
 A:Cross-references: GB:L33339; NID:9659536; PID:AA64432.1; PID:9509539  
 C:Genetics:  
 A:Gene: p52ntk

Query Match 40.0%; Score 12; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 2 PT 3

RESULT 4  
 S83508  
 starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 01-Aug-1994 #sequence\_revision 01-Sep-1995 #text\_change 07 May 1999  
 C:Accession: S83508  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <RES>

Query Match 40.0%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 2 PT 3

RESULT 5  
 S7255  
 ribosomal protein, Y11, mitochondrial, protein and 19S ribosomal subunit  
 C:Species: Saccharomyces cerevisiae  
 A:Variety: strain 0173  
 C:Date: 21-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 07 May 1997  
 C:Accession: S7255  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: Protein  
 A:Residues: 1-4 <XOE>

Query Match 40.0%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 2 PT 3

RESULT 6  
 HOROA  
 proctolin - American cockroach  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
 C:Accession: A01644  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: Protein  
 A:Residues: 1-5 <SRA>  
 A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and phar

Query Match 40.0%; Score 12; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 4 PT 5

RESULT 7  
 A60411  
 proctolin - Atlantic horseshoe crab  
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
 C:Accession: A60411  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: Protein  
 A:Residues: 1-5 <GRO>  
 A:Note: This neuropeptide stimulates cardiac output and hindgut motility in the ho

Query Match 40.0%; Score 12; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 4 PT 5

RESULT 8  
 A02147  
 phagocytosis-stimulating peptide (tuftsin) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 03-Feb-1994  
 C:Accession: A02147  
 C:Reference number: 158407; MUID:9506060; PMID:7970753  
 C:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: Protein  
 A:Residues: 1-4 <NIS>  
 A:Note: a peptide having the same structure, physical properties, and biological acti

R;Fidalgo, B.V.; Najjar, V.A.  
 Biochemistry 6, 3386-3392, 1967  
 A:Reference number: A37502; MUID:68091045; PMID:4163272  
 A:Contents: annotation: immunoglobulin class  
 C:Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils.  
 n is essential for maximum stimulation of the phagocytic activity of neutrophils.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 36.7%; Score 11; DB 2; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTP 4  
 |  
 |  
 Db 1 TTP 3

RESULT 9  
 PT0644  
 T-cell receptor beta chain V-D-J region (111-10) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0644  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711559  
 A:Accession: PT0644  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 36.7%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FT 2  
 |  
 |  
 Db 4 FT 5

RESULT 10  
 E42364  
 flagellar protein fliC - Salmonella typhimurium (fragment)  
 C:Species: Salmonella typhimurium  
 C:Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 12-Sep-1993  
 C:Accession: E42364  
 R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macrabb, R.M.  
 J. Bacteriol. 173, 3564-3572, 1991  
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
 A:Reference number: A42364; MUID:91258342; PMID:1646201  
 A:Accession: E42364  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <VOG>  
 A:Cross-references: GB:M62408

Query Match 30.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTP 4  
 |  
 |  
 Db 3 TLP 5

RESULT 11  
 E60274  
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 1; Dec-1992 #sequence\_revision 1; Dec-1992 #text\_change 30-Sep-1993

C:Accession: E60274  
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A:Title: Isolation and partial characterization of major protein antigens in the cult  
 A:Reference number: A60274; MUID:91099989; PMID:1898899  
 A:Accession: E60274  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <NAG>

Query Match 30.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPT 5  
 |  
 |  
 Db 3 PIT 5

RESULT 12  
 A41225  
 copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)  
 C:Species: Pseudomonas syringae pv. tomato  
 C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
 C:Accession: A41225  
 R;Cha, J.S.; Cooksey, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
 A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer  
 A:Reference number: A41225; MUID:92020961; PMID:1924351  
 A:Accession: A41225  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <CHA>

Query Match 26.7%; Score 8; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TP 3  
 |  
 |  
 Db 4 SP 5

RESULT 13  
 I39964  
 ribosomal protein S4 - Bacillus circulans (fragment)  
 C:Species: Bacillus circulans  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996  
 C:Accession: I39964  
 R;Grundy, F.J.; Henkin, T.M.  
 J. Bacteriol. 174, 6763-6770, 1992  
 A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.  
 A:Reference number: I39963; MUID:93015735; PMID:1400226  
 A:Accession: I39964  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5 <RES>  
 A:Cross-references: GB:M99041; NID:G143471  
 C:Genetics:  
 A:Gene: rpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FT 2  
 |  
 |  
 Db 4 YT 5

RESULT 14  
 I39966  
 ribosomal protein S4 - Bacillus licheniformis (fragment)

C:Species: Bacillus licheniformis  
C:Date: 19-Jul-1996 #sequence\_revision: 19-Jul-1996 #text\_change: 19-Jul-1996  
C:Accession: I39966  
R:Grundy, P.J.; Henkin, T.M.  
J. Bacteriol. 174, 6763-6770, 1992  
A:Title: Characterization of the Bacillus subtilis tpsD regulatory target site.  
A:Reference number: I39963; MUID:93015735; PMID:1400226  
A:Accession: I39966  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross references: GB:M99043; NID:g143473  
C:Genetics:  
A:Gene: tpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2; He+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FT 2  
|  
Db 4 YT 5

RESULT 14  
I39965  
ribosomal protein S4 - Bacillus megaterium (fragment)  
C:Species: Bacillus megaterium  
C:Date: 19-Jul-1996 #sequence\_revision: 19-Jul-1996 #text\_change: 19-Jul-1996  
C:Accession: I39965  
R:Grundy, P.J.; Henkin, T.M.  
J. Bacteriol. 174, 6763-6770, 1992  
A:Title: Characterization of the Bacillus subtilis tpsD regulatory target site.  
A:Reference number: I39963; MUID:93015735; PMID:1400226  
A:Accession: I39965  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross references: GB:M99042; NID:g143473  
C:Genetics:  
A:Gene: tpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2; He+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FT 2  
|  
Db 4 YT 5

Search completed: November 5, 2003, 17:55:16  
Job time: 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:43:22 ; Search time 10 seconds  
(without alignments:  
23,513 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FTPPT 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.4

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	40.0	4	1	RM01 YEAST
2	12	40.0	5	1	PRCT PERAM
3	11	36.7	4	1	TUFT HUMAN
4	11	36.7	5	1	E103 LITRU
5	11	36.7	5	1	PAP2 FARMA
6	11	36.7	5	1	RE31 LITRU
7	11	36.7	5	1	RE32 LITRU
8	8	26.7	5	1	BPP7 ECOLI
9	8	26.7	5	1	PSK DAFIA
10	7	23.3	3	1	THPL PLC
11	7	23.3	4	1	DCXL USETH
12	7	23.3	5	1	SUGA ACHFU
13	6	20.0	4	1	ACH1 ACHFU
14	6	20.0	4	1	FAR3 HERME
15	6	20.0	4	1	FAR4 HERME
16	6	20.0	4	1	FFKA ANTEL
17	6	20.0	4	1	FLRF HERME
18	6	20.0	4	1	FLRN ANTEL
19	6	20.0	4	1	FMRF MACNI
20	6	20.0	4	1	FYRI ANTEL
21	6	20.0	4	1	OCPI OCTMI
22	6	20.0	5	1	AL14 CARMA
23	6	20.0	5	1	E104 LITRU
24	6	20.0	5	1	FARP ASTIR
25	6	20.0	5	1	RE11 LITRU
26	6	20.0	5	1	RE21 LITRU
27	6	20.0	5	1	TPIS CANFA
28	6	20.0	5	1	UC22 MAIZE
29	5	16.7	5	1	BIOM CITR
30	1	3.3	4	1	EC01 HUMAN
31	1	3.3	4	1	OCP3 OCTMI
32	1	3.3	5	1	BI03 CITR
33	1	3.3	5	1	UF01 MOUSE

34 1 3.3 5 1 UXAA CHLTR P38005 chlamydia t  
35 0 0.0 3 1 GRWY HUMAN P01157 homo sapien  
36 0 0.0 3 1 LUXE VIBFI P24272 vibrio fise  
37 0 0.0 4 1 DCMS PSECH P19918 pseudomonas  
38 0 0.0 5 1 TRM3 ECOLI P13973 escherichia

#### ALIGNMENTS

##### RESULT 1

RM01 YEAST STANDARD; PRT; 4 AA.  
AC P36515;1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, last sequence update)  
DT 01-JUN-1994 (Rel. 29, last annotation update)  
DE Mitochondrial 60S ribosomal protein L1 (YmlL) (Fragment).  
GN MRPL1.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91285106; PubMed=2060626;  
RA Grohmann L.; Graack H.-R.; Kruff V.; Choll T.; Goldschmidt-Reisin S.;  
RA Kitakawa M.;  
RT "Extended N-terminal sequencing of proteins of the large ribosomal  
subunit from yeast mitochondria.";  
RL FEBS Lett. 284:51-56(1991).  
DR PIR: S17255; S17255.  
DR SGI: L0002681; XRPUL.  
KW Ribosomal protein; Mitochondrion.  
FT NON TER 4 4  
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0C00000 CRC64;

Query Match 40.0%; Score 12; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TP 3  
DB 3 TP 4

##### RESULT 2

PRCT PERAM STANDARD; PRT; 5 AA.  
AC P01373;1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Proctolin.  
OS Pezoplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Starratt A.N.; Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
in insects.";  
RL Life Sci. 17:263-1256(1975).  
RN [2]  
RP BIOLOGICAL SOURCE.  
RC SPECIES=P.americana;  
RX MEDLINE=91225865; PubMed=6113690;

RA C'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron."  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=C. polyphemus;  
 RX MEDLINE=90287803; PubMed=2356151;  
 RA Groome J.R., Tillinghast E.K., Towmey M.A., Vetrovs A.,  
 RA Watson W.H., III, Hunt E.F., Griffin P.R., Alexander C.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus."  
 RC Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=C. maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangler J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 RT pericardial organs of the shore crab, Carcinus maenas."  
 RL Peptides 7:67-72(1986).  
 RC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINGING MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
 CC 1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC THE CRAB PERICARDIAL ORGANS.  
 DR PIR: A01644; HORCHA.  
 DR PIR: A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B767B54460C380 CRC64.

Query Match 40.0%; Score 12; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 DB 4 PT 5

RESULT 4  
 TUFT HUMAN  
 ID TUFT HUMAN STANDARD; PRT; 4 AA.  
 AC P1859;  
 DT 21 JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phagocytosis-stimulating peptide (Tuftsin).  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartida; Hominidae; Homo  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=72187087; PubMed=4112769;  
 RA Nishizuka K., Constantopoulos A., Sarch P.B., Nappier V.A.;  
 RT "The characteristics, isolation and synthesis of the phagocytosis  
 RT stimulating peptide tuftsin."  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1973).  
 RN [2]  
 RP FUNCTION: BLOOD CLASS.  
 RX MEDLINE=68091045; PubMed=4169272;  
 RA Fida'go B.V., Najjar V.A.;  
 RT "The physiological role of the lymphoid system VII: the stimulatory  
 RT effect of leucophilic gamma globulin (leuckin) on the phagocytic  
 RT activity of human polymorphonuclear leukocyte."  
 RL Biochemistry 6:3396-3392(1967).  
 CC 1- MISCELLANEOUS: AN IGG (CALLED LEUCKIN) BINDS REVERSELY TO THE  
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. DEGRADATION ON THE  
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.  
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC  
 CC ACTIVITY OF NEUTROPHILS.  
 DR PIR: A02147; A02147.  
 DR MIM: 191150; 11

DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006909; P:phagocytosis; NAS.  
 SQ SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTP 4  
 DB 1 TKP 3

RESULT 4  
 E703 LITRU  
 ID E703 LITRU STANDARD; PRT; 5 AA.  
 AC P82059;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 CX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5  
 FT SEQUENCE 5 AA; 633 MW; 66876:F2C9A00000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTTP 4  
 DB 1 FWTP 4

RESULT 5  
 PAP2 PARMA  
 ID PAP2 PARMA STANDARD; PRT; 5 AA.  
 AC P61364;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pardaxin II (PXII) (Fragment).  
 OS Pardachirus marmoratus (Red sea moles sole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Sciaenidae; Pardachirus.  
 OX NCBI\_TaxID=31587;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=87057369; PubMed=3782138;  
 RA Lazarovici P., Primor N., Loew L.M.;  
 RT "Purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the red sea moles sole (Pardachirus  
 RT marmoratus)."  
 RL J. Biol. Chem. 261:16704-16713(1986).  
 CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant



CC properties. Forms voltage-dependent, ion-permeable channels  
 CC in membranes. At high concentration causes cell membrane lysis.  
 CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PARAXIN FAMILY.  
 KW Toxin.  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTP 3  
 Db 3 FFP 5

RESULT 6  
 RE31\_LITRU  
 ID RE31\_LITRU STANDARD; PRT; 5 AA.  
 AC P82072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 3.1.  
 CS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae.  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-Skin secretion;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=MS.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5 5  
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10000000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 Db 4 FT 5

RESULT 7  
 RE32\_LITRU  
 ID RE32\_LITRU STANDARD; PRT; 5 AA.  
 AC P82073;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 3.2.  
 CS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 Db 4 FT 5

RESULT 8  
 BPP7\_BOTIN  
 ID BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 CC Viperidae; Crotalinae; Bothrops.  
 CC NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA MEDLINE=9031557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR: G37196; G37195  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 5;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTP 3  
 Db 3 WAP 5

RESULT 9  
 PSK\_DAUCA  
 ID PSK\_DAUCA STANDARD; PRT; 5 AA.  
 AC P58261;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK  
 DE beta)].  
 OS Daucus carota (Carrot).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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CC Speimaphyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; Campanulids; Apiales; Apiaceae; Daucus.
CX NCBI TaxID:4639;
RN [1]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale M.,
RA Guillemain R.;
RT "Characterization of ovine hypothalamic hypocretinergic
RT TSH-releasing factor."
RL Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES=B.orientalis; Tissue=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin."
RL Chem. Pharm. Bull. 23:330-333(1975).
RN [16]
RP SEQUENCE.
RC SPECIES=N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by new (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor."
RL J. Neurochem. 23:471-478(1974).
CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
DR PIR; A90919; RHTCTO.
DR PIR; A92971; A92971.
DR PIR; A93750; RHSH.
KW Amidation; Pyroglutamate carboxylic acid.
FT MCD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MCD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6C000000000 CRC64;
Query Match 23.3%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 3 P 3
DB 3 P 3
RESULT 11
DCML_PSECH
ID DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTH.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.

```

DR PIR: 250140; PL0140.  
 KW Oxidoreductase; Molybdenum.  
 FT NOK TER 4 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0003000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3  
 |  
 Db 4 P 4

## RESULT 12

SUGA ACHDC STANDARD; PRT; 5 AA.  
 AC P19991; 1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Suboesophageal ganglion; pentapeptide.  
 OS Acheta domestica (House cricket).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 OC Acheta.

CX NCBI TaxID=6997;

RN [1]

RP SEQUENCE.

RA Wicker C., Wicker C.;  
 RT "Isolation and structure of a peptide isolated from the  
 RT suboesophageal ganglion of Acheta domestica (Orthoptera).";

RL Comp. Biochem. Physiol. 88C:185-187(1987).

CC -1 SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL

CC GANGLIA.

DR PIR: JS0319; JS0319.

SQ SEQUENCE 5 AA; 476 MW; 69D76D5DDB0C000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3  
 |  
 Db 4 P 4

## RESULT 13

ACHI ACHFU STANDARD; PRT; 4 AA  
 AC P35904; 1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Achatin-I.

OS Achatina fulica (Giant African snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Stgmurethra; Achatinoidea; Achatinidae; Achatina.

CX NCBI TaxID=6530;

RN [1]

RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.

RA STRAIN=Perussac; TISSUE=Ganglion;

RX MEDLINE=8927355; PubMed=2597281;

RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,

RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Rib E.,

RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.

RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina

RT fulica Perussac containing a D-amino acid residue";

RL Biochem. Biophys. Res. Commun. 160:1015-1020(1999)

RN [2]

RP CHARACTERIZATION.

RC STRAIN=Perussac; TISSUE=Heart atrium;

RX MEDLINE=91264856; PubMed=1675568;

RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Mureoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function.";  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).

RN [3]

RP X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=93014529; PubMed=1399265;

RA Iwashita T., In Y., Doi M., Yasuda-Kamatani Y., Minakata H.,

RA Iwashita T., Nomoto K.;

RT "Crystal structure and molecular conformation of achatin-I

RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a

RL D-amino acid residue.";

RL Int. J. Pept. Protein Res. 39:258-264(1992).

CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY

CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY

CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE

CC HEART BEAT HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.

DR PIR: A32480; A32480.

KW Hormone; D-amino acid.

FT MOD RES 2 2

SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 P 1

|

Db 2 P 2

## RESULT 14

FAR3 HIRME STANDARD; PRT; 4 AA.

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE FMRFamide-like neuropeptide YLRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

CX NCBI TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans S.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 4 4

SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 P 1

|

Db 4 P 4

## RESULT 15

FAR4 HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE FMRFamide-like neuropeptide YMRP-amide.

CS Hirudo medicinalis (Medicinal leech;  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudiniida; Hirudinea;  
 OC Atychtedellida; Hirudiniiformes; Hirudiniidae; Hirudo.  
 OX NCBI\_TaxID:6421;  
 RR [1]  
 RF SEQUENCE  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Colaneri R.L.  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -! SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE)  
 CC FAMILY:  
 KW Neuropeptide; Amidation.  
 FT MCD RES 4 4 AMINATION.  
 SQ SEQUENCE 4 AA; 616 YK; 69CA568B3C000000 CRC64;  
 Query Match 25.0%; Score 67; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1; Seqs 5;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 Qy 1 F 1  
 Db 4 F 4

Search Completed: November 5, 2003, 17:54:37  
 Job time: 10 secs

GenCore version 5.1.6

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OM protein - protein search, using sw mode:

Run on: November 5, 2003, 17:52:17 : Search time 33 seconds  
 (without alignment):  
 39,099 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FRPT 5

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 5

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
 1: sp\_archaea.\*  
 2: sp\_bacteria.\*  
 3: sp\_fungi.\*  
 4: sp\_human.\*  
 5: sp\_invertebrate.\*  
 6: sp\_mammal.\*  
 7: sp\_mhc.\*  
 8: sp\_organelle.\*  
 9: sp\_phase.\*  
 10: sp\_plant.\*  
 11: sp\_rodent.\*  
 12: sp\_virus.\*  
 13: sp\_vertebrate.\*  
 14: sp\_unclassified.\*  
 15: sp\_rvirus.\*  
 16: sp\_bacteriap.\*  
 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	23.1	5	P83308	P83308 Gallus gall
2	5	16.7	5	P83073	P83073 Bacillus ce
3	0	0.0	4	Q08433	Q08433 Rattus sp.
4	0	0.0	5	Q99207	Q99207 hordeum vul

## ALIGNMENTS

RESULT 1  
 P83308 PRELIMINARY; PRT; 5 AA.  
 AC P83308  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

DE FMRFamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA PubMed=6137771;  
 RA Dockray G.J.; Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRFamide";  
 RL Nature 305:329-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 23.3%; Score 7; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3  
 Db 2 P 2

## RESULT 2

P83073 PRELIMINARY; PRT; 5 AA.  
 AC P83073;  
 DT 01-OCT-2001 (TEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TEMBLrel. 18, Last annotation update)  
 DE 88 kDa protein (Fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RN SEQUENCE.  
 RC STRAIN=NCIMB 11796;  
 RA Browne N., Dowds B.C.A.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 FT MCM TER 5  
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 16.7%; Score 5; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2  
 Db 4 T 4

## RESULT 3

Q08433 PRELIMINARY; PRT; 4 AA.  
 ID Q08433  
 AC Q08433;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Gunn.  
 RX MEDLINE=91282755; PubMed=1840486;

RA Sato H., Aono S., Kashiwazata S., Koiwai O.,  
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 RL hyperbilirubinemic Gunn rat.",  
 RL Biochem Biophys Res Commun. 177:1161-1164 (1991).  
 DR EMBL: S18636; AAH19259.1; ..  
 KW Transferase.  
 FT NON TER  
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 8.3e+05;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 T 2

DB 1 N 1

## RESULT 4

Q99607 PRELIMINARY: PRT; 5 AA.  
 AC Q99607;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Alpha amylase (Fragment).  
 GN AMY1 GENE.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID:4511;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91329704; PubMed=1831055;  
 RA Jacobsen J.V., Close T.J.;  
 RT "Control of transient expression of chimaeric genes by gibberellic  
 RT acid and abscisic acid in protoplasts prepared from mature barley  
 RT aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721 (1991).  
 DR EMBL: X54643; CAA38455.1; ..  
 FT NON TER  
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F0C000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 8.3e+05;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 F 1

DB 1 N 1

Search completed: November 5, 2003, 17:05:13  
 Job time : 33 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:48:47 ; Search time 40 Seconds  
(without alignments)  
19,841 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FPPPT 5

Scoring Table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 24275

Minimum DB seq length: 0

Maximum DB seq length: 5

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_19Jun03:

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18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	21	IGF C-epsilon-2 do
2	30	100.0	5	22	peptide P7 derived
3	30	100.0	5	23	Human IGE immunog
4	24	80.0	4	19	NMDA receptor bind
5	24	80.0	4	23	Neuroactive peptid
6	24	80.0	4	23	Neuroactive peptid
7	24	80.0	5	20	Portion of the cor
8	19	63.3	3	19	NMDA receptor bind
9	19	63.3	3	19	NMDA receptor bind

10	19	63.3	3	23	Contiguous hydroxy
11	19	63.3	4	15	Prolyl endopeptida
12	19	63.3	4	23	N. meningitidis LC
13	19	63.3	4	23	Gum arabic glycopr
14	19	63.3	4	23	Contiguous hydroxy
15	19	63.3	5	11	Polypeptide accomp
16	19	63.3	5	15	SV40 T antigen cdc
17	19	63.3	5	15	PHF-tau epitope.
18	19	63.3	5	16	PHF-tau epitope.
19	19	63.3	5	16	AAAR76938
20	19	63.3	5	17	AAW06981
21	19	63.3	5	18	N-acetylglucosam
22	19	63.3	5	19	Peptide determined
23	19	63.3	5	19	Human thrombopoiet
24	19	63.3	5	19	EVH1 ligand motif.
25	19	63.3	5	20	Portion of the cor
26	19	63.3	5	22	Amino acid sequenc
27	19	63.3	5	22	Ena/VASP homology
28	19	63.3	5	22	"L domain" amino a
29	19	63.3	5	22	Colostrinin derive
30	19	63.3	5	22	Colostrinin peptid
31	19	63.3	5	22	Colostrinin peptid
32	19	63.3	5	22	Ewe colostrinin pe
33	19	63.3	5	23	Zyxine VASP bindin
34	19	63.3	5	23	Peptide sequence e
35	19	63.3	5	23	Colostrinin consti
36	19	63.3	5	23	Colostrinin consti
37	19	63.3	5	23	Neural cell regula
38	19	63.3	5	23	Peptide amirio acid
39	19	63.3	5	23	Peptide CycE-5mer
40	19	63.3	5	24	Triketone-inhibito
41	18	60.0	5	19	PPGF retropeptide
42	18	60.0	5	20	Neutrophil-activat
43	18	60.0	5	22	Phosphorylated pep
44	17	56.7	5	16	Immune stimulating
45	17	56.7	5	17	Soybean pepsin dig

#### ALIGNMENTS

##### RESULT 1

AAAB25913

ID AAB25913 standard; Peptide; 5 AA.

XX

AC AAB25913;

XX

DT 05-JAN-2001 (first entry)

XX

DE IGE C-epsilon-2 domain surface exposed epitope peptide P7 SEQ ID NO:7.

XX

KW Epitope; murinope; human; immunoglobulin E; IGE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; anti-allergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.

XX Homo sapiens.

XX

PN W02C0050460-A1.

XX

PD 31-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-EP01455.

XX

PR 25-FEB-1999; 99GB-0004405.

PR 23-MAR-1999; 99GB-0007151.

PR 07-MAY-1999; 99GB-0010537.

PR 07-MAY-1999; 99GB-0010538.

PR 07-AUG-1999; 99GB-0018594.

PR 07-AUG-1999; 99GB-0018603.

PR 07-SEP-1999; 99GB-0021046.

PR 07-SEP-1999; 99GB-0021047.

PR 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027698.  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Larent A, Mason S;  
 DR Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;  
 XX WPI: 2000-522073/53.  
 XX  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 XX Claim 8; Page 5; 129pp; English.  
 XX  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 CC immunogen (II) for treating allergy comprising (i); (2) a vaccine (iii)  
 CC for treating allergies comprising (ii); (3) a ligand (iv) capable of  
 CC recognising E; (4) a pharmaceutical composition (v) comprising (iv);  
 CC (5) a peptide (ia) capable of being recognised by (iv); (6) an immunogen  
 CC (Iia) comprising (ia); and (7) producing (iii) by producing (ii). (i)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (2), (iii) and (iv) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (iv) is useful for identifying mimotopes of E,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (i) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (ii), (iii) and (iv) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (iv) is also useful in diagnosing atopy. AAB25907 to AAB26039 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 30; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPPT 5  
 DB 1 FTPPT 5  
 RESULT 2  
 AAU16638  
 ID AAU16638 standard; Peptide; 5 AA.  
 XX  
 XX  
 XX Peptide P7 derived from Cepsilon2 region of human IgE.  
 DE  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200145745-A2.  
 FN  
 XX 28-JUN-2001.  
 PD  
 XX 21-DEC-2000; 2000WO-GB04935.  
 PF  
 XX 21-DEC-1999; 99GB-0030233.  
 PR  
 XX 22-FEB-2000; 2000GB-0004036.  
 PR  
 XX 22-AUG-2000; 2000GB-0020707.  
 PR  
 XX 22-AUG-2000; 2000GB-0020708.

XX  
 PA (ACAM-) ACAMBIS RES LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Flinn N, Johnson T;  
 XX WP: 2001-521967/57.  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 PT  
 XX Example 4; Page 21; 48pp; English.  
 PS  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 30; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPPT 5  
 DB 1 FTPPT 5  
 RESULT 3  
 ABC00223  
 ID ABC00223 standard; Peptide; 5 AA.  
 XX  
 XX AC AB000223;  
 XX  
 XX 02 SEP 2002 (first entry)  
 DT  
 XX Human IgE immunogenic peptide SEQ ID NO: 7.  
 DE  
 XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; anti-allergic.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200216409-A2.  
 FN  
 XX 28-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-EP09576.  
 PF  
 XX 22-AUG-2000; 2000GB-0020717.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
 PI  
 XX WPI: 2002-489648/52.  
 DR  
 XX  
 XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.  
 PT



XX Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,

XX where the conjugate comprises a disulphide bridge cyclised peptide and an

XX immunogenic carrier. The vaccines can be used in the treatment of

XX allergies. The present sequence is a peptide immunogen derived from human

XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

Qy 1 FTPT 5

Db 1 FTPT 5

RESULT 4

AAW47113

ID AAW47113 standard; peptide; 4 AA.

XX AAW47113;

AC AAW47113;

XX 18-MAY-1998 (first entry)

DE NM2A receptor binding neuroactive peptide 13.

XX NM2A receptor; neuroactive; glycine co-agonist; learning; memory;

KW N-methyl-D-aspartate; pharmaceutical.

XX Synthetic.

OS Rattus sp.

XX W09743306-A1.

XX 26-NOV-1997.

XX 16-MAY-1997; 97WO-US09667.

XX 17-MAY-1996; 96US-0649272.

XX (NEUR ) NEUROTHEAPEUTICS LP.

XX Colley PA, Moskal JR, Yamamoto H;

XX WPI; 1998-008795/01.

XX New neuro-active polypeptide(s) for enhancing learning and memory -

PT have NM2A receptor agonist activity at the glycine binding site

XX Claim 1; Page 23; 38pp; English.

XX This neuroactive peptide can bind to a N-methyl-D-aspartate (NMDA)

CC receptor and is included in a pharmaceutical composition comprising an

CC effective NMDA receptor binding amount of a polypeptide. The products

CC bind to the NMDA receptor at the glycine co-agonist site and effect at

CC least the same biological activity from the NMDA receptor as the binding

CC of glycine. They can be used as NMDA receptor agonists for enhancing

CC learning and memory. They can also be used for the isolation and

CC characterisation of NMDA receptor activity, NMDA receptor tissue

CC localisation and correlation with disease, injury or other

CC pharmacological effects.

XX Sequence 4 AA;

Query Match 80.0%; Score 24; DB 13; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0;

Matches 4; Conservative 0; Mismatches 0;

Qy 2 TPPT 5

Db 1 TPPT 4

RESULT 5

AAE29186

ID AAE29186 standard; peptide; 4 AA.

XX AAE29186;

AC AAE29186;

XX 27-JAN-2003 (first entry)

DE Neuroactive peptide, NT-13.

XX Therapy; hypoxia; neuropathic pain; central nervous system; analgesic;

KW cognitive enhancement; neuroactive peptide; neuroprotective; vasotropic;

KW N-methyl-D-aspartate receptor; NMDA; peptide therapy; nootropic; NT-13.

XX Unidentified.

OS WO200272609-A2.

PN 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07427.

XX 12-MAR-2001; 2001US-275083P.

XX (NYXI-) NYXIS NEURO THERAPIES INC.

XX Moskal JR;

XX WPI; 2002-759835/82.

XX Preventing or treating hypoxia or its effects on the central nervous

PT system, or neuropathic pain in a human, by administering neuroactive

PT peptides or compounds competing with the peptide for binding to

PT N-methyl-D-aspartate receptor -

XX Claim 1; Page 49; 64pp; English.

XX The invention relates to a method for preventing and/or treating hypoxia,

CC neuropathic pain or the effects of hypoxia on the central nervous system,

CC or producing cognitive enhancement in a mammal. The method comprises

CC administering a composition containing neuroactive peptides (designated

CC NT1, NT2, NT3, NT4, NT5, NT6, NT7 or NT8); or a compound that competes

CC with NTs for binding to the N-methyl-D-aspartate (NMDA) receptor. The

CC method is useful for preventing and/or treating hypoxia, neuropathic pain

CC or the effects of hypoxia on the central nervous system, in a mammal

CC (particularly a human). The method is also useful for producing cognitive

CC enhancement in a mammal. The invention is used in peptide therapy. The

XX present sequence is a neuroactive peptide.

SQ Sequence 4 AA;

Query Match 80.0%; Score 24; DB 23; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

Qy 2 TPPT 5

Db 1 TPPT 4

RESULT 6

AAW50692

ID AAW50692 standard; peptide; 4 AA.

XX AAW50692;

XX 08-APR-2002 (first entry)

DE Neuroactive peptide NT-13, for hypoxia treatment.

XX Neuroactive peptide; NT-13; hypoxia; ischaemia; therapy;  
KW N-methyl-D-aspartate; NMDA; agonist; antihypoxic.  
XX Synthetic.

OS WO200198367-A2.

PN 27-DEC-2001.

PP 22-JUN-2001; 2001WO-US:9839.

XX 22 JUN-2000; 2000US-213614P.

XX (NYX1-) NYXIS NEURO THERAPEUTICS INC.

XX Moskal JR, Yamamoto H, Colley PA;

XX WPI; 2002-098225/13.

DE N-PSDB; ABA91366, ABA91367, ABA91369, ABA91369.

XX Use of peptide or amino acid compositions for the treatment of hypoxia  
PT and ischaemia -

PS Claim 1; Page 31; 41pp; English.

XX The present sequence is that of neuroactive peptide NT-13, which  
XX is capable of binding to the N-methyl-D-aspartate (NMDA) receptor.  
XX NT-13 is one of a set of NT family peptides (see ABA90690-92) that  
XX can be used to treat hypoxia and ischaemia. A method of treating  
XX hypoxia by administering a peptide or amino acid composition  
XX comprising a neuroactive peptide, DNA molecules encoding the  
XX neuroactive peptides, and a method of treating the effects of  
XX hypoxia in the central nervous system by administering a  
XX neuroactive peptide, especially NT-13, are claimed. The  
XX neuroactive peptides may be cyclized and may contain (preferably  
XX conservative) amino acid substitutions. NT-13 was shown to be a  
XX partial agonist in a pharmacological NMDA-specific function  
XX assay, a partial agonist in voltage clamp experiments in an  
XX cocult expression system, and a partial agonist in a behavioural  
XX NMDA-specific function assay.

XX Sequence 4 AA:

Query Match 80.0%; Score 24; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPPT 5  
DB 1 TPPT 4

RESULT 7

AAV42926

ID AAV42926 standard; peptide; 5 AA.

XX AAV42926;

XX 20-DEC-1999 (first entry)

XX Portion of the core peptide in the hinge region of IgA1.

XX Immunoglobulin; IgA1; hinge; core; nephropathy; diagnosis.

XX Homo sapiens.

XX WO990663-A1.

XX 07 OCT-1999.

XX 25-MAR-1999; 99WO-JP01525.

XX

PR 31-MAR-1998; 98JP-0101759.

XX (ASAH) ASAH KASEI KOGYO KK.  
PA (KOKU/) KOKUBO T.

XX Kokubo T, Arai K, Toma K;

XX WPI; 1999-591373/5C.

XX Quick, convenient examination of IgA nephropathy by determining  
PT antibody recognizing core peptides in the hinge region of IgA1 -

XX Disclosure; Page 5; 32pp; Japanese.

XX A new method is disclosed for diagnosing IgA nephropathy by determining  
XX an antibody recognising the core peptide in the hinge region of IgA;  
XX contained in a liquid specimen, e.g. blood, serum, plasma, saliva or  
XX urine. The method is quick, convenient, safe and may be automated. Since  
XX there is no need for renal biopsy, the patients suffer little mental  
XX stress, and there is no risk of perirenal bleeding. The present sequence  
XX represents a portion of the core peptide in the hinge region of IgA1.

XX Sequence 5 AA;

Query Match 80.0%; Score 24; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPPT 5  
DB 1 TPPT 4

RESULT 8

AAW47114

ID AAW47114 standard; peptide; 3 AA.

XX AAW47114;

XX 19-MAY-1998 (first entry)

XX NMDA receptor binding neuroactive peptide 14.

XX NMDA receptor; neuroactive; glycine co-agonist; learning; memory;

XX N-methyl-D aspartate; pharmaceutical.

XX Synthetic.

XX Rattus sp.

XX WO9743356 A1.

XX 20-NOV-1997.

XX 16-MAY-1997; 97WC-US08667.

XX 17-MAY-1996; 96US-3649272.

XX (NEUR-) NEUROTHERAPEUTICS LP.

XX Colley PA, Moskal JR, Yamamoto H;

XX WPI; 1998-038795/01.

XX New neuro active polypeptide(s) for enhancing learning and memory -  
PT have NMDA receptor agonist activity at the glycine binding site

XX Claim 5; Page 24; 38pp; English.

XX This neuroactive peptide can bind to a N-methyl-D-aspartate (NMDA)  
XX receptor and is included in a pharmaceutical composition comprising an  
XX effective NMDA receptor binding amount of a polypeptide. The products  
XX bind to the NMDA receptor at the glycine co-agonist site and effect at  
XX least the same biological activity from the NMDA receptor as the binding

CC of glycine. They can be used as NMDA receptor agonists for enhancing  
 CC learning and memory. They can also be used for the isolation and  
 CC characterisation of NMDA receptor activity, NMDA receptor tissue  
 CC localisation and correlation with disease, injury or other  
 CC pharmacological effects.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 Tpp 4  
 |||  
 Db 1 Tpp 3

#### RESULT 9

AAW47115  
 ID AAW47115 standard; peptide; 3 AA.

XX AC AAW47115;

DT 18-MAY-1998 (first entry)

XX DE NMDA receptor binding neuroactive peptide 15.

XX KW NMDA receptor; neuroactive; glycine co-agonist; learning; memory;  
 KW N-methyl-D-aspartate; pharmaceutical.

XX OS Synthetic.  
 OS Rattus sp.

PN WO9743306-A1.

XX PD 20-NOV-1997.

XX PF 16-MAY-1997; 97WO-US08667.

XX PR 17-MAY-1996; 96US-0649272.

XX PA (NEUR-) NEUROTHERAPEUTICS LP.

PI Colley PA, Moskal JR, Yamamoto H;

DR WPI; 1998 008735/01.

XX New neuro-active polypeptide(s) for enhancing learning and memory -  
 have NMDA receptor agonist activity at the glycine binding site

XX Claim 5; Page 24; 38pp; English.

CC This neuroactive peptide can bind to a N methyl D aspartate (NMDA)  
 CC receptor and is included in a pharmaceutical composition comprising an  
 CC effective NMDA receptor binding amount of a polypeptide. The products  
 CC bind to the NMDA receptor at the glycine co-agonist site and effect at  
 CC least the same biological activity from the NMDA receptor as the binding  
 CC of glycine. They can be used as NMDA receptor agonists for enhancing  
 CC learning and memory. They can also be used for the isolation and  
 CC characterisation of NMDA receptor activity, NMDA receptor tissue  
 CC localisation and correlation with disease, injury or other  
 CC pharmacological effects.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Ppt 5  
 |||  
 Db 1 Ppt 3

#### RESULT 10

ABB78522

ID ABB78522 standard; Peptide; 3 AA.

XX AC ABB78522;

XX DT 09-JUL-2002 (first entry)

XX DE Contiguous hydroxyproline sequence SEQ ID NO:213.

XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
 KW HKGP; repetitive proline-rich protein; RRRP; arabinogalactan protein;  
 KW AGP; plant gum.

XX OS Acacia senegal.

OS Synthetic.

PN WO200178503-A2.

XX PD 25-OCT-2001.

XX PF 12-APR-2001; 2001WO-US12136.

XX PR 12-APR-2000; 2000US-0547693.

XX PA (UYOH-) UNIV OHIO.

XX PI Kieliszewski MJ;

XX DR WPI; 2002-04:307/05.

XX Nucleic acids and proteins useful for producing hydroxy-proline rich  
 PT glycoproteins in plants -

XX Claim 9; Page 122; 326pp; English.

CC The present invention describes synthetic genes encoding plant gums and  
 CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
 CC acids that encode them. The nucleic acids, proteins and methods from the  
 CC present invention may be used to produce HRGPs, repetitive proline-rich  
 CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via  
 CC recombinant methodologies. Also described is the expression of synthetic  
 CC genes designed from repetitive peptide sequences, such as glycoproteins  
 CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).  
 CC AB251730 to AB251849 and ABB78401 to ABB78544 represent sequences used  
 CC in the exemplification of the present invention.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 23; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 Tpp 4  
 |||  
 Db 1 Tpp 3

#### RESULT 11

AAR45401

ID AAR45401 standard; peptide; 4 AA.

XX AC AAR45401;

XX DT 11-JUL-1994 (first entry)

XX DE Prolyl endopeptidase inhibitor peptide-10.

XX KW Corn; maize; prolyl endopeptidase; dementia; gamma-zein;  
 KW protease inhibitor; Alzheimer's Disease.

XX OS Synthetic.

XX JP55331072-A.  
 XX  
 XX 14 DEC-1993.  
 XX  
 XX 27-MAY-1992; 92JP-C160354.  
 XX  
 XX 27-MAY 1992; 92JP-C160354.  
 XX  
 XX (AGENCY OF IND SCI & TECHNOLOGY.  
 XX (SHOJI SANGYO CO.  
 XX  
 XX WPI, 1994-022846/03.  
 XX  
 XX Prolyl endopeptidase inhibitors for treating dementia are  
 XX prepared by hydrolysis of corn protein.  
 XX  
 XX Claim 1; Page 2; 8pp; Japanese.  
 XX  
 XX This peptide is one of 10 claimed peptides having prolyl  
 XX endopeptidase inhibitory activity; the peptide is expected to be of  
 XX use for the prophylaxis and treatment of dementia. The peptide is  
 XX synthesised by standard methods.  
 XX  
 XX Sequence 4 AA;  
 XX  
 XX Query Match 63.3%; Score 19; DB 15; Length 4;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 2 TPP 4  
 XX DB 1 TPP 3  
 XX  
 XX RESULT 12  
 XX AB547154  
 XX 13 AB547154 standard; Peptide; 4 AA.  
 XX  
 XX AC AB547154;  
 XX  
 XX DT 19-AUG-2002 (first entry)  
 XX  
 XX DE N. meningitidis LOS peptidic mimotope related peptide #12.  
 XX  
 XX KW Neisseria meningitidis; meningococcus; meningococcal; varicella; LOS;  
 XX lipopolysaccharide; monoclonal antibody; antibacterial; infection;  
 XX antiinflammatory; meningococcal disease.  
 XX  
 XX CS Neisseria meningitidis.  
 XX Synthetic.  
 XX  
 XX PN WO200228859 A2.  
 XX  
 XX PD 11 APR-2002.  
 XX  
 XX PF 03-OCT-2001; 2001WO-EP11409.  
 XX  
 XX PR 03 OCT-2001; 2000GB-0024250.  
 XX  
 XX PA (SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX PL De Bolle XT, Larsson J, Lobet Y, Mouton PY, Pochamp J, Viret P;  
 XX DR WPI, 2002-475596/51.  
 XX  
 XX Novel mimotope of Neisseria meningitidis surface, for treating  
 XX meningococcal disease, comprising a peptide epitope obtainable by  
 XX screening peptide library with a specific monoclonal antibody.  
 XX  
 XX PS Example 5; Page 37; 55pp; English.  
 XX  
 XX The present invention describes mimotopes (1) of a surface of, 9,  
 XX

XX of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis  
 XX comprising a peptide epitope obtained by screening a peptide library  
 XX with a monoclonal antibody (MAB) like 4B12C10, H44/24, H44/58, H44/70  
 XX or H44/78; (1) is antigenically cross-reactive with MAB. (1) have  
 XX antibacterial and antiinflammatory activities, and can be used in  
 XX vaccines. MAB is useful in the identification of (1). (1) or MAB are  
 XX useful as a medicament, and also in the manufacture of a medicament for  
 XX treating or preventing meningococcal disease. (1) and MAB are useful  
 XX for treating a patient suffering from or susceptible to meningococcal  
 XX disease by administering (1) or MAB to the patient. (1) is useful in  
 XX a diagnostic assay for meningococcal infection to detect antibodies  
 XX against 13, 7, 9, LOS and to detect the presence of 13, 7, 9 immunotype  
 XX meningococcus in a sample from a patient. ABN88464 to ABN88487 and  
 XX ABP47326 to ABP47754 represent sequences used in the exemplification  
 XX of the present invention.  
 XX  
 XX Sequence 4 AA;  
 XX  
 XX Query Match 63.3%; Score 19; DB 23; Length 4;  
 XX Best Local Similarity 75.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TPP 4  
 XX DB 1 RPP 4  
 XX  
 XX RESULT 13  
 XX ABB78491  
 XX 1D ABB78491 standard; Peptide; 4 AA.  
 XX  
 XX AC ABB78491;  
 XX  
 XX DT 09-JUL-2002 (first entry)  
 XX  
 XX DE Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:178.  
 XX  
 XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
 XX HRGP; repetitive proline rich protein; RRP; arabinogalactan protein;  
 XX AGP; plant gum.  
 XX  
 XX OS Acacia senegal.  
 XX Synthetic.  
 XX  
 XX PN WO200178503-A2.  
 XX  
 XX PD 25-OCT-2001.  
 XX  
 XX PF 12-APR 2001; 2001WO US12336.  
 XX  
 XX PR 12-APR-2001; 2001US-0547493.  
 XX  
 XX PA (UYCH-) UNIV OHIO.  
 XX  
 XX PI Kieliszewski XG.  
 XX  
 XX DR WPI: 2002-041307/05.  
 XX  
 XX PT Nucleic acids and proteins useful for producing hydroxy-proline rich  
 XX glycoproteins in plants.  
 XX  
 XX PS Claim 5; Page 121; 326pp; English.  
 XX  
 XX The present invention describes synthetic genes encoding plant gums and  
 XX other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
 XX acids that encode them. The nucleic acids, proteins and methods from the  
 XX present invention may be used to produce HRGPs, repetitive proline-rich  
 XX proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via  
 XX recombinant methodologies. Also described is the expression of synthetic  
 XX genes designed from repetitive peptide sequences, such as glycoproteins  
 XX including the peptide sequences of gum arabic glycoprotein (GAGP).  
 XX AB:51730 to AB:51849 and ABB78401 to ABB78544 represent sequences used  
 XX in the exemplification of the present invention.

```

XX SQ Sequence 4 AA;
Query Match 63.3%; Score 19; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPP 4
   |||
Db 1 TPP 3

RESULT 14
ABR78523
ID ABR78523 standard; Peptide; 4 AA.
XX
AC ABR78523;
XX
DT 09-JUN-2002 (first entry)
XX
DE Contiguous hydroxyproline sequence SEQ ID NO:214.
XX
KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
KW HRP; repetitive proline-rich protein; RRP; arabinogalactan protein;
KW AGP; plant gum.
XX
CS Acacia senegal.
OS Synthetic.
XX
PN WC200:78503-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2C01WO-US12336.
XX
PR 12-APR 2000; 2C0JUS-0547693.
XX
PA (UYOH-) UNIV OH:O.
XX
PI Kieliszewski MJ;
XX
DR WPI; 2002-041307/05.
XX
PT Nucleic acids and proteins useful for producing hydroxy-proline rich
PT glycoproteins in plants -
PS Claim 9; Page 122; 326pp; English.
XX
CC The present invention describes synthetic genes encoding plant gums and
CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
CC acids that encode them. The nucleic acids, proteins and methods from the
CC present invention may be used to produce HRGPs, repetitive proline-rich
CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via
CC recombinant methodologies. Also described is the expression of synthetic
CC genes designed from repetitive peptide sequences, such as glycoproteins
CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
CC ABL51730 to ABL51849 and ABR78401 to ABR78544 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 4 AA;
Query Match 63.3%; Score 19; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPP 4
   |||
Db 1 TPP 3

RESULT 15
AAR07911
ID AAR07911 standard; protein; 5 AA.

```

```

XX AAR07911;
AC 18-FEB-1991 (first entry)
DT
XX
DE Polypeptide accompanying fragment of the C-terminus of the p15
DE protein of HIV-1, HIV-2 or HTLV-1 used in vaccine composition.
XX
KW Human lymphotropic diseases; CD5; capsid protein.
XX
OS Synthetic.
XX
PN EP398707-A.
XX
PD 22-NOV-1990.
XX
PF 17-MAY-1990; 90EP-0305325.
XX
PR 17-MAY-1989; 89US-0353021.
XX
PA (SANG-) SANGSTAT MED CORP.
XX
PI Pouletty PJ, Sta K;
XX
DR WPI; 1990-350439/47.
XX
PT Polypeptide comprising core sequence E-P-T-A-P - used, along with
PT antibodies raised against it, for treatment and diagnosis of
PT human lymphotropic diseases.
XX
PS Claim 3; Page 5; 6pp; English.
XX
CC Peptide is used in composition with peptide derived from p15
CC protein of HIV-1, HIV-2 or HTLV-1.
CC Composition is useful in detection of human lymphotropic retrovirus.
CC Anti-idiotypic Abs and vaccines may be prepared, useful in
CC modulation and immunisation against human lymphotropic viruses.
CC See also AAR07908-10.
XX
SQ Sequence 5 AA;
Query Match 63.3%; Score 19; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPP 4
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Db 3 TPP 5

Search completed: November 5, 2003, 17:54:15
Job time : 41 secs

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GenCore version 5.1.6  
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ON protein: - protein search, using sw model

Run on: November 5, 2003, 17:55:28 ; Search time 29 Seconds  
(without alignments)  
29.612 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FTPPT 5

Scoring table: SLOSCM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 10465

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/prodata/2/pubaa/PT\_NEW PUB pep:  
3: /cgn2\_6/prodata/2/pubaa/US06\_NEW PUB pep:  
4: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOVB pep:  
5: /cgn2\_6/prodata/2/pubaa/US07\_NEW PUB pep:  
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Pred. No. is the number of results predicted by change to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	12	US-10-082-014-278 Sequence 278, Appl
2	30	100.0	5	12	US-10-372-076-112 Sequence 132, Appl
3	19	63.3	4	15	US-10-185-815-99 Sequence 99, Appl
4	19	63.3	4	15	US-10-062-623A-23 Sequence 23, Appl
5	19	63.3	5	9	US-09-825-144-15 Sequence 15, Appl
6	19	63.3	5	9	US-09-823-243-3 Sequence 3, Appl
7	19	63.3	5	9	US-09-785-921A-15 Sequence 15, Appl
8	19	63.3	5	10	US-09-861-687-3 Sequence 3, Appl
9	19	63.3	5	12	US-10-247-853-2 Sequence 2, Appl
10	19	63.3	5	12	US-10-247-853-3 Sequence 3, Appl
11	19	63.3	5	12	US-10-192-361-42 Sequence 47, Appl
12	19	63.3	5	15	US-10-281-652-12 Sequence 12, Appl
13	18	60.0	5	15	US-10-252-406-27 Sequence 27, Appl
14	16	53.3	4	15	US-10-211-088-124 Sequence 128, Appl
15	16	53.3	5	15	US-10-206-699-49 Sequence 49, Appl

16	53.3	5	15	US-10-206-699-186	Sequence 186, Appl	
17	15	50.0	4	10	US-09-957-995A-15	Sequence 15, Appl
18	15	50.0	5	9	US-09-054-345-1	Sequence 1, Appl
19	15	50.0	5	9	US-09-858-754-9	Sequence 9, Appl
20	15	50.0	5	10	US-09-861-687-4	Sequence 4, Appl
21	15	50.0	5	12	US-10-316-253-59	Sequence 59, Appl
22	15	50.0	5	12	US-10-232-544-25	Sequence 25, Appl
23	15	50.0	5	12	US-10-302-817A-25	Sequence 25, Appl
24	15	50.0	5	14	US-10-099-895-15	Sequence 15, Appl
25	15	50.0	5	14	US-10-099-895-25	Sequence 25, Appl
26	15	50.0	5	15	US-10-237-850-27	Sequence 27, Appl
27	15	50.0	5	15	US-10-096-986-9	Sequence 9, Appl
28	15	50.0	5	15	US-10-255-733-1	Sequence 1, Appl
29	14	46.7	3	10	US-09-922-261-32	Sequence 32, Appl
30	14	46.7	4	9	US-09-873-737A-21	Sequence 21, Appl
31	14	46.7	4	9	US-09-803-126-17	Sequence 17, Appl
32	14	46.7	4	10	US-09-908-322-71	Sequence 71, Appl
33	14	46.7	4	10	US-09-916-940-3	Sequence 3, Appl
34	14	46.7	4	10	US-09-825-561A-70	Sequence 70, Appl
35	14	46.7	4	10	US-09-871-974-12	Sequence 12, Appl
36	14	46.7	4	11	US-09-783-931-71	Sequence 71, Appl
37	14	46.7	4	12	US-10-181-804A-15	Sequence 15, Appl
38	14	46.7	4	12	US-10-096-550-3	Sequence 3, Appl
39	14	46.7	4	12	US-10-352-704-21	Sequence 21, Appl
40	14	46.7	4	12	US-10-210-023-54	Sequence 54, Appl
41	14	46.7	4	12	US-10-299-991-5	Sequence 5, Appl
42	14	46.7	4	12	US-10-299-991-10	Sequence 10, Appl
43	14	46.7	4	12	US-10-299-991-11	Sequence 11, Appl
44	14	46.7	4	14	US-10-041-030-13	Sequence 13, Appl
45	14	46.7	4	15	US-10-235-552-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-10-082-014-278  
; Sequence 278, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 278  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-278

Query Match 100.0% Score 30; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred.No.5.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTPPT 5  
Db 1 FTPPT 5

RESULT 2  
US-10-372-076-132  
; Sequence 132, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 132  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-132

Query Match 100.0% Score 30; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 FTPT 5

RESULT 3  
US-10-185-815-99  
Sequence 99, Application US/10185815  
Publication No. US20030096354A1  
GENERAL INFORMATION:  
APPLICANT: Flax Corporation, LLC  
APPLICANT: O'Mahony, Daniel  
APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands  
FILE REFERENCE: E1067-20093  
CURRENT APPLICATION NUMBER: US/10/185,815  
CURRENT FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: 60/302,591  
PRIOR FILING DATE: 2001-07-02  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 99  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: polypeptide ligand  
US-10-185-815-99

Query Match 63.3% Score 19; DB 99; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTP 4  
DB 1 TTP 3

RESULT 4  
US-10-062-621A-23  
Sequence 23, Application US/10062621A  
Publication No. US20030108520A1  
GENERAL INFORMATION:  
APPLICANT: Borovsky, Dov  
APPLICANT: DeLoof, Arnold  
APPLICANT: Vethaert, Peter  
TITLE OF INVENTION: Neuropeptides and Their Use for Food Control  
FILE REFERENCE: UF-216C1  
CURRENT APPLICATION NUMBER: US/10/062,621A  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: 09/295,819  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: PCT/US00/10314

PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 23  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NFF peptide  
FEATURE:  
NAME/KEY: Variant  
LOCATION: (1)-(14)  
OTHER INFORMATION: No. US20030108520A1-amidated amino acids  
US-10-062-623A-23

Query Match 63.3% Score 19; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
DB 2 PPT 4

RESULT 5  
US-09-825-144-15  
Sequence 15, Application US/09825144  
Patent No. US2002037286A1  
GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Sechi  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgel Wetland  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7565  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-825-144-15

Query Match 63.3% Score 19; DB 9; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTPT 4  
DB 1 FTPT 4

RESULT 6  
US-09-823-242-3  
Sequence 3, Application US/09823240  
Patent No. US20020048813A1  
GENERAL INFORMATION:  
APPLICANT: Frank B. Gertler  
APPLICANT: James E. Bear  
APPLICANT: Jurgel Wetland  
APPLICANT: Joseph Loureiro  
TITLE OF INVENTION: Methods and Products for Regulating Cell  
TITLE OF INVENTION: Motility  
FILE REFERENCE: M0656/7564 (HCL)  
CURRENT APPLICATION NUMBER: US/09/823,240  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 60/194,564  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 11

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US 09-823-240-3
Query Match      63.3%; Score 19; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FTPT 4
       1 111
Db      1 FTPT 4

RESULT 7
US-09-785-921A-15
; Sequence 15, Application US/C9785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; FILE REFERENCE: LIT-PI-529
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO: 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US 09-785-921A-15
Query Match      63.3%; Score 19; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPT 5
       111
Db      3 PPT 5

RESULT 8
US-09-861-687-3
; Sequence 3, Application US/09861687
; Publication No. US20020193292A1
; GENERAL INFORMATION:
; APPLICANT: Markussen, Jan
; APPLICANT: Jonassen, Ib
; APPLICANT: Havelund, Sverdr
; APPLICANT: Brandt, Jakob
; APPLICANT: Kurtzhals, Peter
; APPLICANT: Harsen, Hertz Per
; APPLICANT: Kaarholm, Niels Christian
; TITLE OF INVENTION: INSULIN DERIVATIVES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020193292A10 No. US20020193292A1disk of No. US200201932
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/C9/861,687
; FILING DATE: 21-May-2001

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/666,360
; FILING DATE: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-247-853-2
Query Match      63.3%; Score 19; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FTPT 5
       111
Db      1 YTPKT 5

RESULT 9
US-10-247-853-2
; Sequence 2, Application US/10247853
; Publication No. US20030138972A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics sa.
; TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
; hybridomas secreting them, antigen recognition of these
; antibodies and their applications
; NUMBER OF SEQUENCES: 3
; STREET: Industriepark-Zwijnaarde 7, box 4
; CITY: Ghent
; COUNTRY: Belgium
; ZIP: B-9052
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/247,853
; FILING DATE: 02-No. US20030138972A1-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/666,360
; FILING DATE: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-247-853-2
Query Match      63.3%; Score 19; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 TPP 4  
|||  
Db 3 TPP 5

RESULT 10  
US-10-247-853-3  
; Sequence 3, Application US/10247853  
; Publication No. US20030138972A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics sa.  
; TITLE OF INVENTION: Monoclonal antibodies specific for HIV-tau,  
; Hybridomas secreting them, antigen recognition of these  
; antibodies and their applications  
; NUMBER OF SEQUENCES: 3  
; STREET: Industriepark-Zwijnaarde 7, box 4  
; CITY: Ghent  
; COUNTRY: Belgium  
; ZIP: B-9032  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/247,853  
; FILING DATE: 02-No. US20030138972A1-1999  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,285  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: C8/666,360  
; FILING DATE: <Unknown>  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 00 32 9 241 07 11  
; TELEFAX: 00 32 9 241 07 99  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US 10 247-853-3

Query Match 63.3%; Score 19; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPP 4  
|||  
Db 3 TPP 5

RESULT 11  
US-10-192-381-47  
; Sequence 47, Application US/10192381  
; Publication No. US20030170807A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WOLFEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HEMER 1b PROTEIN (AS  
; TITLE OF INVENTION: AMENDED)  
; FILE REFERENCE: JNU1580-4  
; CURRENT APPLICATION NUMBER: US/10/192,381  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US/09/377,295  
; PRIOR FILING DATE: 1999-08-18

; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-09-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 47  
; LENGTH: 5  
; TYPE: PPT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: optimal ligand  
US-10-192-381-47

Query Match 63.3%; Score 19; DB 12; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTTP 4  
|||  
Db 1 FTTP 4

RESULT 12  
US-10-281-652-12  
; Sequence 12, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 66/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 5  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-12

Query Match 63.3%; Score 19; DB 15; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTTP 4  
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Db 1 FTTP 4

RESULT 13  
US-10-252-408-27  
; Sequence 27, Application US/10252408  
; Publication No. US20030082736A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, Craig A.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS  
; FILE REFERENCE: A 71592  
; CURRENT APPLICATION NUMBER: US/10/252,408

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; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/08/436,824
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-01-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,242
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Miscellaneous Structure
US-10-252-408-27

Query Match      60.0%; Score 18; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTP 3
Db 3 FTP 5

RESULT 14
US-10-211-088-128
; Sequence 128, Application US/1021108#
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A:el Fusion: Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-128

Query Match      53.3%; Score 16; DB 15; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTPP 4
Db 1 YTPP 4

RESULT 15
US-10-206-699-49
; Sequence 49, Application US/10206699
; Publication No. US20030100510A1
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; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-49

Query Match      53.3%; Score 16; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TPPT 5
Db 2 TPST 5

Search completed: November 5, 2003, 18:00:35
Job time : 29 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX protein - protein search, using sw mode:

Run on: November 5, 2003, 17:53:28 : Search time 21 seconds  
(without alignments)  
10.074 Million cell updates/sec

Title: US-09 914-088-7  
Perfect score: 10  
Sequence: 1 FRPPT 5

Scoring table: BLASTM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 22629

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:  
3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep:  
4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep:  
5: /cgn2\_6/prodata/1/aa/PCUS\_COMB.pep:  
6: /cgn2\_6/prodata/1/aa/backfiles.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	80.0	4	1	US-08-649-272A-13
2	24	80.0	4	3	US-09-105-799-13
3	24	80.0	5	4	US-09-646-154-1
4	19	63.3	3	1	US-08-649-272A-14
5	19	63.3	3	1	US-08-649-272A-14
6	19	63.3	3	3	US-09-105-799-14
7	19	63.3	3	3	US-09-105-799-15
8	19	63.3	4	1	US-07-917-034A-5
9	19	63.3	4	1	US-08-122-546-1
10	19	63.3	4	2	US-08-764-938-1
11	19	63.3	4	3	US-09-195-868-18
12	19	63.3	4	3	US-09-131-052-1
13	19	63.3	4	3	US-09-131-053A-1
14	19	63.3	4	3	US-08-895-590-40
15	19	63.3	5	2	US-08-666-473-6
16	19	63.3	5	2	US-08-666-473-10
17	19	63.3	5	2	US-08-518-967-13
18	19	63.3	5	2	US-08-340-283-3
19	19	63.3	5	2	US-08-967-508-12
20	19	63.3	5	2	US-08-612-858-29
21	19	63.3	5	3	US-08-666-360-2
22	19	63.3	5	3	US-08-666-360-3
23	19	63.3	5	3	US-08-967-506-12
24	19	63.3	5	3	US-08-932-082-3
25	19	63.3	5	4	US-09-646-154-3
26	19	63.3	5	4	US-09-432-285-2
27	19	63.3	5	4	US-09-432-285-3

Sequence 12, Appl  
Sequence 106, App  
Sequence 339, App  
Sequence 12, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 27, Appl  
Patent No. 5395760  
Sequence 22, Appl  
Sequence 38, Appl  
Sequence 6, Appl  
Sequence 22, Appl  
Sequence 19, Appl  
Sequence 3, Appl  
Sequence 48, Appl  
Sequence 9, Appl  
Sequence 27, Appl  
Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-08-649-272A-13  
; Sequence 13, Application US/58649272A  
; Patent No. 5763393  
; GENERAL INFORMATION:  
; APPLICANT: MOSKAL, Joseph R  
; APPLICANT: YAMAMOTO, Hirotsuka  
; APPLICANT: COLLEY, Patricia A  
; TITLE OF INVENTION: Neuroactive Peptides  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKNER & ALLEGRETTI, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,272A  
; FILING DATE: 17-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHAO, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,1204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "NT-13"  
US-08-649-272A-13

Query Match 80.0%; Score 24; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 2 TPPT 5
Db 1 TPPT 4

RESULT 2
US-09-105-799-13
; Sequence 13, Application US/09105799
; Patent No. 6107271
; GENERAL INFORMATION:
; APPLICANT: MOSKAL, Joseph R
; APPLICANT: YAMAMOTO, Hirotsuka
; APPLICANT: COLLEY, Patricia A
; TITLE OF INVENTION: Neuroactive Peptides
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,799
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,272
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,1204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "NT 13"
US-09-105-799 13

Query Match 80.0%; Score 24; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 TPPT 5
Db 1 TPPT 4

RESULT 3
US-09-646-154-4
; Sequence 4, Application US/09646154
; Patent No. 6429024
; GENERAL INFORMATION:
; APPLICANT: KOKUBO, TOHRU
; APPLICANT: ARAI, KENJI
; APPLICANT: TOMA, KAZUNORI
; TITLE OF INVENTION: TEST METHOD FOR IGA NEPHROPATHY
; FILE REFERENCE: KP-9821

Query Match 63.3%; Score 19; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 TPPT 5
Db 1 TPPT 4

Query Match 80.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 TPPT 5
Db 1 TPPT 4

Query Match 80.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/09/646,154
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01525
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Formula amino
; OTHER INFORMATION: acid sequence
US-09-646-154-4

Query Match 80.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 TPPT 5
Db 1 TPPT 4

RESULT 4
US-08-649-272A-14
; Sequence 14, Application US/08649272A
; Patent No. 5763393
; GENERAL INFORMATION:
; APPLICANT: MOSKAL, Joseph R
; APPLICANT: YAMAMOTO, Hirotsuka
; APPLICANT: COLLEY, Patricia A
; TITLE OF INVENTION: Neuroactive Peptides
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,272A
; FILING DATE: 17-MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,1204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "NT-14"
US-08-649-272A-14

Query Match 63.3%; Score 19; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 TPP 4  
 Db 1 TPP 3

## RESULT 5

US-08-649-272A-15  
 ; Sequence 15, Application US/08649272A  
 ; Patent No. 5763393  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
 ; STREET: 10 S. Wacker Drive, Suite 3000  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/649,272A  
 ; FILING DATE: 17-MAY-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CHAO, Mark  
 ; REGISTRATION NUMBER: 37,293  
 ; REFERENCE/DOCKET NUMBER: 95,1204  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-715-1234  
 ; TELEFAX: 312-715-1234  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1  
 ; OTHER INFORMATION: /note= "NT-15"  
 US-08-649-272A-15

Query Match 63.3%; Score 19; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPT 5  
 Db 1 PPT 3

## RESULT 6

US-09-105-799-14  
 ; Sequence 14, Application US/09105799  
 ; Patent No. 6107271  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; APPLICANT: COLLEY, Patricia A  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.

STREET: 10 S. Wacker Drive, Suite 3000  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/105,799  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/649,272  
 FILING DATE: 17-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CHAO, Mark  
 REGISTRATION NUMBER: 37,293  
 REFERENCE/DOCKET NUMBER: 95,1204  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000  
 TELEFAX: 312-715-1234  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: No. 6107271 Relevant  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1  
 OTHER INFORMATION: /note= "NT-14"  
 US-09-105-799-14

Query Match 63.3%; Score 19; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPP 4  
 Db 1 TPP 3

## RESULT 7

US-09-105-799-15  
 ; Sequence 15, Application US/09105799  
 ; Patent No. 6107271  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; APPLICANT: COLLEY, Patricia A  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
 ; STREET: 10 S. Wacker Drive, Suite 3000  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/105,799  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/649,272  
FILING DATE: 17-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,1204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: NO: 6107271 Relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1  
OTHER INFORMATION: /note= "NT-15"  
US-09 105 799.15

Query Match 63.3% Score 19; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
|||  
DB 1 PPT 3

RESULT 8  
US-07-917-034A-5  
Sequence 5, Application US/07917034A  
Patent No. 5427927  
GENERAL INFORMATION:  
APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,  
APPLICANT: Ginter, Dony, Carola  
TITLE OF INVENTION: Process For The Enzymatic Cleavage  
TITLE OF INVENTION: of Recombinant Proteins Using Tga Proteases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS D-OS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/917,034A  
FILING DATE: 19920810  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PC7/EP91/00192  
FILING DATE: 1-Feb-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 39 415-B  
FILING DATE: 10-Dec-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 922.1  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 921.3  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 03 149.7  
FILING DATE: 3-Feb-1990  
ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5427927man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: HUBR 1018  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-917-034A-5

Query Match 63.3% Score 19; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
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DB 1 PPT 3

RESULT 9  
US-08-122-546-1  
Sequence 1, Application US/08122546  
Patent No. 5591593  
GENERAL INFORMATION:  
APPLICANT: Courtenay-Luck, Nigel S  
TITLE OF INVENTION: MINIMCY RECOGNITION UNIT OF PEM MUCIN  
TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jules E Goldberg, Esq.  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/122,546  
FILING DATE: 09/29/93  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24,408  
REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 986-4090  
TELEFAX: (212) 818-9479  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-122-546-1

QY 3 PPT 5  
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DB 2 PPT 4

Query Match 63.3% Score 19; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-08-764-938-1
; Sequence 1, Application US/08764938
; Patent No. 5833943
; GENERAL INFORMATION:
; APPLICANT: Courtenay-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,938
; FILING DATE: December 13, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT/C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-764-938-1
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 PPT 5
Db 2 PPT 4
RESULT 11
US-09-195-868-18
; Sequence 18, Application US/09195868
; Patent No. 609621
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH MD, MICHAEL
; APPLICANT: POT PH.D., DAVID
; APPLICANT: WILLIAMS MDPH, LEWIS T.
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FIRESTONE, LEIGH H.
; REGISTRATION NUMBER: 36,831
; REFERENCE/DOCKET NUMBER: 1182,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2707
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
US-09-195-868-18
Query Match 63.3%; Score 19; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPT 5
Db 1 PPT 3
RESULT 12
US-09-131-052-1
; Sequence 1, Application US/09131052
; Patent No. 6107469
; GENERAL INFORMATION:
; APPLICANT: Courtenay-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/131,052
; FILING DATE: August 7, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REFERENCE/DOCKET NUMBER: JG-EPC-1069C-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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1  FRAGMENT TYPE: internal
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5  Best Local Similarity 100.0%; Pred. No. 2.5e+05;
6  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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8  QY 3 PPT 5
9  DB 2 PPT 4
10
11  RESULT 13
12  US 09-131 053A-1
13  Sequence 1; Application US/09131053A
14  Patent No. 6174691
15  GENERAL INFORMATION:
16  APPLICANT: Courtenay-Luck, Nigel S
17  TITLE OF INVENTION: MINIMUM RECOMBINATION UNIT OF THE MUCIN
18  NUMBER OF SEQUENCES: 18
19  CORRESPONDENCE ADDRESS:
20  ADDRESSEE: Jules E Goldberg, Esq.
21  STREET: 261 Madison Avenue
22  CITY: New York
23  STATE: New York
24  COUNTRY: USA
25  ZIP: 10016-2391
26  MEDIUM TYPE: Floppy disk
27  COMPUTER: IBM PC compatible
28  OPERATING SYSTEM: PC-DOS/MS-DOS
29  SOFTWARE: Patent In Release #1.0, Version #1.25
30  CURRENT APPLICATION DATA:
31  APPLICATION NUMBER: US/09/131 053A
32  FILING DATE: August 7, 1998
33  CLASSIFICATION:
34  PRIOR APPLICATION DATA:
35  APPLICATION NUMBER: US/08/374,888
36  FILING DATE: 19-JAN-1995
37  ATTORNEY/AGENT INFORMATION:
38  NAME: McGowan, Malcolm M.
39  REGISTRATION NUMBER: 39,300
40  REFERENCE/DOCKET NUMBER: 022650-253
41  TELECOMMUNICATION INFORMATION:
42  TELEPHONE: 703-836-6620
43  TELEFAX: 703-836-2021
44  INFORMATION FOR SEQ ID NO: 1:
45  SEQUENCE CHARACTERISTICS:
46  LENGTH: 4 amino acids
47  TYPE: amino acid
48  TOPOLOGY: linear
49  MOLECULE TYPE: protein
50  US-08-895-590-40
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52  Query Match: 63.3%; Score 19; DB 3; Length 4;
53  Best Local Similarity 100.0%; Pred. No. 2.5e+05;
54  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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56  QY 2 PPT 4
57  DB 2 PPT 4
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59  RESULT 15
60  US-08-666-473-6
61  Sequence 6; Application US/08666473
62  Patent No. 6443713
63  GENERAL INFORMATION:
64  APPLICANT: YOSHIDA, Akiyo
65  APPLICANT: TAKEUCHI, Makoto
66  TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
67  TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
68  TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
69  NUMBER OF SEQUENCES: 114
70  CORRESPONDENCE ADDRESS:
71  ADDRESSEE: Foley & Lardner
72  STREET: 3000 K Street, N.W., Suite 500
73  CITY: Washington
74  STATE: D.C.
75  COUNTRY: USA
76  ZIP: 20007-5109
77  COMPUTER READABLE FORM:
78  MEDIUM TYPE: Floppy disk
79  COMPUTER: IBM PC compatible
80  OPERATING SYSTEM: PC-DOS/MS-DOS
81  SOFTWARE: Patent In Release #1.0, Version #1.30
82  CURRENT APPLICATION DATA:
83  APPLICATION NUMBER: US/08/666,473
84  FILING DATE: 19 SEP 1996
85  CLASSIFICATION: 435
86  PRIOR APPLICATION DATA:

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APPLICATION NUMBER: WO PCT/JP95/02238  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-22:01  
FILING DATE: 09-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-2691:1  
FILING DATE: 31-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16897/837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 9C4136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08 666-473-6

Query Match 63.3%; Score 19; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Cy 2 TPP 4  
Db 2 TPP 4

Search completed: November 5, 2003, 17:56.31  
Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw mode:

Run on: November 5, 2003, 17:59:59 ; Search time 13 Seconds  
(without alignments)  
96.169 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68  
Sequence: 1 CLEGGQVMDVLL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1925

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : p1R 76:•  
1: p1r1:•  
2: p1r2:•  
3: p1r3:•  
4: p1r4:•

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	32.4	7	B34818	vicilin 57K chain
2	21	30.9	8	A28719	thymic humoral fac
3	21	30.9	10	G58501	48K bile/gallblad
4	20	29.4	9	A60427	macrophage cyto
5	20	29.4	10	GXHU1	gastric juice pep
6	20	29.4	11	PS0259	19K protein 325
7	19	27.9	12	PN0160	ribosomal protein
8	18	26.5	13	A33660	osteoclast functi
9	18	26.5	13	S47357	T-cell antigen rec
10	18	26.5	13	S66235	sperr motility inh
11	17	25.0	6	P70804	T-cell receptor be
12	17	25.0	6	PT0857	T-cell receptor be
13	17	25.0	7	PT0543	T-cell receptor be
14	17	25.0	10	S10926	inhibin beta-A cha
15	17	25.0	10	PC4442	cytochrome c553
16	17	25.0	10	PH1592	Ig H chain V-D-J r
17	17	25.0	12	G49410	complex polypept
18	17	25.0	12	C58502	58K bile and gallb
19	17	25.0	12	S43013	hypothetical prote
20	17	25.0	12	S36899	ribosomal protein
21	17	25.0	12	PH1611	Ig H chain V-D-J r
22	17	25.0	12	PH1581	Ig H chain V-D-J r
23	16	23.5	9	A37027	macrophage chemot
24	16	23.5	10	A32543	cardioexcitatory n
25	16	23.5	10	A56633	neomycin suppressin
26	16	23.5	10	A32195	Na+/K+-exchanging
27	16	23.5	11	S19301	endo-1,4-beta-xyla
28	16	23.5	11	A34243	hydrocaphorin - Ja
29	16	23.5	12	T46754	hypothetical prote

30 16 23.5 12 2 JQ2308 hypothetical 1.4K  
31 16 23.5 12 2 JQ2318 hypothetical 1.4K  
32 16 23.5 12 2 PH1172 T-cell receptor al  
33 16 23.5 13 2 S65612 tubulin alpha-chai  
34 15 22.1 6 2 B34835 dnAA protein - Pse  
35 15 22.1 6 2 C26997 unspecific monocoy  
36 15 22.1 10 2 PH0807 T-cell receptor al  
37 15 22.1 10 2 PH0946 T-cell receptor be  
38 15 22.1 10 2 E86128 hypothetical prote  
39 15 22.1 11 2 S14087 parasporal crystal  
40 15 22.1 11 2 S18385 NADP-cytochrome P4  
41 15 22.1 11 2 H84382 hypothetical prote  
42 15 22.1 12 2 S29764 alpha-macroglobuli  
43 15 22.1 12 2 S48209 zinc-metallophosph  
44 15 22.1 12 2 I40663 bma protein - Clos  
45 15 22.1 12 2 PH1587 Ig H chain V-D-J r

#### ALIGNMENTS

RESULT 1  
B34818  
vicilin 57K chain - Pigeon pea (fragment)  
C:Species: Cajanus cajan (pigeon pea)  
C>Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C:Accession: B34818  
R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.  
A:Reference number: A34818; MUID:90165956; PMID:2306256  
A:Accession: B34818  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MAW>

Query Match 32.4%; Score 22; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLEGG 5  
DB 3 CMESG 7

RESULT 2  
A28719  
thymic humoral factor gamma 2 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1993  
C:Accession: A28719  
R:Burststein, Y.; Buchner, V.; Pecht, M.; Trainin, N.  
Biochemistry 27, 4066-4071, 1988  
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an im  
A:Reference number: A28719; MUID:88326920; PMID:3261994  
A:Accession: A28719  
A:Molecule type: protein  
A:Residues: 1-8 <BUR>

Query Match 30.9%; Score 21; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDG 5  
DB 1 LEDG 4

RESULT 3  
G58501  
48K bile/gallbladder stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C>Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C:Accession: G58501

R:Binette, J.P.; Binette, M.B.

Submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: G58501

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <BIN>

A:Experimental source: human bile and gallbladder stones

A>Note: 1 Ser and 4-Glu were also found

Query Match 30.9%; Score 21; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.7e-03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0;

QY 2 LEDGQVM 8

|||||

DB 4 VEDGRAL 10

#### RESULT 4

A60427

A:Description: cytotoxicity-inducing factor, 29K - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence\_revision: 12-Feb-1993 #text\_change 18-Jun-1993

C:Accession: A60427

R:Cones, C.M.; Prince, C.A.; Williams, J.S.

Exp. Hematol. 19, 704-709, 1991

A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing

A:Reference number: A60427; MUID:91372355; PMID:11629970

A:Accession: A60427

A:Molecule type: protein

A:Residues: 1-9 <GR>

A>Note: the sequence from the text on page 705 is inconsistent with that from page 708

C:Keywords: cytokine

Query Match 29.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 86.0%; Pred. No. 2.4e-04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IENQ 6

|||||

DB 4 LEDSQ 9

#### RESULT 5

GXHU

A:Description: gastric juice peptide - human

C:Species: Homo sapiens (man)

C:Date: 20-Jun-2000 #sequence\_revision: 20-Jun-2000 #text\_change 20-Jun-2000

C:Accession: A01628

R:Heathcote, J.G.; Washington, R.J.

Int. J. Protein Res. 2, 117-126, 1973

A:Title: Peptides of normal human gastric juice

A:Reference number: A01628; MUID:75150663; PMID:544848

A:Accession: A01628

A:Molecule type: protein

A:Residues: 1-10 <HFA>

A>Note: a second peptide lacking 1-Leu, but otherwise identical in composition with the

C:Superfamily: unassigned animal peptides

C:Keywords: stomach

Query Match 29.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2e-03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEDGQVMDV 10

|||||

DB 1 LAAGKVEISD 10

#### RESULT 6

PS0259

39K protein 3225 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995

C:Accession: PS0259

R:Tsugita, A.; Kano, M.

submitted to JIPID, April, 1993

A:Reference number: PS0209

A:Accession: PS0259

A:Molecule type: protein

A:Residues: 1-11 <TSC>

A:Experimental source: callus

C:Comment: molecular weight 39K, pI 5.7.

Query Match 29.4%; Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.2e-03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDGQVM 8

|||||

DB 4 EDGPV 9

#### RESULT 7

PN0160

A:Description: ribosomal protein S16 - fungus (Fusarium sporotrichoides) (fragment)

C:Species: Fusarium sporotrichoides

C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 11-Nov-1994

C:Accession: PN0160

R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot

A:Reference number: PN0160

A:Accession: PN0160

A:Molecule type: protein

A:Residues: 1-12 <FUK>

C:Keywords: protein biosynthesis; ribosome

Query Match 27.9%; Score 19; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3.5e-03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VMDVD 11

|||||

DB 6 VMDVD 10

#### RESULT 8

A33660

A:Description: osteoclast functional antigen alpha chain - green monkey (fragment)

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 23-Mar-1995

C:Accession: A33660

R:Davies, J.; Warwick, J.; Totty, N.; Philp, R.; Helfrich, M.; Horton, M.

J. Cell. Biol. 109, 1817-1826, 1989

A:Title: The osteoclast functional antigen, implicated in the regulation of bone resor

A:Reference number: A33660; MUID:96009054; PMID:2477382

A:Accession: A33660

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <DAV>

A:Experimental source: a green monkey kidney Vero cell line

Query Match 26.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5.7e-03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 MDVD 11

|||||

DB 3 MDVD 6

#### RESULT 9

```

S47357
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
R:Lehrer, P.J.
submitted to the EMBL Data Library, August, 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-23 <USH>
A:Cross-references: EMBL:Z35691; NID:9527451; PDB:1A84750.1; PDB:3527452
C:Keywords: T-cell receptor

Query Match      26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 5.7e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CLEGGQVMD 9
| | |
Db 1 CASSGRSTD 9

RESULT 13
S46235
sperm motility inhibitor protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S46235
R:Iwamoto, T.; Hironaka, H.; Furuchi, Y.; Wada, K.; Satoh, M.; Osada, T.; Gao
FEBS Lett. 368, 420-424, 1995
A:Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle an
A:Reference number: S46233; MUID:95361914; PMID:7635190
A:Accession: S46235
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <WA>
A:Note: Pro-6 was also found

Query Match      26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDCQVM 8
| | |
Db 7 DDGGV 12

RESULT 11
PT3604
T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT3604
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT5059; MUID:91277601; PMID:1711558
A:Accession: PT3604
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      25.0%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGG 6
| | |
Db 4 DGG 6

RESULT 12
PT0657
T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0657
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0657
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      25.0%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGG 6
| | |
Db 4 DGG 6

RESULT 13
PT0543
T-cell receptor beta chain V-D-J region (126-1BE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0543
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0543
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      25.0%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGG 6
| | |
Db 4 DGG 6

RESULT 14
SI0926
inhibin beta-A chain - African clawed frog (fragment)
N:Alternate names: activin A; mesoderm-inducing factor
C:Species: Xenopus laevis (African clawed frog)
C:Date: 18-Feb-1994 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: SI0926
R:Smith, J.C.; Price, B.M.J.; van Nimmen, K.; Huylebroeck, D.
Nature 345, 729-731, 1990
A:Title: Identification of a potent Xenopus mesoderm-inducing factor as a homologue o
A:Reference number: SI0926; MUID:90294906; PMID:2113615
A:Accession: SI0926
A:Molecule type: protein
A:Residues: 1-10 <NAT>
C:Superfamily: inhibin
C:Keywords: hormone

Query Match      25.0%; Score 17; DB 2; Length 10;

```

Best Local Similarity 75.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 4 DGV 7  
 DB 5 DGV 8

RESULT 15  
 PC4442  
 Cytochrome c553 - Desulfovibrio desulfuricans (fragment)  
 C:Species: Desulfovibrio desulfuricans  
 C:Date: 28-Mar-1998 #sequence\_revision 28-Mar-1998 #text\_change 07 May-1999  
 C:Accession: PC4442  
 R:Aubert, C.; Leroy, G.; Bianco, P.; Forest, E.; Pruschi, M.; Della, A.  
 Biochem. Biophys. Res. Commun. 242, 213-218, 1998  
 A:Title: Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.  
 A:Reference number: PC4442, XUID:9810281; PMID:9439638  
 A:Accession: PC4442  
 A:Molecule type: protein  
 A:Residues: 1-10 <ADB>  
 A:Experimental source: strain G201  
 C:Comment: This protein is involved in the formate reduction pathway.

Query Match: 25.0%; Score 17; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDG 5  
 DB 2 EDG 4

Search completed: November 5, 2003, 18:04:16  
 Job time : 14 secs

GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 17:56:33 ; Search time 9.5 seconds  
(without alignments)  
64,352 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: 1 CLECGQVMDVDLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127963 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 596

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	29.4	10	1 GAGU HUMAN	P01359 homo sapien
2	19	27.9	12	1 V23K WSSV	P82005 white spot
3	18	26.5	8	1 ACT_CARGA	P80729 carcinus ra
4	17	25.0	10	1 APE_CARGI	P80474 capnocytop
5	17	25.0	13	1 UHAI HUMAN	P40928 homo sapien
6	16	23.5	8	1 PLP BRANA	P81727 brassica ra
7	16	23.5	10	1 FARP_LCCMI	P38553 ocusta mig
8	16	23.5	10	1 LOMS_EUMA	P21144 leucophaea
9	16	23.5	10	1 XALE_KLEFN	P55564 lebsstella
10	16	23.5	12	1 HS9A_RAT	P42993 rattus norv
11	16	23.5	13	1 GER2_HORVI	P28526 leodeut vul
12	15	22.1	9	1 D1_NEPNO	P24816 neptrops no
13	15	22.1	10	1 PPCK_FASHE	P30525 fasciola he
14	15	22.1	10	1 SPI_HALRO	Q10997 halocynthia
15	15	22.1	12	1 XYL4_STRVN	P14405 streptococ
16	15	22.1	13	1 GER1_HORVU	P28525 leodeut vul
17	14	20.6	9	1 FARD_CALVO	P41868 calliphora
18	14	20.6	10	1 UPA2_HUMAN	P30088 homo sapien
19	14	20.6	11	1 CA41_LITIC	P82091 litoria cit
20	14	20.6	11	1 R2T_CCNAM	P42341 conopholis
21	14	20.6	12	1 CXAI_CONIM	P50382 conus imper
22	14	20.6	12	1 PA2B_VIPBO	P11859 vipera beru
23	14	20.6	13	1 ACT7_SOYBN	P15527 glycine max
24	14	20.6	13	1 ADFB_TENMC	P83109 tenebrio mo
25	14	20.6	13	1 IDHA_CANFA	P54816 canis fami
26	14	20.6	13	1 TEJA_RANJA	P81307 rana japoni
27	14	20.6	13	1 UN10_CLOPA	P81345 clostridium
28	13.5	19.9	9	1 UF02_MOUSE	P38640 mus musculu
29	13	19.1	8	1 WPI_FERAT	P83195 perkinsus a
30	13	19.1	9	1 DNFI_LCCM	P16319 ocusta mig
31	13	19.1	9	1 IPVR_RHOVI	P32902 rhodopseudo
32	13	19.1	9	1 RE42_LITRU	P82075 litoria rub
33	13	19.1	9	1 UPA6_HUMAN	P30092 homo sapien

34 13 19.1 10 1 COXO\_RAT P80432 rattus norv  
35 13 19.1 10 1 SP34\_DICMU P81545 dictyostell  
36 13 19.1 10 1 UXA6\_CHLIR P38007 chlamydia c  
37 13 19.1 10 1 VEG6\_BACSU P80699 bacillus su  
38 13 19.1 11 1 CA21\_LITIC P82087 litoria cit  
39 13 19.1 11 1 FARP\_PENMO P83321 penaeus mon  
40 13 19.1 11 1 RRPL\_CHAV P13179 chandipura  
41 13 19.1 12 1 CD14\_LITXA P56245 litoria xan  
42 13 19.1 12 1 CD14\_LITXA P56246 litoria xan  
43 13 19.1 12 1 HCYB\_MEGCR Q10584 megathura c  
44 13 19.1 12 1 OPS3\_DROVI P17645 drosophila  
45 13 19.1 13 1 FIBB\_RABIT P14478 oryctolagus

## ALIGNMENTS

RESULT 1  
GAGU\_HUMAN  
ID GAGU\_HUMAN STANDARD; PRT; 10 AA.  
AC P01359;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Gastric juice peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75150968; PubMed=5538385;  
RA Heathcote J.G., Washington R.J.;  
RT "Peptides of normal human gastric juice."  
RL Int. J. Protein Res. 2:117-126(1970).  
DR PIR; AC1628; GXHU1.  
DR MIM; 137220;  
DR GO; GO:0007596; P:digestion; NAS  
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.  
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.  
SQ SEQUENCE 10 AA; 1004 MW; CFEEC6AB02C3387D CRC64;  
Query Match 29.4%; Score 20; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEDGQVMDVD 11  
| | | | |  
DB 1 LAAGKVELSD 10

RESULT 2  
V23K\_WSSV  
ID V23K\_WSSV STANDARD; PRT; 12 AA.  
AC P82005;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 23 kDa structural polypeptide (Fragment).  
OS White spot syndrome virus (WSSV).  
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.  
OX NCBI\_TaxID=92652;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=South Carolina;  
RX MEDLINE=20214217; PubMed=10752552;  
RA Wang Q., Poulos B.T., Lightner D.V.;  
RT "Protein analysis of geophilic isolates of shrimp white spot syndrome virus."  
RL Arch. Virol. 145:263-274(2000).  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.  
FT NON\_TER :2 12  
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

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Query Match      27.9%; Score 19; DB 1; Length 12;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 2 LEQGVMDVLL 12
   |||
Db 1 MFGNLTNDV 11

RESULT 3
ACT_CARMA
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created);
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 15-JUL-1999 (Rel. 38, Last annotation update);
DE Actin (Fragment);
CS Carcinus maenas (Common shore crab) (Green crab);
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eulacostraca; Eucarida; Decapoda; Ploceymata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus;
OX NCBI_TaxID=6759;
RN 1;
RP SEQUENCE.
RA Lachaise F., Sornet G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Encodine 5:23-32(1996);
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBICITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 kDa.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR034001; Actin.
DR InterPro; IPR034001; Actin like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB32CAAB3 CRC64;

Query Match      24.5%; Score 18; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 9 DVDLL 12
   |||
Db 3 DVC: 6

RESULT 4
APE_CAPGI
ID APE_CAPGI STANDARD; PRT; 10 AA.
AC P8574;
DT 01-OCT-1996 (Rel. 34, Created);
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 01-OCT-1996 (Rel. 34, Last annotation update);
DE Aminopeptidase (SC 3.4.11.-) (Fragment);
OS Capnocytophaga gingivalis;
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN 1;
RP SEQUENCE.
RA STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574432;
RA Spratt L.A., Greenman C., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence

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factor";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1306 MW; 0CC0A6DB43772694 CRC64;

Query Match      25.0%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 9 DVDLL 13
   |||
Db 1 DVMXL 5

RESULT 5
UHA1_HUMAN
ID UHA1_HUMAN STANDARD; PRT; 13 AA.
AC P40928;
DT 01-FEB-1995 (Rel. 31, Created);
DT 01-FEB-1995 (Rel. 31, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Unknown protein from 2D-page of heart (Spot 4304) (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.7, ITS MW IS: 35.5 kDa.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1380 MW; 6617BA7A1E06AB1B CRC64;

Query Match      25.0%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 EDG 5
   |||
Db 7 EDG 9

RESULT 6
PLP_BRANA
ID PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created);
DT 15-JUL-1999 (Rel. 38, Last sequence update);
DT 30-MAY-2000 (Rel. 39, Last annotation update);
DE Plasmidial lipid-associated protein (Fragment).
CS Brassica napus (Rape);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN 1;
RP SEQUENCE.
RA STRAIN=CV TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;

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RA Hernandez-Finzon I., Ross J.H.E., Barnes K.A., Darant A.P.,
RA Murphy D.J.:
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAEOPLAST, A TAPETUM-
CC SPECIFIC ELASTIDIAL LIPID ORGANELLE.
CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.
FT NCN TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 VMDVD 11
DB :VIDVN 5

RESULT 7
FARP_LOCM1 STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistocerca gregaria (PDVDFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=768732;
RA Schoofs L., Holman G.M., Paemen L., Veehaert E., Avelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
RT (Schistocerca gregaria) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system.
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of FMRFamide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1999).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVARY SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543.
KW Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVD 11
DB 2 DVD 4

RESULT 8
LCMS_LEUMA STANDARD; PRT; 10 AA.
AC P21144; P41497;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucomyosuppressin (LMS) (Leu-MS).
OS Leucomyosuppressin (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin,
RT an insect neuropeptide that inhibits spontaneous contractions of the
RT cockroach hindgut.";
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
CC PROCTODEUM (HINDGUT).
KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid
FT MOD RES 10
FT MOD RES 10 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVD 11
DB 2 DVD 4

RESULT 9
MALE_KLEPN STANDARD; PRT; 10 AA.
AC Q05564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein);
DE (MMSp) (Fragment).
GN MALE
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=93211295; PubMed=9459773;
RA Bachellier S., Perrin D., Hofnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMES) are present in the
RT genome of Klebsiella.";
RL Mol. Microbiol. 7:537-544(1993).
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEMOTAXIS TOWARD MALTOLOGOSACCHARIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EYEL: X68329; CAA48406.1; -
DR InterPro: IP006061; SBP_dcm1.
DR PROSITE: PS01037; SBP_BACTERIAL.1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1159 MW; 8F59D04415A6BDDA CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEDGQ 6
DB 1 LKDAQ 5

RESULT 10
ID HS9A_RAT STANDARD; PRT; 12 AA.
AC P2935;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (fragment).
GN HSPCA
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
KN [1]
RP SEQUENCE
RC STRAIN: Sprague-Dawley; TISSUE: Liver;
RX MEDLINE=2159977; PubMed=1173232;
RA Langer T.; Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver."
RL Protoplasma 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro: IP002404; Hsp90.
DR PROSITE: PS02238; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation;
FT MCD_RES 4 4 PHOSPHORYLATION;
FT MCD_RES 6 6 PHOSPHORYLATION;
FT NON_TER 12 12
FT SEQUENCE 12 AA; 1432 MW; DE47C122CAB6C1B6 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 12;
Best Local Similarity 42.9%; Pred. No. 6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDCQMD 9
DB 2 EETGQD 8

RESULT 11
ID GER2_HORVU STANDARD; PRT; 14 AA.
AC P28526;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Germin 352 (fragment).
OS Hordeum vulgare (Barley).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RV [1]
RP SEQUENCE.
RC STRAIN=cv. CM 72; TISSUE=Root;
RA Hurkman W.J., Tao H.P., Tanaka C.K.;
RT "Germin-like polypeptides increase in barley roots during salt
RT stress."
RL Plant Physiol. 97:366-374(1991).
CC -!- FUNCTION: MAY PLAY A ROLE IN ALTERING THE PROPERTIES OF CELL
CC WALLS DURING GERMINATIVE GROWTH.
CC -!- SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY
CC HEXAMER) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
CC -!- TISSUE SPECIFICITY: ROOTS AND COLEOPTILE. IN ROOTS, PRESENT IN
CC THE MATURE REGION, BUT NOT IN THE TIP. NOT DETECTED IN LEAVES.
CC -!- INDUCTION: INCREASED BY SALT STRESS IN ROOTS AND DECREASED BY SALT
CC STRESS IN COLEOPTILE.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE GERMIN FAMILY.
DR InterPro: IPR001929; Germin.
DR PROSITE: PS00725; GERMIN, PARTIAL.
KW Apoplast; Cell wall; Glycoprotein; Multigene family.
FT NON_TER 10 10
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLED 4
DB 10 C1AD 13

RESULT 12
ID NEPCO STANDARD; PRT; 9 AA.
AC P24816;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Gastrin/cholecystokinin-like peptide D1.
OS Nephrops norvegicus (Norway lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Decapoda; Stomatopoda; Euphausiidae; Decapoda; Ploceyerata; Astacidea;
OC Nephropoidea; Nephropidae; Nephrops.
OX NCBI_TaxID=6929;
RV [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=92082847; PubMed=1747388;
RA Pavet P., Kegeles G., Sedlmeyer D., Keller R., van Wormhoudt A.;
RT "Structure and biological activity of crustacean gastrointestinal
RT peptides identified with antibodies to gastrin/cholecystokinin."
RL Biochimie 73:1233-1239(1991).
CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: S47432; S47432.
KW Hormone.
SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match 22.1%; Score 15; DB 1; Length 9;
Best Local Similarity 25.6%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDCQ 6
DB 2 EDCQ 5

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RESULT 13
PECK_FASHE STANDARD; PRT; 10 AA.
AC P80525;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative phosphoenolpyruvate carboxylase [GTP] EC 4.1.1.32
DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
DE protein 1) (Fragment)
OS Fasciola hepatica (Liver fluke)
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
CX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Kalcevic J., Ashman K., Meudsen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins."
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2)
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
CC FAMILY.
DR InterPro: IPR003364; PEP_carboxykin.
DR PROSITE; PS00505; PEPCK_GTP; PARTIAL.
KW Lyase; Decarboxylase; GTP-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1069 MW; 839346187AA9C97A CRC64;

Query Match 22.1%; Score 15; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DQGVN 8
DB 6 DGEAV 10

RESULT 14
SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
C. 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment)
OS Halcynethia toretzi (Sea squirt)
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Stolidobranchia; Pyrosida; Halcynethia.
CX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX ISSUE=Hemolymph;
RX MEDLINE=96321333; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000 Da proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Halcynethia
RT toretzi."
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Enzyme
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 22.1%; Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;

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Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDQQ 6
DB 3 KDGE 6

RESULT 15
XYLA_STRVN STANDARD; PRT; 12 AA.
ID XYLA_STRVN STANDARD; PRT; 12 AA.
AC P14405;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment)
GN XYLA.
OS Streptomyces violaceoruber.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=1935;
RN [1]
RP SEQUENCE.
RX STRAIN=LMG 7183;
RX MEDLINE=90104230; PubMed=2604694;
RA Vangrypeere W., Ange C., Kersters-Hilderson H., Tempat P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping."
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR HAMAP; MF_00455; 1.
DR InterPro: IPR001998; Xylose isom.
DR PROSITE; PS00173; XYLOSE_ISOMERASE_1; PARTIAL.
DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
FT NON_TER 1 1
FT ACT_SITE 5 5
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1375 MW; E749268EB1AAAAA1 CRC64;

Query Match 22.1%; Score 15; DB 1; Length 12;
Best Local Similarity 63.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 DVGAL 13
DB 6 DDCJH 10

Search completed: November 5, 2003, 18:02:29
Job time : 10.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:59:29 ; Search time 27.5 Seconds

(without alignments)  
121.989 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: CLEGGQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 266

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

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Pred. No. is the number of results predicted by CompuGen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	36.8	9	11 Q9QZAB	Q9QZAB mus musculus
2	20	29.4	12	12 Q89243	Q89243 woodchuck h
3	19	27.9	9	4 Q96P97	Q96P97 homo sapien
4	19	27.9	9	10 Q8LPT5	Q8LPT5 zea mays (m
5	19	27.9	10	10 Q8LPT7	Q8LPT7 zea mays (m
6	19	27.9	12	10 Q8LPT6	Q8LPT6 zea mays (m
7	19	27.9	13	12 Q9PBX5	Q9PBX5 duck hepatic
8	18	26.5	11	6 Q9TRX0	Q9TRX0 sus scrofa
9	18	26.5	11	7 Q29831	Q29831 homo sapien
10	18	26.5	11	11 P97755	P97755 rattus norv
11	18	26.5	12	4 Q9NTR7	Q9NTR7 homo sapien
12	18	26.5	13	5 Q9TWR4	Q9TWR4 titus serr
13	17	25.0	8	4 Q9P285	Q9P285 homo sapien
14	17	25.0	8	11 Q9GV15	Q9GV15 rattus sp.
15	17	25.0	11	6 P83128	P83128 bos indicus
16	17	25.0	11	13 Q9QWA2	Q9QWA2 gallus gall

17	17	25.0	12	2 Q912U8	Q912U8 acinetobact
18	17	25.0	12	2 Q52112	Q52112 acinetobact
19	17	25.0	12	2 Q8GMV1	Q8GMV1 acinetobact
20	17	25.0	12	2 Q8GMT8	Q8GMT8 acinetobact
21	17	25.0	12	2 Q8GML2	Q8GML2 acinetobact
22	17	25.0	12	10 Q9S918	Q9S918 beta vulgar
23	17	25.0	13	4 Q9UP58	Q9UP58 homo sapien
24	17	25.0	13	7 Q19690	Q19690 homo sapien
25	17	25.0	13	8 Q94RE2	Q94RE2 leptomonas
26	16	23.5	8	13 Q90493	Q90493 eopasaltia
27	16	23.5	9	6 Q9XT05	Q9XT05 macropus ru
28	16	23.5	9	10 Q42452	Q42452 tritricum ae
29	16	23.5	9	10 Q9FSZ2	Q9FSZ2 cicer ariet
30	16	23.5	10	13 Q8L7F5	Q8L7F5 hevea bras
31	16	23.5	10	10 P82938	P82938 hordeum vul
32	16	23.5	10	11 Q9QV57	Q9QV57 mus sp. pro
33	16	23.5	11	5 Q23876	Q23876 dictyosteli
34	16	23.5	11	10 Q19784	Q19784 gossypium h
35	16	23.5	11	11 Q9QVF6	Q9QVF6 mus musculu
36	16	23.5	12	4 Q9UGS1	Q9UGS1 homo sapien
37	16	23.5	12	6 P81127	P81127 bos indicus
38	16	23.5	13	4 Q8WY56	Q8WY56 homo sapien
39	16	23.5	13	10 Q9S8N1	Q9S8N1 hordeum vul
40	15	22.1	7	4 Q15897	Q15897 homo sapien
41	15	22.1	8	11 Q9ET18	Q9ET18 mus spratus
42	15	22.1	8	11 Q9ET17	Q9ET17 mus caroli
43	15	22.1	8	11 Q9ET16	Q9ET16 mesocricetu
44	15	22.1	9	1 Q50832	Q50832 methanococc
45	15	22.1	9	2 P72149	P72149 pseudomonas

#### ALIGNMENTS

RESULT :

```

Q9QZAB
ID Q9QZAB PRELIMINARY; PRT; 9 AA.
AC Q9QZAB:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C-type lectin DC11 (Fragment).
GN DC11
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.;
RT "Dendritic cell regulation of DC11 mRNA expression.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192526; AAF04843.1;
DR MGD; MGI:2136650; Dcl1.
KW Lectin.
FT NON_TER
SQ SEQUENCE 9 AA; 994 MW; 342161ABI72EBAB7 CRC64;

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Query Match 36.8%; Score 25; DB 11; Length 9;  
Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY i CLEGGQ 6  
|||  
Db 4 CLEGG 9

RESULT 2

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Q89243
ID Q89243 PRELIMINARY; PRT; 12 AA.
AC Q89243:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

```

```
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update);
DE Core protein (Fragment).
CS Woodchuck hepatitis B virus.
CC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
CX NCBI_TaxID=35269;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W64;
RX MEDLINE=87219879; PubMed=3582979;
RA Etienne J., Moroy T., Trepo C., Tiollais F., Buchdala M.A.;
RT "Nucleotide sequence of the woodchuck hepatitis virus surface antigen
RNAs and the variability of three overlapping viral genes.";
RC Gene 500:207-214(1986).
DR EMBL; M15954; AAA69576.1; -
DR InterPro; IPR02006; Hepatitis_core.
DR Pfam; PF03906; Hepatitis_core.1.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1388 MW; 22ABC172F2132E47 CRC64;

Query Match 29.4%; Score 20; DB 12; Length 12;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 MDVD 11
DB 1 MDID 4

RESULT 3
Q96P97 PRELIMINARY; PRT; 9 AA.
AC Q96P97;
DT 01 DEC-2001 (TrEMBLrel. 19, Created);
DT 01 DEC-2001 (TrEMBLrel. 19, Last sequence update);
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Reptin52 Protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Kim D.Y., Han T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in C3H/10T1/28 clone 8 ordered
RT differential display PCR."
RL Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401216; AAU02172.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 981 MW; 5CDDAA681A1813 CRC64;

Query Match 27.9%; Score 19; DB 47; Length 9;
Best Local Similarity 60.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQVMD 9
DB 3 GETMD 7

RESULT 4
Q9LPT5 PRELIMINARY; PRT; 9 AA.
AC Q9LPT5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Pnicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (JUL 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094308; AAM21834.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; 5C5B2D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 9;
Best Local Similarity 42.9%; Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 2 KDEVVD 8
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RP SEQUENCE FROM N.A.
RC STRAIN=CV. C123;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094310; AAM21836.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; 5C5B2D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 9;
Best Local Similarity 42.9%; Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 2 KDEVVD 8

RESULT 5
Q8LPT7 PRELIMINARY; PRT; 10 AA.
AC Q8LPT7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Pnicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094308; AAM21834.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1048 MW; 5C5B7D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 3 KDEVVD 9

RESULT 6
Q8LPT6 PRELIMINARY; PRT; 12 AA.
AC Q8LPT6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Pnicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094308; AAM21834.1; -
FT NON_TER 1
SQ SEQUENCE 12 AA; 1048 MW; 5C5B7D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 3 KDEVVD 9
```

RT elite-raize inbred lines";  
 RJ Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY094309; AAM21835.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1260 MW; 5055EDBD451AA3A3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 12;  
 Best Local Similarity 42.9%; Pred. No. 1.e+04; 1; Indels 0; Gaps 0;  
 Matches 3; Conservative 3; Mismatches 0;

QY 3 LEDGQVMD 9  
 DB 5 KODEVVD 11

## RESULT 7

Q9PX85 PRELIMINARY; PRT; 13 AA.

AC Q9PX85  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 170 kDa DHBV pre-S region binding protein (Fragment).  
 OS Duck hepatitis B virus (DHBV).  
 OC Viruses; Retroviridae; Hepadnaviridae; Avihepadnavirus.  
 CX NCBI\_TaxID=12639;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96013813; PubMed=7474130;  
 RA Tong S., Li J., Wands J.R.;  
 RT "Interaction between duck hepatitis B virus and a 170-kilodalton  
 RT cellular protein is mediated through a neutralizing epitope of the pre-  
 RT S region and occurs during viral infection."  
 RL J. Virol. 69:7106-7112(1995).  
 SQ SEQUENCE 13 AA; 1397 MW; DC478FE0149C772 CRC64;

Query Match 27.9%; Score 19; DB 12; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.e+04; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 3; Mismatches 0;

QY 2 LEDGQV 7  
 DB 1 VREGKV 6

## RESULT 8

Q9TRX0 PRELIMINARY; PRT; 11 AA.

AC Q9TRX0  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Lanosterol 14 alpha-demethylase, cytochrome P 45014X (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91316123; PubMed=1859829;  
 RA Sono H., Sonoda Y., Sato Y.;  
 RT "Purification and characterization of cytochrome P 45014X (lanosterol-  
 RT 14 alpha-demethylase) from pig liver microsomes."  
 RL Biochim. Biophys. Acta 1078:388-394(1991).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1084 MW; 8A7ASCBC2AA72661 CRC64;

Query Match 26.5%; Score 18; DB 6; Length 11;  
 Best Local Similarity 44.4%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 QYMDVLDL 13

DB 1 GLLTGLDLL 9

## RESULT 9

Q29831 PRELIMINARY; PRT; 11 AA.

AC Q29831  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gene fragment encoding human histocompatibility antigen HLA-DR alpha  
 DE (exon 2).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83169718; PubMed=6403940;  
 RA Das H.K., Biro P.A., Cohen S.N., Erlich H.A., von Gabain A.,  
 RA Lavrance S.K., Lemaux P.G., McDevitt H.O., Peterlin B.M., Schulz M.F.,  
 RA Sood A.K., Weissman S.M.;  
 RT "Use of synthetic oligonucleotide probes complementary to genes for  
 RT human HLA-DR alpha and beta as extension primers for the isolation of  
 RT 5' specific clones."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1531-1535(1983).  
 DR EMBL; V03525; CAA23784.1;  
 SQ SEQUENCE 11 AA; 1230 MW; 9378714E0865B1EA CRC64;

Query Match 26.5%; Score 18; DB 7; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 1.4e+04; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 3;

QY 1 CLEDGQVW 8  
 DB 3 CDHSGRVL 13

## RESULT 10

P97755 PRELIMINARY; PRT; 11 AA.

AC P97755  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
 DE Secretogranin II (SQII) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96143805; PubMed=8756552;  
 RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;  
 RT "Cell-specific expression of the rat secretogranin II promoter."  
 RL Endocrinology 137:3815-3822(1996).  
 DR EMBL; AF107301; -; NOT\_ANNOTATED\_CDS.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 26.5%; Score 18; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLE 3  
 DB 1 CLE 3

## RESULT 11

Q9NTR7 PRELIMINARY; PRT; 12 AA.

Q9NTR7

```
AC QNTW7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update);
DE D378N1C.1 (Eyes absent (Drosophila) homolog 4) (Fragment);
GN EY44;
CS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Dunn M.;
RL Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL121959; CAB92069.1;
FT NCN TER 12
SQ SEQUENCE 12 AA; 1394 MW; C15EA7952D472AB6 CRC64;

Query Match 26.5%; Score 15; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEDGQ 6
DB : MEDSQ 5

RESULT 12
QNTW4
ID QNTW4 PRELIMINARY; PRT; 13 AA.
AC QNTW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update);
DE Peptide 7-BRADYKININ potentiator;
OS Tityus serrulatus (Brazilian scorpion);
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Eutherozoa; Euthera; Insecta;
OX NCBI_TaxID=6887;
RN [1];
RP SEQUENCE
RX MEDLINE=9424945; PubMed=8212046;
RA Ferreira L.A., Alves E.W., Henriques O.E.;
RC "Peptide T, a novel bradykinin potentiator isolated from Tityus
RT serrulatus scorpion venom.";
RL Toxicon 31:941-947(1993);
FT NON TER 1
SQ SEQUENCE 13 AA; 1694 MW; 3539E90443E230755044

Query Match 26.5%; Score 15; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDGQMDVD 11
DB 2 KGGYPVEYD 10

RESULT 13
Q9P395
ID Q9P285 PRELIMINARY; PRT; 3 AA.
AC Q9P285;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update);
DE Clotting factor VIII (Fragment);
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Shibata M., Shima M., Morichika S., Yoshida A.;
RC "Human clotting factor VIII gene, junction region";
RL Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB040872; BAA34312.1;
FT NCN TER 1
SQ SEQUENCE 3 AA; 866 MW; 1C16987AAB05BDD3 CRC64;
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RT exon 4 through 7.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB040872; BAA34312.1;
FT NCN TER 1
FT NCN TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 25.0%; Score 17; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDG 5
DB 4 EDG 6

RESULT 14
Q9QV15
ID Q9QV15 PRELIMINARY; PRT; 8 AA.
AC Q9QV15;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE 18 kDa cell growth factor (Fragment);
OS Rattus sp.;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE
RX MEDLINE=92028975; PubMed=1656977;
RA Milner P.G.;
RC "Simian sarcoma virus transformation of normal rat kidney fibroblasts
RT is associated with markedly increased basic fibroblast growth factor
RL expression.";
RL Biochem. Biophys. Res. Commun. 180:423-430(1991);
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 907 MW; B0787AAB07673AFA CRC64;

Query Match 25.0%; Score 17; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDG 5
DB 5 EDG 7

RESULT 15
P83129
ID P83129 PRELIMINARY; PRT; 11 AA.
AC P83129;
DT 01-JUN-2002 (TrEMBLrel. 21, Created);
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update);
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE Pregnancy-associated glycoprotein (Fragment);
OS Bos indicus (Zebu);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos;
OX NCBI_TaxID=9915;
RN [1];
RP SEQUENCE, AND GLYCOSYLATION.
RC TISSUE=Placenta;
RA Sousa N.M., Remy B., El Amri B., Figueiredo J.R., Beckers J.F.;
RC "Characterization of pregnancy-associated glycoproteins extracted from
RT zebu (Bos indicus) placentas removed at different gestational
RT periods.";
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- EFM: GLYCOSYLATED.
KW Glycoprotein;
FT NCN TER 1; 11
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SO SEQUENCE 11 AA; 1234 MW; CE8EA47EA0586B5D CRC64;  
Query Match: 25.0%; Score 17; DB 6; Length 11;  
Best Local Similarity 30.0%; Pred. No. 2.1e+04;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 4 DGQVMDVLL 13  
Lh 1 DKNAVIGDL 10

Search completed: November 5, 2003, 18:03:38  
Job time : 29.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:56:03 ; Search time 34.5 Seconds  
(without alignments)  
59.810 Million cell updates/sec

Title: US-09-914-088-8

Perfekt score: 68

Sequence: 1 CLFDQGVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 299364

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	13	21 AAB20872	Antiallergy peptid
2	68	100.0	13	21 AAB25914	PI mimotope peptid
3	68	100.0	13	22 AAU16639	Peptide P15 deriv
4	68	100.0	13	22 AAB51028	IgE peptide #6. M
5	68	100.0	13	23 AABJ00224	Human IgE immunoge
6	64	94.1	13	21 AABJ00224	PI mimotope peptid
7	64	94.1	13	22 AABJ00224	Peptide P15q deriv
8	64	94.1	13	22 AABJ00224	Human IgE cyclic i
9	55	80.9	13	21 AAB25916	PI mimotope peptid

10	55	80.9	13	22 AAU16641	Peptide P15p deriv
11	55	80.9	13	23 AABJ00226	Human IgE immunoge
12	51	75.0	10	21 AAB25929	PI mimotope peptid
13	51	75.0	10	22 AAU16654	Peptide P15t deriv
14	51	75.0	10	23 AABJ00228	Human IgE immunoge
15	50	73.5	13	23 AABJ00541	Human IgE cyclic i
16	47	69.1	9	21 AAB20867	Immunoglobulin E
17	47	69.1	9	21 AAB25907	IgE C-epsilon-2 do
18	47	69.1	9	22 AAU16632	Peptide P1 derived
19	47	69.1	9	22 AAB51023	IgE peptide #1. M
20	47	69.1	9	23 AABJ00217	Human IgE immunoge
21	45	66.2	10	24 AABJ00507	Immunoglobulin E (
22	35	51.5	9	24 AABJ00509	Human immunoglobul
23	34	50.0	7	21 AAB25923	PI mimotope peptid
24	34	50.0	7	22 AAU16648	Peptide P15s deriv
25	34	50.0	7	23 AABJ00227	Human IgE immunoge
26	34	50.0	9	24 AABJ00506	Human immunoglobul
27	34	50.0	10	24 AABJ00506	Immunoglobulin E (
28	33	48.5	11	21 AAB26010	Peptide ESB1/6etc
29	33	48.5	11	22 AAU16735	Human IgE C-epsilon
30	33	48.5	11	23 AABJ00265	Human CYP3A4 speci
31	31	45.6	11	19 AAB84026	Human immunoglobul
32	30	44.1	9	24 AABJ00510	Human CYP3A4 speci
33	30	44.1	12	21 AAB25949	Human immunoglobul
34	30	44.1	12	21 AAB26040	PI mimotope (PTmAb
35	30	44.1	12	22 AAU16674	Human IgE C-epsilon
36	30	44.1	12	22 AAU16765	Peptide #15 derive
37	30	44.1	12	23 AABJ00337	Peptide EED147/173
38	30	44.1	12	23 AABJ00386	Human IgE cyclic i
39	29	42.6	9	24 AABJ00386	Human IgE cyclic i
40	29	42.6	10	22 AABJ00386	Human immunoglobul
41	29	42.6	10	22 AABJ00386	Arabidopsis thalia
42	28	41.2	7	23 AABJ00386	Arabidopsis thalia
43	28	41.2	9	23 AABJ00386	Oplophorus gracili
44	28	41.2	10	23 AABJ00386	Human 125p5C8 epit
45	28	41.2	10	23 AABJ00386	Cobra CVF1 factor
					Selective targetin

#### ALIGNMENTS

RESULT 1  
AAB20872  
ID AAB20872 standard; peptide; 13 AA.  
XX  
AC AAB20872;  
XX  
DT 03-JAN-2001 (first entry)  
XX  
DE Antiallergy peptide mimotope sequence SEQ ID NO:10.  
XX  
IM Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;  
XX  
KM prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
XX  
KW malaria; cytotoxic; antiallergic; nontropic; neuroprotective;  
XX  
KW protozoacide; Alzheimer's disease; allergy.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Modified-site 13  
FT Location/Qualifiers /note= "amidated"  
XX  
FN WO2000050077-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 22-FEB-2000; 2003WO-EP01457.  
XX  
PR 25-FEB-1999; 99GB-0004405.  
XX  
PR 25-FEB-1999; 99GB-0004408.  
XX  
PR 25-FEB-1999; 99GB-0004412.  
XX  
PR 13-AUG-1999; 99GB-0019260.  
XX





PA (ACNM-) ACNYS RES LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PI P:inn N, Johnson T;  
 XX WPI; 2001-521967/57.  
 DR  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases -  
 XX  
 XX Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins); to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 100.0%; Score 68; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEDGQVMDVLL 13  
 |||||  
 DB 1 CLEDGQVMDVLL 13  
 |||||

RESULT 4  
 AAB51028  
 ID AAB51028 standard; Peptide; 13 AA.  
 XX  
 AC AAB51028;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE IgE peptide #6.  
 XX  
 KW Vaccine; immunoglobulin E; IgE; anti-allergy.  
 XX  
 CS Mammalia.  
 XX  
 PN WC200074716-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 06 JUN-2000; 2000WO-EP05164.  
 XX  
 PR 08-JUN-1999; 99GB-0013327.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Priee's J;  
 XX  
 DR WPI; 2001-091150/10.  
 XX  
 CC New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual  
 PT susceptible to an allergic response  
 XX  
 XX Claim 5; Page 20; 26pp; English.

XX  
 CC The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 CC such peptide from IgE. The composition is useful as a vaccine or for  
 CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 100.0%; Score 68; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEDGQVMDVLL 13  
 |||||  
 DB 1 CLEDGQVMDVLL 13  
 |||||

RESULT 5  
 AABJ00224  
 ID AABJ00224 standard; Peptide; 13 AA.  
 XX  
 AC AABJ00224;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 8.  
 XX  
 KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; antiallergic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216409-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EP09576.  
 XX  
 PR 22-AUG-2000; 2000GB-0020717.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Friede M, Mason S, Turnell WG, Vinals Bassols VC;  
 XX  
 DR WPI; 2002-489648/52.  
 XX  
 PT Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier -  
 XX  
 PS Claim 4; Page 9; 45pp; English.  
 XX  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulphide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 100.0%; Score 68; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEDGQVMDVLL 13  
 |||||  
 DB 1 CLEDGQVMDVLL 13  
 |||||

RESULT 6

AAB25917  
 ID AAB25917 standard; Peptide; 13 AA.  
 XX  
 AC AAB25917;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE P1 mimotope peptide P15q SEQ ID NO:11.  
 XX  
 KW Epitope; micropeptide; human; immunoglobulin E (IgE); Cepsilon 2 domain;  
 KW allergic disease; immunoprophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200050460-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 22-FEB-2000; 2000WO-EP01455.  
 XX  
 PR 25-FEB-1999; 99GB-0004405.  
 PR 29-MAR-1999; 99GB-0007151.  
 PR 07-MAY-1999; 99GB-0010537.  
 PR 07-MAY-1999; 99GB-0010538.  
 PR 07-AUG-1999; 99GB-0018594.  
 PR 07-AUG-1999; 99GB-0018603.  
 PR 07-SEP-1999; 99GB-0021046.  
 PR 07-SEP-1999; 99GB-0021047.  
 PR 23-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dwyer M, Fricke M, Greenwood J, Hewitt E, Lambert A, Mason S;  
 PI Randall P, Turnell WG, Van Mechelen MP, Vinals G, Bassols JC;  
 XX  
 WP 2000-572073/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 14; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a protein, a polypeptide, a peptide or an isolated  
 CC surface exposed group/epitope (PI) of a protein, a polypeptide, a peptide or an  
 CC immunoglobulin E (IgE), or its mimotope. Also, the invention describes a  
 CC immunogen (II) for treating allergy comprising (i) a vaccine (III)  
 CC for treating allergies comprising (iii); (iv) a mimic (IV); capable of  
 CC recognising E1; (4) a pharmaceutical composition (V) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (III) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of P1.  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (I) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25917 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 94.1%; Score 64; DP 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00059;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVCL 12  
 DB : CLEGGQVMDVCL 12  
 RESULT 7  
 AAU16642  
 ID AAU16642 standard; Peptide; 13 AA.  
 XX  
 AC AAU16642;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Peptide P15q derived as mimotope of Cepsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0220145745-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 21-DEC-2000; 2000WO-GB04935.  
 XX  
 PR 21-DEC-1999; 99GB-0030231.  
 PR 22-FEB-2000; 2000GB-0004096.  
 PR 22-AUG-2000; 2000GB-0020707.  
 PR 22-AUG-2000; 2000GB-0020708.  
 XX  
 PA (ACAM) ACAMBI RES LTD.  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Flinn N, Johnson T;  
 XX  
 WP 2801-521967/57.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 XX  
 PS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce a  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 94.1%; Score 64; DP 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00059;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVCL 12  
 DB : CLEGGQVMDVCL 12

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RESULT 8.
ID ABJ00312 standard; Peptide; 13 AA.
XX AC ABJ00312;
XX DT 02-SEP-2002 (first entry)
XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 9a.
XX KW immunogen; human; IgE; immunoglobulin E; allergy; three other linkage;
XX KW vaccine; antiallergic; cyclic.
XX OS Homo sapiens.
XX PN WO200216439-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-EP09576.
XX PR 22-AUG-2000; 2000GB-0020717.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;
XX WI; 2002-489648/52.
XX PT Conjugate for use in vaccine for treatment of allergy, comprises
XX PT disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 11; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a cyclic peptide immunogen derived
XX CC from human immunoglobulin E (IgE) suitable for use in the invention.
XX SQ Sequence 13 AA;
Query Match 94.1%; Score 64; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLERGGQVMDVDL 12
Db 1 CLERGGQVMDVDL 12
RESULT 9
ID AAB25916 standard; Peptide; 13 AA.
XX AC AAB25916;
XX DT 05-JAN-2001 (first entry)
XX DE P1 mimotope peptide P15p SEQ ID NO: 10.
XX KW Epitope; mimotope; human; immunoglobulin E; IgE; C epsilon 2 domain;
XX KW allergic disease; immunoprophylaxis; immunotherapy; antiallergic;
XX KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX KW allergy; atopy.
XX OS Homo sapiens.
XX PN WC2000050460 A1.
XX PD 31-AUG-2000.
XX PF 22-FEB-2000; 2000WO-EP01455.
XX PR 25-FEB-1999; 99GB-0004405.
XX PR 29-MAR-1999; 99GB-0007151.
XX PR 07-MAY-1999; 99GB-0010517.
XX PR 07-MAY-1999; 99GB-0010518.
XX PR 07-AUG-1999; 99GB-0018594.
XX PR 07-AUG-1999; 99GB-0018603.
XX PR 07-SEP-1999; 99GB-0021046.
XX PR 29-SEP-1999; 99GB-0021047.
XX PR 29-OCT-1999; 99GB-0025619.
XX PR 23-NOV-1999; 99GB-0027698.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX WI; 2000-572073/53.
XX PT Peptides useful for treating, preventing and ameliorating allergic
XX PT diseases, comprising an isolated surface exposed group of a specific
XX PT domain from immunoglobulin E.
XX PS Disclosure; Page 9; 129pp; English.
XX CC The present invention describes a peptide (I) comprising an isolated
XX CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of
XX CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
XX CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
XX CC for treating allergies comprising (II); (3) a ligand (IV) capable of
XX CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);
XX CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
XX CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (7)
XX CC can have antiallergic and immunosuppressive activities, and can be used
XX CC as a vaccine and histamine release inhibitor. (1), (II) and (III) are
XX CC useful in medicine and in the manufacture of medicaments for treating
XX CC and preventing allergies. (IV) is useful for identifying mimotopes of P1,
XX CC in medicine and also in manufacturing medicaments for treating
XX CC allergies. (I) is useful in diagnostics and in the affinity purification
XX CC of circulating anti-IgE antibodies from blood. (I), (II) and (III) are
XX CC useful for treating a patient susceptible to or suffering from allergies.
XX CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
XX CC peptide sequences which are used in the exemplification of the present
XX CC invention.
XX SQ Sequence 13 AA;
Query Match 90.9%; Score 55; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LEDGGQVMDVDL 12
Db 2 LEDGGQVMDVDL 12
RESULT 10
AAU1664;
ID AAU16641 standard; Peptide; 13 AA.
XX AC AAU1664;
XX DT 07-NOV-2001 (first entry)
XX DE Peptide P15p derived as mimotope of Cepsilon2 region of human IgE.
XX KW Human; linkage technology; conjugated compound; carrier vehicle;
XX KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;
XX KW IgE mediated disease; antibody response.
XX OS Homo sapiens.

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OS Synthetic.
XX PN W0200145745-A2.
XX PC 28 JUN-2002.
XX PF 21-FEB-2000; 2000WC GR04935.
XX PP 21-FEB-1999; 99GB-C030233.
XX PR 22-FEB-2000; 2000GB-C004036.
XX PS 22-AUG-2000; 2000GB-C020752.
XX PT 22-AUG-2000; 2000GB-C020758.
XX PA (ACAM:) ACAMBIS RES LTD.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Ffynn N. Johnson T;
XX PS WPI: 2001-521947/57.
XX PT A linkage comprising an immunogenic conjugate useful treatment of IgE
XX PT mediated diseases.
XX PS Example 4; Page 21; 49pp; English.
XX CC The present invention relates to linkage methodology for use in the
XX CC conjugation of compounds (e.g. peptides) to carrier vehicles
XX CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX CC biological and immunological constructs. The invention provides a
XX CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX CC protein) for use in a pharmaceutical composition or a vaccine. The
XX CC invention describes peptides derived from or mimotopes of the
XX CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E
XX CC (IgE) which are used to produce conjugated compounds. The compounds or
XX CC compositions of the invention are useful in the manufacture of a
XX CC medicament for the treatment of IgE-mediated diseases. The invention
XX CC allows for controlled conjugation of a peptide epitope (antigen) to a
XX CC protein so as to form an immunogenic conjugate which may be able to
XX CC raise a protective antibody response in an animal or human patient.
XX CC AAL16632-AAL16913 represent peptides derived from C1 mimotopes of
XX CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
XX PS Sequence 13 AA;
XX CC
XX CC Query Match 80.9%; Score 55; DB 22; Length 12;
XX CC Best Local Similarity 100.0%; Fred. No. 0.018;
XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 LEDGQVMDVL 12
XX CC |||||
XX CC Db 2 LEDGQVMDVL 12
XX CC |||||
XX CC
XX CC RESULT 12
XX CC AAB25929
XX CC ID AAB25929 standard; Peptide: 10 AA.
XX CC
XX CC AC AAB25929;
XX CC
XX CC DT C5-JAN-2001 (first entry)
XX CC
XX CC DE P1 mimotope peptide P1st SEQ ID NO:23.
XX CC
XX CC KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX CC allergic disease; immunophylaxis; immunotherapy; anti-allergic;
XX CC immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX CC allergy; atopy.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN W0200150450-A1.
XX CC
XX CC PD 31-AUG-2000.
XX CC
XX CC PF 22-FEB-2000; 2000WC-EP01455.
XX CC
XX CC PR 25-FEB-1999; 99GB-C004425.
XX CC PR 29-MAR-1999; 99GB-C007151.
XX CC PR 07-MAY-1999; 99GB-C010537.
XX CC PR 07-MAY-1999; 99GB-C010538.
XX CC PR 07-AUG-1999; 99GB-C018594.
XX CC PR 07-AUG-1999; 99GB-C018603.
XX CC PR 07-SEP-1999; 99GB-C021046.
XX CC PR 07-SEP-1999; 99GB-C021047.
XX CC PR 29-OCT-1999; 99GB-0025619.
XX CC PR 23-NOV-1999; 99GB-C027698.
XX CC
XX CC PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX CC (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX CC
XX CC Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX CC Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX CC WPI: 2000-572074/53.

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XX 22-AUG-2000; 2000GB-C020717.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;
XX
XX WPI: 2002-489648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy, comprises
XX PT disulfide bridge cyclised peptide and immunogenic carrier.
XX
XX PS Claim 4; Page 9; 45pp; English.
XX
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a peptide immunogen derived from human
XX CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX PS Sequence 13 AA;
XX CC
XX CC Query Match 80.9%; Score 55; DB 23; Length 13;
XX CC Best Local Similarity 100.0%; Fred. No. 0.018;
XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 LEDGQVMDVL 12
XX CC |||||
XX CC Db 2 LEDGQVMDVL 12
XX CC |||||
XX CC
XX CC RESULT 12
XX CC AAB25929
XX CC ID AAB25929 standard; Peptide: 10 AA.
XX CC
XX CC AC AAB25929;
XX CC
XX CC DT C5-JAN-2001 (first entry)
XX CC
XX CC DE P1 mimotope peptide P1st SEQ ID NO:23.
XX CC
XX CC KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX CC allergic disease; immunophylaxis; immunotherapy; anti-allergic;
XX CC immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX CC allergy; atopy.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN W0200150450-A1.
XX CC
XX CC PD 31-AUG-2000.
XX CC
XX CC PF 22-FEB-2000; 2000WC-EP01455.
XX CC
XX CC PR 25-FEB-1999; 99GB-C004425.
XX CC PR 29-MAR-1999; 99GB-C007151.
XX CC PR 07-MAY-1999; 99GB-C010537.
XX CC PR 07-MAY-1999; 99GB-C010538.
XX CC PR 07-AUG-1999; 99GB-C018594.
XX CC PR 07-AUG-1999; 99GB-C018603.
XX CC PR 07-SEP-1999; 99GB-C021046.
XX CC PR 07-SEP-1999; 99GB-C021047.
XX CC PR 29-OCT-1999; 99GB-0025619.
XX CC PR 23-NOV-1999; 99GB-C027698.
XX CC
XX CC PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX CC (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX CC
XX CC Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX CC Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX CC WPI: 2000-572074/53.

```

XX Peptides useful for treating, preventing and ameliorating allergic  
PT Diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E -  
XX  
XX  
PS Disclosure; Page 9; 129pp; English.  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (i), (2) a vaccine (III)  
CC for treating allergies comprising (II), (3) a ligand (IV) capable of  
CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
CC (Iia) comprising (Ia), and (7) producing (III) by producing (II). (I)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies. (I) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood. (II), (III) and PC are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. AAH25307 to AAH26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 10 AA;  
Query Match 75.0%; Score 51; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 10; Conservative C; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEDGQVMVDV 11  
DB 1 LEDGQVMVDV 10  
RESULT 13  
AAU16654  
ID AAU16654 standard; Peptide; 10 AA.  
AC AAU16654;  
XX  
XX 07-NOV-2001 (first entry)  
XX Peptide P13: derived as mimotope of Cepsilon2 domain of human IgE.  
XX Human; linkage technology; conjugated compound; carrier vehicle;  
KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E.  
KW IgE mediated disease; antibody response.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS WC200145745-A2.  
XX  
XX 28-JUN-2001.  
XX  
XX 21-DEC-2000; 2000WO-GB04935.  
XX  
XX 21-DEC-1999; 99GB-0030233.  
PR 22-FEB-2000; 2000GB-0004096.  
PR 22-AUG-2000; 2000GB-0020707.  
PR 22-AUG-2000; 2000GB-0020708.  
XX  
XX (ACAV-) ACAMBIS RES LTD.  
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX F.irm N, Johnson, T;  
XX WPI; 2001-521967/57.  
XX

PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases -  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
CC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimotopes of the  
CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
CC (IgE) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IgE mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope (antigen) to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
XX  
SQ Sequence 10 AA;  
Query Match 75.0%; Score 51; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEDGQVMVDV 11  
DB 1 LEDGQVMVDV 10  
RESULT 14  
ABJ00228  
ID ABJ00228 standard; Peptide; 10 AA.  
AC ABJ00228;  
XX  
XX 02-SEP-2002 (first entry)  
XX Human IgE immunogenic peptide SEQ ID NO: 12.  
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic.  
XX Homo sapiens.  
OS WO200016409-A2.  
PN  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EP09576.  
XX  
XX 22-AUG-2000; 2000GB-3020717.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-); PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX WPI; 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier -  
XX  
XX Claim 4; Page 9; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
CC

```

XX SQ Sequence 10 AA:
Query Match 75.0%; Score 51; DB 24; Length 10;
Best local Similarity 100.0%; Pred. NO. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKDGQWMD 11
   |||||
DB 1 LKDGQWMD 10

RESULT 15
AB020541
ID AB020541 standard; Peptide; 10 AA.
XX AC AB020541;
XX DT 02-SEP-2002 (first entry)
XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 115.
XX EE Immunogen; human; IgE; immunoglobulin E; allergy; thio ether linkage;
XX FF vaccine; anti-allergic; cyclic.
XX GS Homo sapiens.
XX HN WP000216409-A2.
XX ID 29-SEP-2002.
XX EE 17 AUG-2001; 2001WO-EP09576.
XX EE 22-AUG-2000; 2000GB 0020717.
XX EE (SMR) SYNTHESINE BEECHAM BIOLOGICALS.
XX EE (PDB) PEPTIDE THERAPEUTICS LTD
XX EE Friede M, Mason S, Turnell WJ, Vinals Bassalis YJ.
XX EE WPI: 2001 409648/52.
XX EE Conjugate for use in vaccine for treatment of allergy, comprises
XX EE disulfide bridge cyclized peptide and immunogenic carrier.
XX EE Claim 4; Page 16; 45pp; English.
XX EE The present invention relates to conjugates of a cyclic peptide in vaccines,
XX EE where the conjugate comprises a disulfide bridge cyclized peptide and an
XX EE immunogenic carrier. The vaccine can be used in the treatment of
XX EE allergies. The present sequence is a cyclic peptide conjugate derived
XX EE from human immunoglobulin E (IgE) suitable for use in the invention.
XX SQ Sequence 10 AA:
Query Match 73.5%; Score 50; DB 23; Length 10;
Best local Similarity 100.0%; Pred. NO. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKDGQWMD 9
   |||||
DB 1 LKDGQWMD 9

Search completed: November 5, 2003, 18:01:56
CPU time : 34.5 secs

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OX protein - protein search, using sw model

Run on: November 5, 2003, 19:03:44 ; Search time 22 seconds  
(without alignments)  
101.488 Million cell updates/sec

Title: US-09-914-088-8  
Perfect score: 68  
Sequence: 1 CLEGGQVMDVDLL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 segs, 171749292 residues

Total number of hits satisfying chosen parameters: 99933

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/2/pubaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/2/pubaa/US07\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*  
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18: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by the search to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	72.1	10	12	US-10-082-014-282
2	49	72.1	10	12	US-10-372-076-136
3	47	69.1	9	12	US-10-082-014-273
4	47	69.1	9	12	US-10-372-076-127
5	45	66.2	10	12	US-10-144-188-55
6	34	50.0	10	12	US-10-144-188-60
7	29	42.6	10	12	US-09-572-270A-1084
8	29	42.6	10	12	US-09-572-270A-1086
9	28	41.2	7	10	US-09-842-164-12
10	28	41.2	10	10	US-09-925-442-1
11	27	39.7	13	11	US-09-862-151-1
12	26	38.2	10	11	US-09-572-404B-2983
13	25.5	37.5	12	11	US-09-922-568-4
14	25	36.8	10	15	US-10-155-922-72
15	25	36.8	11	11	US-09-863-049A-77

Sequence 11, Appl  
Sequence 2, Appl1  
Sequence 6, Appl1  
Sequence 10, Appl  
Sequence 14, Appl  
Sequence 18, Appl  
Sequence 22, Appl  
Sequence 434, Appl  
Sequence 556, Appl  
Sequence 475, Appl  
Sequence 475, Appl  
Sequence 502, Appl  
Sequence 613, Appl  
Sequence 502, Appl  
Sequence 613, Appl  
Sequence 8, Appl1  
Sequence 22, Appl  
Sequence 1418, Appl  
Sequence 47, Appl  
Sequence 55, Appl  
Sequence 20, Appl  
Sequence 1189, Appl  
Sequence 535, Appl  
Sequence 633, Appl  
Sequence 458, Appl  
Sequence 591, Appl  
Sequence 102, Appl  
Sequence 196, Appl  
Sequence 504, Appl  
Sequence 163, Appl

## ALIGNMENTS

RESULT 1  
US-10-082-014-282  
; Sequence 282, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4364/85124  
; CURRENT APPLICATION NUMBER: US/10/082.014  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 282  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-282

Query Match 72.1%, Score 49; DB 12; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.03;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LEDGQVMDVD 11  
Db 1 MEDGQVMDVD 10

RESULT 2  
US-10-372-076-136  
; Sequence 136, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS



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? FILE REFERENCE: 4564/87179
? CURRENT APPLICATION NUMBER: US/10/372,076
? CURRENT FILING DATE: 2003-02-21
? PRIOR APPLICATION NUMBER: 10/080,299
? PRIOR FILING DATE: 2002-02-21
? PRIOR APPLICATION NUMBER: 10/082,014
? PRIOR FILING DATE: 2002-02-22
? NUMBER OF SEQ ID NOS: 308
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 136
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-372-076 136
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Query Match 72.1%; Score 49; DB 12; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0%;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 LEDGQVMDVD 11
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Db 1 MEDGQVMDVD 10
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RESULT 3
US-10-082-014-273
? Sequence 273, Application US/10082014
? Publication No. US2003018588A1
? GENERAL INFORMATION:
? APPLICANT: Barker, Ashley J.
? TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
? FILE REFERENCE: ICC-130.0 4564/85124
? CURRENT APPLICATION NUMBER: US/10/082,014
? CURRENT FILING DATE: 2002-02-22
? PRIOR APPLICATION NUMBER: 09/930,915
? PRIOR FILING DATE: 2001-08-15
? NUMBER OF SEQ ID NOS: 290
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 273
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-082-014-273
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Query Match 69.1%; Score 47; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 0.0%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EDGQVMDVD 11
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Db 1 EDGQVMDVD 9
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RESULT 4
US-10-372-076-127
? Sequence 127, Application US/10372076
? Publication No. US20030196645A1
? GENERAL INFORMATION:
? APPLICANT: Paule, Mark
? APPLICANT: Fiedler, Martin
? TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
? FILE REFERENCE: 4564/87179
? CURRENT APPLICATION NUMBER: US/10/372,076
? CURRENT FILING DATE: 2003-02-21
? PRIOR APPLICATION NUMBER: 10/380,299
? PRIOR FILING DATE: 2002-02-21
? PRIOR APPLICATION NUMBER: 10/082,014
? PRIOR FILING DATE: 2002-02-22
? NUMBER OF SEQ ID NOS: 308
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 127
? LENGTH: 9
? TYPE: PRT
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? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-372-076-127
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Query Match 69.1%; Score 47; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 EDGQVMDVD 11
   :|:|||||
Db 1 EDGQVMDVD 9
```

```
RESULT 5
US-10-144-188-55
? Sequence 55, Application US/10144188
? Publication No. US20030170212A1
? GENERAL INFORMATION:
? APPLICANT: Cai, Zeling
? APPLICANT: Jackson, Michael R.
? APPLICANT: Peterson, Per A.
? APPLICANT: Shi, Weixing
? APPLICANT: Kong, Yan
? APPLICANT: Degraw, Juli
? TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specif
? FILE REFERENCE: PR10010 ORT-1627
? CURRENT APPLICATION NUMBER: US/10/144,188
? CURRENT FILING DATE: 2002-05-13
? PRIOR APPLICATION NUMBER: 60/291,300
? PRIOR FILING DATE: 2001-05-15
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 55
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Peptide antigen
US-10-144-188-55
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Query Match 66.2%; Score 45; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 LEDGQVMDVD 10
   :|:|||||
Db 2 LEDGQVMDVD 10
```

```
RESULT 6
US-10-144-188-60
? Sequence 60, Application US/10144188
? Publication No. US20030170212A1
? GENERAL INFORMATION:
? APPLICANT: Cai, Zeling
? APPLICANT: Jackson, Michael R.
? APPLICANT: Peterson, Per A.
? APPLICANT: Shi, Weixing
? APPLICANT: Kong, Yan
? APPLICANT: Degraw, Juli
? TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specif
? FILE REFERENCE: PR10010 ORT-1627
? CURRENT APPLICATION NUMBER: US/10/144,188
? CURRENT FILING DATE: 2002-05-13
? PRIOR APPLICATION NUMBER: 60/291,300
? PRIOR FILING DATE: 2001-05-15
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 60
? LENGTH: 10
? TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144 188-60

Query Match          50.0%; Score 34; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GQVMDVD 12
DB 1 GQVMDVD 7

RESULT 7
US-09-572-270A-1084
; Sequence 1084, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572.270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1084
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in (AVA-P1 CR T4:20,300) AND AVA-P2
US-09-572-270A-1084

Query Match          42.6%; Score 29; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 2 GQVLEVD 8

RESULT 8
US-09-572-270A-1086
; Sequence 1086, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572.270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1086
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in (AVA-P1 CR T4:20,300) AND AVA-P2
US-09-572-270A-1086

Query Match          42.6%; Score 29; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 3 GQVLEVD 9

RESULT 9
US-09-842-164-12
; Sequence 12, Application US/09842164
```

```
; Patent No. US20020102687A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Satoshi
; TITLE OF INVENTION: Luciferase and Photoprotein
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842.164
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JAPAN 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Oplophorus gracilirostris
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(7)
; OTHER INFORMATION: PRT, 35 kDa protein, partial
US-09-842-164-12

Query Match          41.2%; Score 28; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 5.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 1 GQVMDMD 7

RESULT 10
US-09-925-442-3
; Sequence 3, Application US/09925442
; Patent No. US20020103346A1
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; BREDEHORST, REINHORST
; KOCK, MICHAEL
; FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/925.442
; FILING DATE: 10-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/017,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US 09-925 442-3

Query Match 41.2%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EDGQVMDVL 12
DB 1 EDGFIADSL 10

RESULT 11
US-09-862-151-1
; Sequence 1, Application US/0986215;
; Publication No. US20030092746A;
; GENERAL INFORMATION:
; APPLICANT: Hagmann, William K.
; APPLICANT: DeLaszlo, Stephen E.
; APPLICANT: Kamerecka, Theodore
; APPLICANT: MacCoss, Malcolm
; TITLE OF INVENTION: SUBSTITUTED AMINO ACID DERIVATIVES AS
; TITLE OF INVENTION: INHIBITORS OF CELL ADHESION
; FILE REFERENCE: 23688
; CURRENT APPLICATION NUMBER: US/09/862,151
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/206,181
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-151-1

Query Match 39.7%; Score 27; DB 11; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QEDGGQMDV 10
DB 1 QHHPLELV 10

RESULT 12
US-09-572-404B-2983
; Sequence 2983, Application US/09572404B
; Publication No. US20010078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 2983
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in GUYVED OR GUYED OR KED-1 OR RETOC OR GUCIA4
; OTHER INFORMATION: CORP6 at 314-323 and may interact with sequence 2984 in this pate
US 09-572-404B 2983

Query Match 38.2%; Score 26; DB 11; Length 10;
Best Local Similarity 44.4%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QEDGGQMD 9
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DB 2 CPSEGSVID 10

RESULT 13
US-09-922-568-2
; Sequence 2, Application US/09922568
; Publication No. US20030049842A1
; GENERAL INFORMATION:
; APPLICANT: Barot, U. et al.
; TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS WITH GRADED
; TRANSCRIPTIONAL POTENTIAL
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,568
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,027
; FILING DATE: 23-May-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: BBI 088CPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-922-568-2

Query Match 37.5%; Score 25.5; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 2 QEDGGVMDVL 13
DB 4 QEDGS...DLVL 12

RESULT 14
US-10-155-922-72
; Sequence 72, Application US/10155922
; Publication No. US20030086891A1
; GENERAL INFORMATION:
; APPLICANT: Hira, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hakari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPETIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 4673920022
; CURRENT APPLICATION NUMBER: US/10/155,922
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;; CURRENT FILING DATE: 2002-05-23  
;; PRIOR APPLICATION NUMBER: PCT/JP01/0469;  
;; PRIOR FILING DATE: 2001-06-04  
;; PRIOR APPLICATION NUMBER: JP 2000-166903  
;; PRIOR FILING DATE: 2000-06-05  
;; PRIOR APPLICATION NUMBER: JP 2001-347340  
;; PRIOR FILING DATE: 2001-11-13  
;; PRIOR APPLICATION NUMBER: JP 2001-347338  
;; PRIOR FILING DATE: 2001-11-13  
;; PRIOR APPLICATION NUMBER: JP 2001-171175  
;; PRIOR FILING DATE: 2001-12-05  
;; PRIOR APPLICATION NUMBER: JP 2001-371366  
;; PRIOR FILING DATE: 2001-12-05  
;; NUMBER OF SEQ ID NOS: 156  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 72  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Construct  
;; NAME/KEY: VARIANT  
;; LOCATION: 7  
;; OTHER INFORMATION: Xaa - Any Amino Acid  
US 10-155-922-72

Query Match 36.8%; Score 25; DB 11; Length 11;  
Best Local Similarity 80.0%; Pred. NC 4.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 CLEGG 5  
DB 6 CXEDG 10

RESULT 15  
US-03-863 049A-77  
;; Sequence 77, Application US/09863049A  
;; Publication No. US2003032055A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kerwick, Sue J.  
;; APPLICANT: Nelson, David L.  
;; APPLICANT: Aradhya, Swaroop  
;; APPLICANT: D'Urso, Michele  
;; APPLICANT: Wolfendin, Hayley  
;; APPLICANT: Munnich, Arnold  
;; APPLICANT: Smahi, Asmae  
;; APPLICANT: Israel, Alain  
;; APPLICANT: Poustka, Annemarie  
;; APPLICANT: Lewis, Richard A  
;; APPLICANT: Levy, Moise  
;; APPLICANT: Heiss, Nina  
;; TITLE OF INVENTION: Diagnosis and Treatment of Mutual Conditions Associated with Des  
;; FILE REFERENCE: HO-201961US1  
;; CURRENT APPLICATION NUMBER: US/09/863,049A  
;; CURRENT FILING DATE: 2001-05-22  
;; PRIOR APPLICATION NUMBER: US 60/206,223  
;; PRIOR FILING DATE: 2000-05-22  
;; NUMBER OF SEQ ID NOS: 77  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 77  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Human  
US-03-863 049A-77

Query Match 36.8%; Score 25; DB 11; Length 11;  
Best Local Similarity 66.7%; Pred. NC 4.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 CLEGG 6

Db  
4 CLEGG 9

Search completed: November 5, 2003, 18:11:58  
Job time : 23 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 18:30:39 : Search time 14 Seconds  
(without alignments)  
39.289 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: 1 CLEGGQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 11:645

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A-COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PTCUS-COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	45.6	11	4	US-09-057-897-13
2	28	41.2	7	4	US-09-042-164A-10
3	28	41.2	10	1	US-08-447-411-46
4	28	41.2	10	2	US-08-662-227-3
5	29	41.2	10	4	US-09-017-947-3
6	28	41.2	13	2	US-08-162-081B-13
7	28	41.2	13	2	US-08-780-872-13
8	28	41.2	13	3	US-09-085-957-13
9	27	39.7	8	4	US-09-057-937-15
10	27	39.7	10	2	US-08-724-548-28
11	27	39.7	10	2	US-08-724-548-23
12	27	39.7	10	3	US-07-978-674B-28
13	27	39.7	10	3	US-07-978-674B-29
14	27	39.7	12	3	US-09-238-438-8
15	27	39.7	13	4	US-09-341-435-57
16	26	38.2	8	1	US-08-571-985-20
17	26	38.2	8	2	US-09-116-766-20
18	26	38.2	11	3	US-07-861-458C-110
19	25.5	37.5	12	3	US-08-888-082A-2
20	25.5	37.5	12	3	US-08-257-781-9
21	25.5	37.5	12	3	US-09-577-027-2
22	25.5	37.5	12	5	PCT-US95-07157-9
23	25	36.8	8	1	US-08-571-985-26
24	25	36.8	8	2	US-09-116-766-26
25	25	36.8	10	4	US-08-398-852B-6
26	25	36.8	12	2	US-08-617-929-32
27	24	35.3	8	4	US-09-127-815D-2

28	24	35.3	8	4	US-09-127-815D-6	Sequence 6, Appl
29	24	35.3	8	4	US-09-127-815D-10	Sequence 10, Appl
30	24	35.3	8	4	US-09-127-815D-14	Sequence 14, Appl
31	24	35.3	8	4	US-09-127-815D-18	Sequence 18, Appl
32	24	35.3	8	4	US-09-127-815D-22	Sequence 22, Appl
33	24	35.3	9	3	US-09-371-710-25	Sequence 25, Appl
34	24	35.3	9	3	US-09-648-386-25	Sequence 25, Appl
35	24	35.3	11	2	US-08-726-308A-134	Sequence 134, App
36	24	35.3	11	3	US-08-836-480-38	Sequence 38, Appl
37	24	35.3	11	3	US-09-562-897-38	Sequence 38, Appl
38	24	35.3	13	1	US-07-842-089E-13	Sequence 13, Appl
39	24	35.3	13	1	US-07-842-089E-19	Sequence 19, Appl
40	24	35.3	13	1	US-08-264-485-13	Sequence 13, Appl
41	24	35.3	13	1	US-08-264-485-19	Sequence 19, Appl
42	24	35.3	13	2	US-08-580-988A-19	Sequence 19, Appl
43	23	33.8	8	1	US-08-346-455B-47	Sequence 47, Appl
44	23	33.8	8	3	US-08-977-221-47	Sequence 47, Appl
45	23	33.8	8	4	US-09-483-831B-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1  
US-09-057-897-13  
; Sequence 13, Application US/09057897  
; Patent No. 6300476  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Anthony Y.H.  
; APPLICANT: Wang, Regina W.  
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
; TITLE OF INVENTION: Cytochrome P450 3A4  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-057-897-13

Query Match 45.6%; Score 31; DB 4; Length 11;  
Best Local Similarity 63.6%; Red. No. 14;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CLEGGQVMDV 11  
DB 1 CLEDTOKHRV 11

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RESULT 2
US-09-842-164A-12
; Sequence 12, Application US/09842:164A
; Patent No. 6544754
; GENERAL INFORMATION:
; APPLICANT: INOUE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842,164A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Opicphorus graciliorostris
US-09-842-164A-12

Query Match 41.2%; Score 28; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 2,56-05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 5 GQVMDV 11
DB 1 GQVMDV 7

RESULT 3
US-09-447-411-46
; Sequence 46, Application US/08447:411
; Patent No. 5733243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING CBRA C3, CVP1, AND CVP2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/043,747
; APPLICATION NUMBER: 07-APR-1993
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243mar F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAI UR
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
US-08-447-411-46

Query Match 41.2%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 EDGQVMDV 12
DB 1 EDGFIADSDI 10

RESULT 4
US-08-662-227-3
; Sequence 3, Application US/08662:227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.O.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14 JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-662-227-3

Query Match 41.2%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 EDGQVMDV 12
DB 1 EDGFIADSDI 10

RESULT 5
US-09-017-947-3
; Sequence 3, Application US/09017:947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
```

APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,947  
FILING DATE:  
CLASSIFICATION:

Prior Application Data:  
APPLICATION NUMBER: US 08/662,227  
FILING DATE: 14-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-2X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
MOLECULE TYPE: peptide

Query Match 41.2%; Score 28; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 44;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EDGQVMDVDL 12  
DB 1 EDGFIADSDI 10

RESULT 6  
US-08-162-081B-13  
Sequence 13, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Query Match 41.2%; Score 28; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQVMDVD 11  
DB 1 DDGQLFHID 9

RESULT 7  
US-08-780-872-13  
Sequence 13, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US 08-780-872-13

Query Match: 41.2%; Score 29; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
:|:|:|:|:  
DB 1 DDGQWMDV 9

## RESULT 2

US-09-085-957-13  
Sequence 13, Application US/09085957  
Patent No. 6274327  
GENERAL INFORMATION:  
APPLICANT: Hales, Ian Donald; Fry, Michael John; Drand, Eric  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Olsu, Masayuki; Panayiotou, George; Volinnia,  
APPLICANT: Stefano; Golt, Ivan Tarasovich  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb st-1440  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/152,041  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/02961  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasquardini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LMD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9203  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-085-957-13

Query Match: 41.2%; Score 29; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
:|:|:|:|:  
DB 1 DDGQWMDV 9

## RESULT 9

US-09-057-897-15  
Sequence 15, Application US/09057897  
Patent No. 6300476  
GENERAL INFORMATION:  
APPLICANT: Lu, Anthony Y.H.  
APPLICANT: Wang, Regina W.  
TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
TITLE OF INVENTION: Cytochrome P450 3A4  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2080  
CITY: Rahway  
STATE: NJ  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,897  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19902  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (732)594-3905  
TELEFAX: (732)594-4720  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
APPLICATION TYPE: peptide  
US-09-057-897-15

Query Match: 39.7%; Score 27; DB 4; Length 8;  
Best Local Similarity 53.3%; Pred. No. 25e+05;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLEDTG 6  
:|:|:|:|:  
DB 1 CLEDTG 6

## RESULT 10

US-08-724-549-28  
Sequence 28, Application US/08724548  
Patent No. 5830637  
GENERAL INFORMATION:  
APPLICANT: Frank, Ronald  
APPLICANT: Guler, Sinan  
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR  
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
TITLE OF INVENTION: PROCESS  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joseph T. Eisele  
ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
ADDRESSEE: Levy, Eisele and Richard  
STREET: 711 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.

Query Match: 41.2%; Score 29; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
:|:|:|:|:  
DB 1 DDGQWMDV 9



ZIP: 10017-4059  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 3.3:  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,548  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/978,674  
FILING DATE: 03/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: EISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,331  
REFERENCE/DOCKET NUMBER: 2727-68 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 687-6000  
TELEFAX: (212) 682-3485  
TELEX: (212) 426767  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
US-08-724 548 28

Query Match 39.7%; Score 27; DB 2; Length 10;  
Best local Similarity 50.0%; Pred. No. 67;  
Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Qy 3 EDGQVMDVLL 12  
||| :|||  
Db 1 DGGPLDXDL 10

RESULT 11  
US-08-724-548-29  
; Sequence 29, Application US/08724548  
; Patent No. 5896637  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Ronald  
; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR  
; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Joseph T. Eisele  
; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
; ADDRESSEE: Levy, Eisele and Richard  
; STREET: 711 Third Avenue  
; CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-4059  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 3.3:  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,548  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/978,674  
FILING DATE: 03/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: EISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,331  
REFERENCE/DOCKET NUMBER: 2727-68 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 687-6000  
TELEFAX: (212) 682-3485  
TELEX: (212) 426767  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
US-08-724-548-29

Query Match 39.7%; Score 27; DB 2; Length 10;  
Best local Similarity 50.0%; Pred. No. 67;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 DGQVMDVLL 13  
||| :|||  
Db 1 DGGPLDXDL 10

RESULT 12  
US-07-978-674B-28  
; Sequence 28, Application US/07978674B  
; Patent No. 6040423  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Ronald  
; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR  
; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Joseph T. Eisele  
; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
; ADDRESSEE: Levy, Eisele and Richard

1 RESULT :  
 2 US-07 974 604B-29  
 3 Sequence 29, Application US/0797864B  
 4 Patent No 6040423  
 5  
 6 GENERAL INFORMATION:  
 7 APPLICANT: Frank, Ronald  
 8 APPLICANT: Guert, Sinan  
 9  
 10 TITLE OF INVENTION: PROCESS FOR THE RAPID DYEING OF CO  
 11 TITLE OF INVENTION: SUPPORT-BOUND OR FREE PETITION OF  
 12 TITLE OF INVENTION: CIGONUCLEOTIDES, A FLAT MATERIAL  
 13 TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
 14 TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
 15 TITLE OF INVENTION: PROCESS  
 16  
 17 NUMBER OF SEQUENCES: 54  
 18  
 19 CORRESPONDENCE ADDRESS:  
 20 ADDRESSEE: Joseph T. Eisele

RESULT 14  
US-09-238-448-B  
Sequence 8, Application US/59238448  
Patent No. #238925  
GENERAL INFORMATION:  
APPLICANT: Sarpson, Hugh A.  
TITLE OF INVENTION: Method for Determining Likelihood of Developing  
TITLE OF INVENTION: Immunological Tolerance  
FILE REFERENCE: HS 100  
CURRENT APPLICATION NUMBER: US/59/238,448  
CURRENT FILING DATE: 1999-01-26  
EARLIER APPLICATION NUMBER: 60/673,271  
EARLIER FILING DATE: 1994-11-30  
NUMBER OF SEQ. ID NOS.: 10

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-238-448-8
```

```
Query Match 39.7% Score 27; DB 3; Length 12;
Best Local Similarity 83.3% Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDGQVM 8
   |||
Db 5 EDGKVM 10
```

```
RESULT 15
US-09-341-435-57
; Sequence 57, Application US/09341435
; Patent No. 651196;
; GENERAL INFORMATION:
; APPLICANT: TAKAHASHI, TOSHIYA
; APPLICANT: SAITO, NOBUO
; APPLICANT: TAKESHIGE, HIDEYUKI
; APPLICANT: TANAKA, TOSHIAKI
; APPLICANT: KAINOH, MIE
; TITLE OF INVENTION: CYCLIC PEPTIDES AND MEDICINAL USE THEREOF
; FILE REFERENCE: 2109-14
; CURRENT APPLICATION NUMBER: US/09/341,435
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/JP98/05096
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic peptide
US-09-341-435-57
```

```
Query Match 39.7% Score 27; DB 4; Length 13;
Best Local Similarity 40.0% Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGSGQVMGV 10
   ||||
Db 1 CLGSGEHLGV 10
```

```
Search completed: November 5, 2003, 18:04:57
Job time : 15 secs
```

GenCore version 5.1.2  
Copyright (c) 1993-2003 Computer 1.1

EM protein protein search, using sw model

Run on: November 5, 2003, 17:00:59 / Search time is 8 hours

without alignment  
56,163 million cell operators/sec

Title: US-09-914-088 11

Percent score: 73

Sequence: 1 GLENGQWQVQVQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616942 residues

Total number of hits satisfying chosen parameters: 1026

Minimum DB seq length: 6

Maximum DB seq length: 13

Post-processing: Minimum Match of

Maximum Match 100%

Listing first 45 summaries

Database: PIR261\*

1: PIR261\*

2: PIR261\*

3: PIR261\*

4: PIR261\*

Pred. No. is the number of results predicted by name. Here a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	34	12	Q02106	hypothetical 1.4K protein - tomato chloroplast
2	25	34	12	Q02106	hypothetical 1.4K protein - tomato chloroplast
3	22	30	7	P44114	hypothetical protein - Arabidopsis thaliana
4	21	29	8	A28113	hypothetical protein - Arabidopsis thaliana
5	21	28	10	G58511	hypothetical protein - Arabidopsis thaliana
6	20	27	10	A60419	hypothetical protein - Arabidopsis thaliana
7	20	27	10	G58511	hypothetical protein - Arabidopsis thaliana
8	19	27	11	G58511	hypothetical protein - Arabidopsis thaliana
9	19	26	12	PS0283	hypothetical protein - Arabidopsis thaliana
10	19	26	12	PS0283	hypothetical protein - Arabidopsis thaliana
11	18	26	13	S01243	hypothetical protein - Arabidopsis thaliana
12	18	24	10	A32295	hypothetical protein - Arabidopsis thaliana
13	18	24	13	A33660	hypothetical protein - Arabidopsis thaliana
14	18	24	13	S47357	hypothetical protein - Arabidopsis thaliana
15	17	24	13	S62335	hypothetical protein - Arabidopsis thaliana
16	17	24	12	140645	hypothetical protein - Arabidopsis thaliana
17	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
18	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
19	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
20	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
21	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
22	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
23	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
24	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
25	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
26	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
27	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
28	17	23	16	PT0624	hypothetical protein - Arabidopsis thaliana
29	16	21	9	A33660	hypothetical protein - Arabidopsis thaliana

cardioexcitatory n  
neomycin suppressin  
endo-1,4-beta-xyla  
H-hyoscyamine  
hypothetical prote  
T-cell receptor A  
ig heavy chain DJ  
tubulin alpha-chain  
dnaA protein Pse  
T-cell receptor al  
T-cell receptor be  
parapara crystal  
NADP-cytochrome P4  
hypothetical prote  
alpha-macroglobulin  
zinc-metallophosph

ALIGNMENTS

RESULT 1

Q02106  
hypothetical 1.4K protein - tomato chloroplast (strain Toko)  
C:Species: chloroplast Lycopersicon esculentum (tomato)  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995  
C:Accession: Q02106  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 91, 13 20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)  
A:Reference number: Q02106  
A:Accession: Q02106  
A:Molecule type: DNA  
A:Residues: 1-12 <RAW>  
A:Experimental source: strain Toko  
A:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 34.2% Score 25; DB 2; length 12;  
Best Local Similarity 50.0%; Pied No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QV R MPVDLC 13  
Eb 4 1 1 1 1 1 1 1 1 1 1 1

RESULT 2

Q02108  
hypothetical 1.4K protein - potato chloroplast  
C:Species: chloroplast Solanum tuberosum (potato)  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996  
C:Accession: Q02108; Q02113  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 91, 13 20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)  
A:Reference number: Q02106  
A:Accession: Q02108  
A:Molecule type: DNA  
A:Residues: 1-12 <RAW>  
A:Experimental source: cv. W53-4  
A:Accession: Q02113  
A:Molecule type: DNA  
A:Residues: 1-12 <RAW>  
A:Experimental source: cv. W53-4  
A:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 34.2% Score 25; DB 2; length 12;  
Best Local Similarity 50.0%; Pied No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LEDGQV 13  
DB 4 LEDGQV 9

RESULT 4

QSpecies: B34618  
CDate: 13-Jun-1993 #sequence\_revision 13-Jun-1993 #text\_change 18-Jun-1993  
CAccession: B34618  
RJones, C.M., Prince, J.A., Williams, J.S.  
Exp. Heratol. 19, 704-709, 1991  
ATitle: Purification and amino acid analysis of a human macrophage cytotoxicity-induc-  
AReference number: A54427; PMID:9315597; PMID:217424  
AAccession: B34618  
AStatus: preliminary  
AMolecule type: protein  
AResidues: 1-7 <YAN>

Query Match 30.43; Score 20; DB 2; Length 9;  
Best Local Similarity 60.04; Pred. No. 2.5e+01;  
Matches 1; Conservative 0; Mismatches 1; Indels 0;

QY 1 LEDGQV 5  
DB 4 LEDGQV 9

RESULT 4

QSpecies: A28719  
CDate: 30-Sep-1989 #sequence\_revision 40-Sep-1993 #text\_change 18-Jun-1993  
CAccession: A28719  
RBaron, V., Pecht, M., Trainin, N.  
Biochemistry 27, 4864-4871, 1988  
ATitle: Thymic humoral factor gamma-2, purification and amino acid sequence of an immun-  
AReference number: A28719; PMID:882674; PMID:287474  
AAccession: A28719  
AMolecule type: protein  
AResidues: 1-9 <YAN>

Query Match 29.43; Score 20; DB 2; Length 9;  
Best Local Similarity 60.04; Pred. No. 2.5e+01;  
Matches 1; Conservative 0; Mismatches 1; Indels 0;

QY 1 LEDGQV 4  
DB 1 LEDGQV 4

RESULT 4

QSpecies: G54501  
CDate: 03-Feb-1997 #sequence\_revision 03-Feb-1997 #text\_change 11-Apr-1997  
CAccession: G54501  
RBinette, J.P., Binette, M.B.  
submitted to the Protein Sequence Database, October 1997  
AReference number: A54501  
AAccession: G54501  
AStatus: preliminary  
AMolecule type: protein  
AResidues: 1-11 <SPIN>  
AExperiment: 1; source: human bile and gallbladder  
ANote: 1, 2, 3, and 4 glu were also found

Query Match 28.87; Score 20; DB 2; Length 11;  
Best Local Similarity 42.94; Pred. No. 2.5e+01;  
Matches 3; Conservative 0; Mismatches 1; Indels 0;

QY 2 LEDGQV 8  
DB 4 LEDGQV 1

RESULT 6

QSpecies: A60427  
CDate: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
CAccession: A60427  
RJones, C.M., Prince, J.A., Williams, J.S.  
Exp. Heratol. 19, 704-709, 1991  
ATitle: Purification and amino acid analysis of a human macrophage cytotoxicity-induc-  
AReference number: A60427; PMID:9317233; PMID:1909970  
AAccession: A60427  
AMolecule type: protein  
AResidues: 1-9 <YAN>

ANote: the sequence from the text on page 706 is inconsistent with that from page 705  
CKeywords: cytokine

Query Match 27.43; Score 20; DB 2; Length 9;  
Best Local Similarity 80.04; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEDGQV 6  
DB 5 LEDGQV 9

RESULT 7

QSpecies: A01628  
CDate: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
CAccession: A01628  
RHeathcote, J.G., Washington, R.C.  
Int. J. Protein Res. 2, 117-126, 1970  
ATitle: Peptides of normal human gastric juice.  
AReference number: A01628; PMID:7515095; PMID:5539385  
AAccession: A01628  
AMolecule type: protein  
AResidues: 1-10 <HEA>

ANote: a second peptide lacking 1 Leu, but otherwise identical in composition with the  
CSuperfamily: unclassified animal peptides  
CKeywords: stomach

Query Match 27.43; Score 20; DB 2; Length 10;  
Best Local Similarity 60.04; Pred. No. 2.5e+01;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEDGQV 11  
DB 1 LEDGQV 10

RESULT 8

QSpecies: PS0259  
CDate: 03-Feb-1997 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
CAccession: PS0259  
RItogiya, A., Kato, M.  
submitted to JIPID, April 1993  
AReference number: PS0259  
AAccession: PS0259  
AMolecule type: protein  
AResidues: 1-11 <SPIN>  
AExperiment: 1; source: human bile and gallbladder  
ANote: 1, 2, 3, and 4 glu were also found

Query Match 27.43; Score 20; DB 2; Length 11;  
Best Local Similarity 42.94; Pred. No. 2.5e+01;  
Matches 3; Conservative 0; Mismatches 1; Indels 0;



A:Molecule type: Protein  
A:Residues: 113 <LMA>  
A:Note: P106 was also found

Query Match 24.0% Score 10.5; DB: 1; Length: 113;  
Best Local Similarity 50.0%; P106: No. 7; Length: 113;  
Matches 3; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 3 EGGVW 12  
DB 7 EGGVW 12

RESULT 15  
140663  
bma protein: Clostridium cochlearium filament.  
C:Species: Clostridium cochlearium  
C:Date: 12-Aug-1996 #sequence\_revision 12 Aug 1996 #ext. #dupes 1 #Oct-1999  
C:Accession: 140663; S47465  
R:Zeilger, C.; Beatrice, B.; Leubacher, D.; Buschel, W.  
R:J. Biochem. 226: 577-585, 1994  
A:Title: Characterization of the coenzyme B12-dependent glutamate mutase from Clostridium  
A:Reference number: 140659; NCBI:950948.6; F010749.251  
A:Accession: 140663  
A:Status: preliminary; translated from db/EMBL/DBS  
A:Molecule type: DNA  
A:Residues: 112 <RES>  
A:Cross references: EMBL: X80997; NID: J510036; PDB: 1A5A; 1A 1; 1A5A; 1A10  
C:Genebank:  
A:Gene: bma

Query Match 24.0% Score 10.5; DB: 1; Length: 113;  
Best Local Similarity 50.0%; P106: No. 9; Length: 113;  
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 6 QVNVVLC 13  
DB 2 KIVV 10 5

Search completed: November 5, 2003, 18:54:16  
Run time: 1.13 secs









1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY  
 2- SUBUNIT: Homodimer (by similarity)  
 3- SUBCELLULAR LOCATION: Cytoplasmic  
 4- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN B FAMILY.  
 5- INFORMATION: P0201494, Hsp90.  
 6- PROSITE: PS00298, HSP90; PARTIAL.  
 7- CHARACTER: ATP-binding; Heat shock; Phosphorylation  
 8- MOD\_RES 4 4 PHOSPHORYLATION (BY IS NA KINA-B-ARY  
 9- SIMILARITY)  
 10- MOD\_RES 5 6 PHOSPHORYLATION (BY IS NA KINA-B-ARY  
 11- SIMILARITY)  
 12- MOD\_RES 12 12 SIMILARITY  
 13- SEQUENCE 12 AA: 1432 WW; DE470120CABADIR6 144;  
 14- Query Match 21.9%; Score 16; DB 1; Length 14;  
 15- Best Local Similarity 42.9%; Pred No. 6.7e-03;  
 16- Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 17- CY 3 EETQWQ 7  
 18- DB 2 EETQWQ 8  
 19- RESULT 19  
 20- ID NC40 SCYRN STANDARD; PRT: 12 AA  
 21- AC P596A  
 22- DT 01-NOV-1999 (Rel. 35, Created)  
 23- DT 01-NOV-1999 (Rel. 35, Last sequence update)  
 24- DT 15-DEC-1999 (Rel. 37, Last annotation update)  
 25- DE Early nodulin 40.  
 26- GN ENO40  
 27- OS Glycine max (soybean)  
 28- CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 29- CC Spermatophyta; Magnoliophyta; eudicotyledons; Asteridiales; Papilionales;  
 30- CC Genus: I. Fabaceae; Fabaceae; Papilionaceae; Phaseolus; Glycine;  
 31- CC NCBI TaxID: 4471  
 32- RN 1  
 33- PP SEQUENCE FROM N.A.  
 34- RA STRAIN: N. Williams  
 35- RX MEDLINE 9418161; PubMed 8220464;  
 36- RA Yamaoka, A.; Kikuchi, S.; Hoshikawa, I.; Kikuchi, A.; Kikuchi, S.;  
 37- RA Sato, T.; van Kamen, A.; Besseling, R.; Kikuchi, S.; Kikuchi, S.;  
 38- RI "Characterization of GmERD40, a protein with a conserved ERD domain,  
 39- RI Specific expression during soybean root nodulation." Plant Physiol 113: 562-569 (1993)  
 40- RI Plant 113: 562-569 (1993)  
 41- CC FUNCTION: REGULATES THE ACTIN CYTOSKELETON IN ROOT NODULATION  
 42- CC GROWTH REGULATOR THAT ALTERS THE ACTIN CYTOSKELETON  
 43- CC SIMILARITY  
 44- CC DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF ROOT NODULATION  
 45- CC  
 46- CC THIS SWISS PRO entry is copyrighted. It is provided under a license agreement  
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 53- CC  
 54- CC EM50, X69164; NCT\_ANNOTATED\_CUS  
 55- CC NODULATION  
 56- CC SEQUENCE 12 AA: 1391 WW; SC600046 1400 1404  
 57- CC  
 58- CC Query Match 21.9%; Score 16; DB 1; Length 14;  
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 65- CC RESULT 14  
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 67- AC P2481E  
 68- DT 01-MAR-1992 (Rel. 21, Created)  
 69- DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 70- DT 01-MAR-1992 (Rel. 21, Last annotation update)  
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 75- CC Nephropoda; Nephropidae; Nephrops  
 76- CC NCBI TaxID: 6829  
 77- RN 11  
 78- PP SEQUENCE  
 79- CC TISSUE: STOMACH  
 80- RX MEDLINE 9208294; PubMed 1741385;  
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 84- RI Biochimie 73: 1219-1231 (1991)  
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 461- RI peptides identified with antibodies to gastrin/cholecystokinin."  
 462- RI Biochimie 73: 1219-1231 (1991)  
 463- CC FUNCTION: MAY INTERFERE WITH DIGESTION PROCESSES IN CRUSTACEANS.  
 464- CC SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 465- CC PRT: 9 AA  
 466- CC  
 467- CC CY 1 EETQWQ 4  
 468- CC DB 1 EETQWQ 4  
 469- CC  
 470- CC RESULT 12  
 471- ID D1 NEPNO STANDARD; PRT: 9 AA  
 472- AC P2481E  
 473- DT 01-MAR-1992 (Rel. 21, Created)  
 474- DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 475- DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 476- DE Gastrin/cholecystokinin-like peptide D1  
 477- OS Nephrops norvegicus (Norway lobster)  
 478- CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 479- CC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Astacidea;  
 480- CC Nephropoda; Nephropidae; Nephrops  
 481- CC NCBI TaxID: 6829  
 482- RN 11  
 483- PP SEQUENCE  
 484- CC TISSUE: STOMACH  
 485- RX MEDLINE 9208294; PubMed 1741385;  
 486- RA Favrel, P.; Keger, J.; Sedwimer, D.; Keller, R.; van Wormhoudt, A.;  
 487- RI "Structure and biological activity of crustacean gastrointestinal  
 488- RI peptides identified with antibodies to gastrin/cholecystokinin."  
 489- RI Biochimie 73: 1219-1231 (1991)  
 490- CC FUNCTION: MAY INTERFERE WITH DIGESTION PROCESSES IN CRUSTACEANS.  
 491- CC SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 492- CC PRT: 9 AA  
 493- CC  
 494- CC CY 1 EETQWQ 4  
 495- CC DB 1 EETQWQ 4  
 496- CC  
 497- CC RESULT 12  
 498- ID D1 NEPNO STANDARD; PRT: 9 AA  
 499- AC P2481E  
 500- DT 01-MAR-1992 (Rel. 21, Created)  
 501- DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 502- DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 503- DE Gastrin/cholecystokinin-like peptide D1  
 504- OS Nephrops norvegicus (Norway lobster)  
 505- CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 506- CC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Astacidea;  
 507- CC Nephropoda; Nephropidae; Nephrops  
 508- CC NCBI TaxID: 6829  
 509- RN 11  
 510- PP SEQUENCE  
 511- CC TISSUE: STOMACH  
 512- RX MEDLINE 9208294; PubMed 1741385;  
 513- RA Favrel, P.; Keger, J.; Sedwimer, D.; Keller, R.; van Wormhoudt, A.;  
 514- RI "Structure and biological activity of crustacean gastrointestinal  
 515- RI peptides identified with antibodies to gastrin/cholecystokinin."  
 516- RI Biochimie 73: 1219-1231 (1991)  
 517- CC FUNCTION: MAY INTERFERE WITH DIGESTION PROCESSES IN CRUSTACEANS.  
 518- CC SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 519- CC PRT: 9 AA  
 520- CC  
 521- CC CY 1 EETQWQ 4  
 522- CC DB 1 EETQWQ 4  
 523- CC  
 524- CC RESULT 12  
 525- ID D1 NEPNO STANDARD; PRT: 9 AA  
 526- AC P2481E  
 527- DT 01-MAR-1992 (Rel. 21, Created)  
 528- DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 529- DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 530- DE Gastrin/cholecystokinin-like peptide D1  
 531- OS Nephrops norvegicus (Norway lobster)

```

SQ SEQUENCE 9 AA: 1028 MW: 60ECT9VA6D9592VB CFC64;
Query Match 20.5%; Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDGQ 6
DB 2 EDGQ 5

RESULT 13
PCKK_FASHE STANDARD: PRT: 10 AA
AC PRG525;
DT 01-FEB-1996 (Rel. 33, Created);
DT 01-FEB-1996 (Rel. 33, Last sequence update);
DT 01-NOV-1997 (Rel. 35, Last annotation update);
DE Putative phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.31);
DE (Phosphoenolpyruvate carboxy-ase) (PEPCK) (Newly expressed juvenile
protein 1) (Fragment);
DE Fasciola hepatica (liver fluke);
DE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
DE Schistosomidae; Schistosomatidae; Fasciolidae; Fasciolidae; Fasciolidae;
CX NCBI_TaxID=6592;
RN [1];
RP SEQUENCE;
RX MEDLINE=95166593; PubMed=763732;
RA Kraljevic J., Ashman K., Veessen E.;
PT "Fasciola hepatica: rapid identification of newly expressed juvenile
proteins";
RG Biochem. Biophys. Res. Commun. 233:163-174(1997);
CC 1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GMP + phosphoenolpyruvate
+ CO2;
CC 1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE (GTP)
FAMILY;
DE InterPro: IPR003364; PEP carboxykin.
DR PROSITE: PS00505; PEPCK_GTP; PARTIAL
KW Lyase; Decarboxylase; GTP-binding;
FT KKWTF
IC 10
SQ SEQUENCE 10 AA: 1069 MW: 8193A6157AA9787A CFC64;

Query Match 20.5%; Score 15; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EDGQ 6
DB 2 EDGQ 10

RESULT 14
SPI_FALBC STANDARD: PRT: 10 AA
AC Q10497;
DT 01-OCT-1996 (Rel. 34, Created);
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 15-DEC-1996 (Rel. 37, Last annotation update);
DE Serine proteinase inhibitor (Fragment);
DE Halcorymba korezi (Sea squirt);
DE Eukaryota; Metazoa; Chordata; Urochordata; Ascidacea;
CX NCBI_TaxID=7729;
RN [1];
RP SEQUENCE;
RX TISSUE: Hemolymph; PubMed=8753295;
RA Shishikura F., Abe T., Ohtake S., Iizuka K.;
DE "Purification and characterization of a 59,000 Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halcorymba
korezi";
RG Corp. Biochem. Biophys. 154B:1-9 (1999);
CC 1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME ACTIVITY
```

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CC 1- SUBUNIT: MONOMER;
CC 1- SIMILARITY: BELONGS TO THE SERPIN FAMILY;
DR InterPro: IPR00215; Serpin;
DR PROSITE: PS00284; SERPIN; PARTIAL;
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma;
FT NKNTER
IC 10
SQ SEQUENCE 10 AA: 1104 MW: 4225C73B1B187AA3 CFC64;

Query Match 20.5%; Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDGQ 6
DB 3 EDGQ 6

RESULT 15
LICH_BACLI STANDARD: PRT: 12 AA
AC P82907;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Lichenus licheniformis;
CC Bacillus licheniformis;
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
CX NCBI_TaxID=1402;
RN [1];
RP SEQUENCE;
RC STRAIN=26L-10/3RA;
RX MEDLINE=21460732; PubMed=11578300;
RA Patrak P., Kaushik J.K., Grover S., Batish V.K.;
PT "Purification and characterization of a bacteriocin-like compound
(Ribocin) produced anaerobically by Bacillus licheniformis isolated
from water buffalo";
RT J. Appl. Microbiol. 91:636-645(2001);
RN [2];
RP SEQUENCE;
RC STRAIN=26L-10/3RA;
RA Patrak P.;
PT "Biochemical characterization and molecular genetics of bacteriocin
produced by a selected tamen bacterial isolate";
RG Thesis (1999), National Dairy Research Institute / Karnal, India;
CC 1- FUNCTION: OXGEN LABILE BACTERIOICIN LIKE, HAS ANTIBACTERIAL
ACTIVITY;
CC 1- SUBCELLULAR LOCATION: secreted;
KW Antibiotic; Bacteriocin;
SQ SEQUENCE 12 AA: 1414 MW: 1C05B56CFC4AEEB0 CFC64;

Query Match 20.5%; Score 15; DB 1; Length 12;
Best Local Similarity 16.7%; Pred. No. 9e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 EDGQ 13
DB 1 ISIEIC 6

Search completed: November 5, 2003, 18:02:29
Job time : 3.5 secs
```

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OK protein protein: search, using sw model

Run on: November 5, 2003, 17:59:29 Search time: 0.18 seconds  
Database alignment: 121,986 Multiple PDB updates/sec

Title: US-09-914-088-11  
Perfect score: 73  
Sequence: 1 CLEGGQVNDLQ 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 3.5

Searches: H1525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 13

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 sum-ratios

Database: SPTREXEL23

- 1: sp archaea
- 2: sp bacteria
- 3: sp fungi
- 4: sp human
- 5: sp invertebrates
- 6: sp mammal
- 7: sp plant
- 8: sp euglenae
- 9: sp phage
- 10: sp plant
- 11: sp rodent
- 12: sp virus
- 13: sp vertebrate
- 14: sp unclassified
- 15: sp virus
- 16: sp bacteria
- 17: sp archaea

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SYNVARIES

Result No.	Score	Query Match	Length	DB ID	Identification
1	25	34.2	9	1: Q3QZAB	Q3QZAB mus musculus
2	20	27.4	12	10 Q92LCA	Q92LCA trifolium r
3	20	27.4	12	12 C89243	C89243 woodchuck h
4	20	27.4	13	2 Q37543	Q37543 pseudomonas
5	19	26.0	9	4 Q96P97	Q96P97 homo sapien
6	19	26.0	9	10 Q8LPT7	Q8LPT7 zea mays lm
7	19	26.0	10	10 Q8LPT7	Q8LPT7 zea mays lm
8	19	26.0	12	10 Q8LPT7	Q8LPT7 zea mays lm
9	19	26.0	13	3 Q75014	Q75014 schizosacch
10	19	26.0	13	12 Q9PXB-	Q9PXB- duck hepaci
11	18	24.7	10	2 Q50012	Q50012 mycobacteri
12	18	24.7	11	7 Q29811	Q29811 homo sapien
13	18	24.7	11	7 Q7791A	Q7791A schizosacch
14	18	24.7	11	11 P37355	P37355 lat is norv
15	18	24.7	12	4 Q9T87	Q9T87 homo sapien
16	18	24.7	13	5 Q9T874	Q9T874 trifolium seri

Q46012 clostridium  
Q9P285 homo sapien  
Q9QV15 rattus sp.  
Q77912 oreochromis  
Q77888 oreochromis  
Q77883 oreochromis  
Q77887 oreochromis  
Q77910 oreochromis  
Q90W32 gallus gali  
Q93208 acinetobact  
Q52112 acinetobact  
Q8GMV1 acinetobact  
Q8GMV8 acinetobact  
Q8GM12 acinetobact  
Q9LYF5 mus musculu  
Q8QGS1 xenopus lae  
Q9UPE8 homo sapien  
Q19690 homo sapien  
Q90493 eopsaltria  
Q9X105 macropus ru  
Q42452 tritium ae  
Q9FS22 cicer ariet  
Q35013 mexicodogyne  
Q81715 hevea bras  
P82938 tordecum vu  
Q9GVE7 mus sp. pro  
Q23876 dictyostell  
Q39784 scsypium h  
Q9UGS1 homo sapien

# ALIGNMENTS

RESULT 1

Q3QZAB PRELIMINARY: PRI: 9 AA.

ID Q3QZAB  
AC Q3QZAB  
DT 01-MAY-2000 (TREMURel. 13, Created)  
CT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)  
DB C-type lectin DC11 (Fragment)  
GN DC11  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID:10052;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.  
RT "Condition cell regulation of DC11 mRNA expression."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
LR EMBL: AF192526; AA:04843.1;  
DR MGD: YGI:213650; DC11.  
KW Lectin.  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 594 MW, 34216:AB172EBAB7 CRC64;

Query Match 34.2%; Score 25; DB 11; Length 9;

Best Local Similarity 66.7%; Pred No. 8.3e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY : CLEGGQ 6

Do : CLEGGQ 5

RESULT 2

Q8LLC3 PRELIMINARY: PRI: 12 AA.

ID Q8LLC3

AC Q8LLC3

DT 01-OCT-2002 (TREMURel. 19, Created)

DT 01-OCT-2002 (TREMURel. 12, Last sequence update)

```

DT C1-OCT-2001 (TEMBLrel. 22, last annotation update)
DE Early nodulin endodermis
DS Trifolium repens (creeping white clover)
SC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids; Rosidae;
OC eumecostas; Fabales; Fabaceae; Papilionoideae; Trifoliales;
CX NCBI TaxID:3899;
RN 1;
RP SEQUENCE FROM N.A.
RA MEDLINE=22111131; PubMed 12114569;
RA Varkanyi-Basic E., White D.W.;
RT "The White Clover erod4 Gene Family: Expression Patterns of ER Types
RT of Genes Indicate a Role in Vascular Function";
RL Plant Physiol. 129:1107-1118(2002);
DR EMBL: AF424440; AAC81037.1;
SQ SEQUENCE 12 AA: 1405 MW: 306956RBURB2A2145944.
Query Match 27.4% Score 20 DB 16; Length 12;
Best Local Similarity 75.0% Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 VMDLLC 13
DB 11
DB 1 MLD 4

RESULT 3
Q89243 PRELIMINARY: PRT: 17 AA.
AC Q89243;
DT C1-NOV-1996 (TEMBLrel. 01, Created);
DT C1-NOV-1996 (TEMBLrel. 01, Last sequence update);
DT C1-OCT-2001 (TEMBLrel. 18, Last annotation update);
DE Gene protein (fragment);
OS Woodchuck hepatitis B virus;
OC Viruses; Retroviruses; Hepadnaviridae; with replicative
CX NCBI TaxID:35369;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN W64;
RX MEDLINE=8711989; PubMed:3582979;
RA Scheraga J., Varley T., Trepo C., Trilliv L., Pouchard M.;
RT "Nucleotide sequence of the woodchuck hepatitis virus surface
RT protein and the variability of three coding regions";
RL Gene 500:231-244(1991);
LP EMBL: Y55049; AAC83576.1;
DR InterPro:IPR00064; Hepatitis vir;
DR Pfam:PF00064; Hepatitis core;
FT MEN TER 13 12
SQ SEQUENCE 17 AA: 1398 MW: 214000EPLRER 13
Query Match 27.4% Score 20 DB 16; Length 17;
Best Local Similarity 75.0% Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 MVE 11
DB 11
DB 1 MLD 4

RESULT 4
Q89243 PRELIMINARY: PRT: 17 AA.
AC Q89243;
DT C1-NOV-1996 (TEMBLrel. 01, Created);
DT C1-NOV-1996 (TEMBLrel. 01, Last sequence update);
DT C1-NOV-1998 (TEMBLrel. 08, Last annotation update);
DE Plus expression protein (fragment);
OS Pseudomonas syringae;
OC Bacteria; Proteobacteria; Gammaproteobacteria;
OC Pseudomonadales; Pseudomonas;
CX NCBI TaxID:317;

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RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN W64;
RX MEDLINE=96134973; PubMed 8550460;
RA Roine E., Nann C.M., Paulin L., Romantschuk M.;
RT "Characterization of genes required for plus expression in
RT Pseudomonas syringae pathovar phaseolicola";
RL J. Bacteriol. 178:410-417(1996);
DR EMBL: L28837; AAC61390.1;
FT MEN TER 13 13
SQ SEQUENCE 17 AA: 1406 MW: 30915F7933495045 CRC64;
Query Match 27.4% Score 20 DB 2; Length 13;
Best Local Similarity 42.9% Pred. No. 8.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 VMDVLLC 13
DB 11
DB 7 LGVSLC 13

RESULT 5
Q96P97 PRELIMINARY: PRT: 9 AA.
AC Q96P97;
DT C1-DEC-2001 (TEMBLrel. 19, Created);
DT C1-DEC-2001 (TEMBLrel. 19, Last sequence update);
DT C1-DEC-2001 (TEMBLrel. 19, Last annotation update);
DE Reptin52 protein (fragment);
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
CX NCBI TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.-J., Jung H.M., Kim D.-Y., Huh T.-L., Kim Y.H.;
RT "Characterization of TPA responsive genes in U937 cells using ordered
RT differential display PCR";
RL Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases;
DR EMBL: AF401216; AAC10172.1;
FT MEN TER 1 1
SQ SEQUENCE 9 AA: 981 MW: 500DA0A681A51873 CRC64;
Query Match 46.0% Score 19 DB 4; Length 9;
Best Local Similarity 80.0% Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCMQ 1
DB 1
DB 3 GCMQ 7

RESULT 6
Q81275 PRELIMINARY: PRT: 9 AA.
AC Q81275;
DT C1-OCT-2002 (TEMBLrel. 32, Created);
DT C1-OCT-2002 (TEMBLrel. 32, Last sequence update);
DT C1-OCT-2002 (TEMBLrel. 32, Last annotation update);
DE Beta-expansin like protein (fragment);
OS Zea mays (maize);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Monocotyledons; Poales; Poaceae;
OC PACAO; Clade; Pan-Poaceae; Andropogoneae; Zea;
CX NCBI TaxID:4573;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN CV 0233;
RA Chung A.S., Galloway R.S., Jung M., Dolan M., Smith C.S., Tinney S.;
PA Galloway R.S., Finkelsch J.A.;
RT "ZmP1, a beta-expansin, and ZmP2, a putative and linkage disequilibrium in
RT maize, maize, and rice";
RL Submitted Apr. 2002 to the EMBL/GenBank/DBJ databases;

```







RN (1)  
 RP SEQUENCE FROM N.A.  
 PA Query X.1  
 PR Submitted MAY-2003 to the EMBL/GenBank/TrEMBL databases  
 DR EMBL; Accession: CAB92069.1; 1  
 FT NON-TER 12  
 SQ SEQUENCE 12 AA: 1594 MW: 115479.14  
 Query Match 24.74; Score 16; 1H 4; 100% 129  
 Residual Similarity 60.04; Pred. No. 129+24  
 Matches 3; Conservative 1; Mismatches 1; Indels 1; Gaps 0;  
 CY 2 LDDGV  
 DD :  
 : MEDG  
 : MEDG

Search completed: November 5, 2003, 18:01:39  
 Job time : 27.5 secs

GenCore version 5.1.6  
Copyright (c) 1993-2003 CoreGen Ltd.  
Query protein: protein search, using sw-maze.  
Run on: November 6, 2003, 17:56:23 / search (us-09-914-088-11.clos)  
10 hits, 5.11e-6, 0.01 / 84444800

Title: US-09-914-088-11  
Perfect score: 13  
Sequences: 1, CDS:US09-914-088-11  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
Searched: 1187463 seqs, 15872653 residues  
Total number of hits satisfying chosen parameters: 293464  
Minimum DB seq length: 0  
Maximum FP seq length: 13  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database	Accession	Length	Score	Match	Length	ID	Description
1	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	73	100.0	13	AA025917	PI mimotope peptide
2	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	73	100.0	13	AAU16642	Peptide P155 deriv
3	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	73	100.0	13	AAU00312	Human IgE cyclic i
4	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	Antiallergic
5	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	PI mimotope peptide
6	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	PI mimotope peptide
7	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	Peptide P155 deriv
8	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	Peptide P155 deriv
9	/SUS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT	13	64	87.7	13	AA025917	PI mimotope peptide

Find No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	ID	Description
1	73	100.0	13	AA025917	PI mimotope peptide
2	73	100.0	13	AAU16642	Peptide P155 deriv
3	73	100.0	13	AAU00312	Human IgE cyclic i
4	64	87.7	13	AA025917	Antiallergic
5	64	87.7	13	AA025917	PI mimotope peptide
6	64	87.7	13	AA025917	PI mimotope peptide
7	64	87.7	13	AA025917	Peptide P155 deriv
8	64	87.7	13	AA025917	Peptide P155 deriv
9	64	87.7	13	AA025917	PI mimotope peptide

10	64	87.7	13	ABJ00624	Human IgE immuno
11	64	87.7	13	ABJ00626	Human IgE immuno
12	51	69.9	10	AA025929	PI mimotope peptide
13	51	69.9	10	AAU16654	Peptide P155 deriv
14	51	69.9	10	ABJ00624	Human IgE immuno
15	50	68.5	13	ABJ00641	Human IgE cyclic i
16	47	64.4	9	AA025907	Immunoglobulin E
17	47	64.4	9	AA025907	IgE C-epsilon 2 do
18	47	64.4	9	AA025907	Peptide P155 deriv
19	47	64.4	9	AA025907	IgE peptide #1
20	47	64.4	9	AA025907	Human IgE immuno
21	46	61.6	10	AA025907	Immunoglobulin E
22	35	47.9	9	AA025907	Human immunoglob
23	34	46.6	7	AA025923	PI mimotope peptide
24	34	46.6	7	AAU16648	Peptide P155 deriv
25	34	46.6	7	AAU16648	Human IgE immuno
26	34	46.6	7	ABJ00627	Human immunoglob
27	34	46.6	13	AA025907	Immunoglobulin E
28	33	45.2	13	AA025916	PI mimotope peptide
29	33	45.2	13	AAU16661	Peptide #2 deriv
30	33	45.2	13	ABJ00324	Human IgE cyclic i
31	32	43.8	12	AA025943	PI mimotope (PTMab
32	32	43.8	12	AA026042	Human IgE C-epsilo
33	32	43.8	12	AAU16674	Peptide #15 deriv
34	32	43.8	12	AAU16674	Peptide SED-47/173
35	32	43.8	12	ABJ00337	Human IgE cyclic i
36	32	43.8	12	ABJ00386	Human IgE cyclic i
37	32	43.8	13	AA025935	PI mimotope SQ ID
38	32	43.8	13	AAU16660	Peptide #1 deriv
39	32	43.8	13	ABJ00323	Human IgE cyclic i
40	31	42.5	11	AA026026	Human CYP3A4 spec
41	31	41.1	9	AA025910	Human immunoglob
42	29	39.7	8	AAU16637	Membrane dipeptida
43	29	39.7	9	AA025908	Human immunoglob
44	29	39.7	10	AA026444	Arabidopsis thalia
45	29	39.7	10	AA026446	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AA025917	
ID	AA025917 standard; peptide; 13 AA.
XX	AA025917
AC	AA025917
DT	05 JAN 2001 (first entry)
DE	PI mimotope peptide P155 SEQ ID NO:11.
XX	
KW	Epitope: mimotope; human; immunoglobulin E; IgE; C-epsilon:2 domain;
KW	allergic disease; immunoprecipitation; immunotherapy; antiallergic;
KW	immunoprecipitation; vaccine; histamine release inhibitor; immunogen;
KW	allergy; atopy.
OS	HOLO ENZYME.
XX	
PN	WO2000010400.A1.
XX	
PD	31-AUG 2000.
XX	
PF	22-FEB-2000; 2000WO-EP01455.
XX	
PR	25-FEB-1999; 99GB-0004405.
PR	29-MAR-1999; 99GB-0007151.
PR	07-MAY-1999; 99GB-0010537.
PR	07-MAY-1999; 99GB-0010538.
PR	07-AUG-1999; 99GB-0018584.
PR	07-AUG-1999; 99GB-0018653.
PR	07-SEP-1999; 99GB-0021046.
PR	07-SEP-1999; 99GB-0021047.
PR	09-OCT-1999; 99GB-0025619.



PT disulfide bridge cyclized peptide and immunogenic carrier  
 PS Claim 4, Page 11, 45pp; English.  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide or antigen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%, Score 24, DB 21, Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5, 40-61;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQWMDVLC 13  
 Db 1 CLEGGQWMDVLC 13  
 RESULT 4  
 AAB25914  
 ID AAB25914 standard; peptide; 13 AA  
 XX  
 AC AAB25914  
 XX  
 DT 03 JAN 2001 (first entry)  
 XX  
 DE Antiallergy peptide mimotope sequence SEQ ID NO:11  
 KW Immunoglobulin E (IgE); immunogenic; immunogen; Protein E; vaccine;  
 KW prostate cancer; haemophilus influenzae; vaccine; infectious disease;  
 KW malaria; cytotoxic; antiallergic; nocturnal; neurodegenerative;  
 KW proinflammatory; Alzheimer's disease; allergy  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2002050400 A1.  
 XX  
 PD 31 AUG 2002  
 XX  
 PF 22 FEB 2003; 2002WO-EP01455.  
 XX  
 PS 25-FEB 1999; 99GB 0004405.  
 PR 29-MAR 1999; 99GB 0002152.  
 PR 07-MAY 1999; 99GB 0005592.  
 PR 07-MAY 1999; 99GB 0005598.  
 PR 07-AUG 1999; 99GB 0006594.  
 PR 07-AUG 1999; 99GB 0006621.  
 PR 07-SEP 1999; 99GB 0021046.  
 PR 07-SEP 1999; 99GB 0021047.  
 PR 29-OCT-1999; 99GB 0025619.  
 PR 23-NOV 1999; 99GB 0027698.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 PI Ramsdell B, Turnell WG, Van Mechelen WP, Vinals De Bassols YC;  
 DR WPI: 2000-57207/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 10, Page 18, 53pp; English.  
 CC The present invention describes an immunogen comprising a peptide  
 CC (1a) and a carrier (1b) derived from protein E of hemophilus influenzae  
 CC or its fragments. Also described are (1a) vaccine compositions comprising  
 CC an exemplar (1c) preparation of (1), comprising a carrier (1b) and  
 CC a protein E or its fragment, and (1) preparation of a vaccine (1d) for  
 CC prophylactic formulation (1) with an exemplar (1c) and (1b) starting  
 CC antigen, noctropic, neuroprotective and flat (1e) the immunogen  
 CC (1c) and the vaccine are useful for the treatment of (1f) and (1g).

CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (1) induces high levels of antipeptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC mimotope peptide sequence, which can be used in an immunogen of the  
 CC present invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 87.3%, Score 64, DB 21, Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0, 0015;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQWMDVLC 12  
 Db 1 CLEGGQWMDVLC 12  
 RESULT 5  
 AAB25914  
 ID AAB25914 standard; peptide; 13 AA  
 XX  
 AC AAB25914  
 XX  
 DT 05 JAN 2001 (first entry)  
 XX  
 DE PI mimotope peptide PT15, SEQ ID NO:8.  
 KW Epi-ope; mimotope; human; immunoglobulin E (IgE); C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2002050400 A1.  
 XX  
 PD 31 AUG 2002  
 XX  
 PF 22 FEB 2003; 2002WO-EP01455.  
 XX  
 PS 25-FEB 1999; 99GB 0004405.  
 PR 29-MAR 1999; 99GB 0002152.  
 PR 07-MAY 1999; 99GB 0005592.  
 PR 07-MAY 1999; 99GB 0005598.  
 PR 07-AUG 1999; 99GB 0006594.  
 PR 07-AUG 1999; 99GB 0006621.  
 PR 07-SEP 1999; 99GB 0021046.  
 PR 07-SEP 1999; 99GB 0021047.  
 PR 29-OCT-1999; 99GB 0025619.  
 PR 23-NOV 1999; 99GB 0027698.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 PI Ramsdell B, Turnell WG, Van Mechelen WP, Vinals De Bassols YC;  
 DR WPI: 2000-57207/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 14, Page 9, 129pp; English.  
 CC The present invention describes a peptide (1) comprising an isolated  
 CC surface exposed epitope (E1) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are (1) an  
 CC immunogen (1a) for treating allergy comprising (1); (2) a vaccine (1b)  
 CC for treating allergy comprising (1); (3) a ligand (1c) capable of  
 CC for treating allergy comprising (1); (4) a pharmaceutical composition (1d)  
 CC comprising (1); (5) a pharmaceutical composition (1e) comprising (1);

CC (5) a peptide that capable of being recognised by IgE, (6) an immunogen  
CC (11a) comprising (1a), and (7) producing (11), by producing (11), (1)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor, (11), (1b) and (11c) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies, (11) is useful for identifying mimotopes of PI,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies, (7) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood, (11), (11b) and (11c) are  
CC useful for treating a patient susceptible to or suffering from allergies,  
CC (11) is also useful in diagnosing atopy, AAR25907 to AAR26099 represent  
CC peptide sequences which are used in the exemplification of the present  
XX invention.

XX Sequence 13 AA:  
XX  
XX Query Match 87.0%, Score 64, DB 21, Length 13;  
XX Best Local Similarity 100.0%, Pred. NC 0.5015;  
XX Matches 12, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY : CLEDGQWMDVLC 12  
: CLEDGQWMDVLC 12

RESULT 6  
AAR25916  
ID AAR25916 standard, Peptide, 13 AA.  
XX  
XX AC AAR25916;  
XX

XX 05 JAN 2001: first entry;  
XX  
XX PE mimotope peptide P15p SEQ ID NO: 10;  
XX  
XX Epitope; mimotope; human; immunoglobulin E (IgE); C-terminal domain;  
XX allergic disease; immunophylaxis; immunotherapy; anti-allergy;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.

XX Home stations;  
XX Synthesis;  
XX WO200014519 A2  
XX 28 JUN 2001.  
XX 21 DEC 2000: 2000G-0504935.  
XX 21 DEC 1999: 99GB-003233.  
XX 22-FEB-2000: 2000GB-000496.  
XX 22-AUG-2000: 2000GB-002307.  
XX 22-AUG 2000: 2000GB-0020708.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
XX (SEPT) SEPTIDE THERAPEUTICS LTD.  
XX  
XX Dyson M, Fride M, Greenwood J, Hewitt E, Lee J, A. Vanden B,  
XX Randall E, Turnell WG, Van Mechelen ME, Vignali R, Ruppels V,  
XX  
XX Will 1999: 000195/53.  
XX  
XX Reported useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated substance extracted from a C-terminal  
XX domain from immunoglobulin E  
XX  
XX (1) a peptide, (2) a vaccine, (3) a ligand (4) capable of  
XX

CC The present invention describes a peptide (1) comprising an isolated  
CC surface exposed group; epitope (2) of C-terminal-2 domain (3) of  
CC immunoglobulin E (IgE) or its mimotope. Also described are: (1) an  
CC immunogen (11) for treating allergy comprising (11), (2) a vaccine (11)  
CC for treating allergies comprising (11), (3) a ligand (11) capable of  
CC recognising (11), (4) a pharmaceutical composition (PC) comprising (11),  
CC (5) a peptide (11a) capable of being recognised by (11), (6) an immunogen  
CC (11a) comprising (11a) and (7) producing (11), by producing (11), (1)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor, (11), (11b) and (11c) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies, (11) is useful for identifying mimotopes of PI,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies, (11) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood, (11), (11b) and (11c) are  
CC useful for treating a patient susceptible to or suffering from allergies,  
CC (11) is also useful in diagnosing atopy, AAR25907 to AAR26099 represent  
CC peptide sequences which are used in the exemplification of the present  
XX invention.

XX Sequence 13 AA:  
XX  
XX Query Match 87.0%, Score 64, DB 21, Length 13;  
XX Best Local Similarity 100.0%, Pred. NC 0.5015;  
XX Matches 12, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY : CLEDGQWMDVLC 13  
: CLEDGQWMDVLC 13

RESULT 7  
AAR16639  
ID AAR16639 standard, Peptide, 13 AA.  
XX  
XX AC AAR16639;  
XX

XX 07 NOV 2001: first entry;  
XX  
XX PEptide f15 derived as mimotope of C-terminal region of human IgE.  
XX Human, linkage technology; conjugated compound; carrier vehicle;  
XX epitope; C-terminal; C-terminal; C-terminal; C-terminal; C-terminal;  
XX IgE mediated disease; antibody response.  
XX Home stations;  
XX Synthesis;  
XX WO200014519 A2  
XX 28 JUN 2001.  
XX 21 DEC 2000: 2000G-0504935.  
XX 21 DEC 1999: 99GB-003233.  
XX 22-FEB-2000: 2000GB-000496.  
XX 22-AUG-2000: 2000GB-002307.  
XX 22-AUG 2000: 2000GB-0020708.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
XX (SEPT) SEPTIDE THERAPEUTICS LTD.  
XX  
XX Farnham R, Johnson T,  
XX WPL 2001: 521967/53.  
XX  
XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
XX mediated diseases  
XX  
XX Example 1: 1999: 1-11, English.  
XX  
XX The present invention is directed to linker technology for use in the  
XX construction of conjugates and peptides, carrier vehicles

(e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimetics of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human leucodermulin E (LgE), which are used to produce conjugated compounds, the components of compositions of the invention are useful in the manufacture of a medicament for the treatment of LgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope containing a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient.

AAD16613-AAD16618 represent peptides derived from or mimetics of the Cepsilon2/Cepsilon3/Cepsilon4 region of human LgE

Sequence 13 AA:

Query Match: 57.9% Score E4: FR 22; Length 10.  
Best Local Similarity 100.0%; Pred.No. 0 Gaps  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY : CEDAGQWVDV 12  
IIIIIIIII  
DB : I CEDAGQWVDL 12

RESULT 4  
AAD16641  
ID : AAD16641 standard, Peptide, 13 AA  
XX  
AA16641:  
XX  
07-RAW 2001: first entry  
XX  
Peptide: P15P derived as "mimetic of Cepsilon4 region of human LgE"  
XX  
Human linkage technology, conjugated compound, carrier vehicle;  
KW epitope; Cepsilon2/ Cepsilon3; Cepsilon4; Immunization (in E);  
XX LGE mediated disease; Antibody response.  
XX  
Homo sapiens.  
OS Synthetic.  
CS  
IN W22014-045-AA.  
XX  
EF 2R JUN 2001.  
XX  
F1 21-EPT 2001, 2000GB 0B04345  
XX  
F2 21-FEC-1999; 99GB-0G10233.  
F3 22-FEB-2000; 2000GB-0A04096.  
F4 22-JUN 2000; 2000GB-0C20707.  
F5 22-AUG-2000; 2000GB 0C20708.  
XX  
TACAP: ACAMERIS RES LTD,  
PA (SMK); SMT/KLINE BEECHAN BIOLOGICALS  
XX  
F1 Flinn N. Johnson T;  
XX  
WB1: 2001-021967/53.  
XX  
XX  
FT A linkage comprising an immunogenic substrate useful treatment of LgE  
BT mediated diseases -  
XX  
PS Example 4: Page 21: 48pp; English.  
XX  
XX The present invention relates to linkage methods only for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
QC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimetics of the Cepsilon2,  
CC Cepsilon3 or Cepsilon4 regions of human leucodermulin E (LgE), which  
CC are used to produce conjugated compounds, the components of compo-

CC	Capsilone2, Capsilone3 or Capsilone4 regions of human immunoglobulin E
CC	IgE) which are used to produce conjugated compounds. The compounds or
CC	compositions of the invention are useful in the manufacture of a
CC	medicament for the treatment of IgE mediated diseases. The invention
CC	allows for controlled conjugation of a peptide epitope (antigen) to a
CC	protein so as to form an immunogenic conjugate which may be able to
CC	raise a protective antibody response in an animal or human patient.
CC	AAU16622 AAU16333 represent peptides derived from or mimotopes of
CC	the Capsilone2/Capsilone3/Capsilone4 region of human IgE.
XX	
XX	Sequence    ? AA;
SQ	
	Query Match                 87.7%; Score 64; DB 22; Length 13;
	Best Local Similarity 100.0%; Pred. No. 0.0015;
	Matches    12; Conservative    0; Mismatches    0; Gaps    0;
QY	2 IEGGQWQVDEL 13 
D6	2 IEGGQWQVDEL 13
RESULT 9	
AAB51028	
ID	AAB51028 standard; Peptide; 13 AA.
XX	
XX	AAB51028:
XX	
DT	21-MAR-2001 (first entry)
XX	
DE	I95 peptide #6.
XX	
KW	Vaccine; Immunoglobulin E; IgE; anti-allergy.
XX	
CS	Mammalia.
XX	
FN	WO200074716-A2.
XX	
PC	14-DEC 2000.
XX	
Pf	56-JUN-2000; ZOOWC EP05164.
XX	
PR	28-JUN-1999; 99GH-001127.
XX	
PA	GENVIK : SMITHKLINE BEECHAM BIOLOGICALS.
XX	
Pt	Principals 0.
XX	
DR	WPI: 2001-0-1154716.
XX	
PT	New vaccine comprising allergy peptides linked by an inert carrier,
ET	useful for boosting an anti-allergy immune response in an individual
Pt	susceptible to an allergic response -
XX	
PS	Claim 5; Page 27; 26pp; English.
XX	
CC	The present invention relates to a composition comprising allergy
CC	peptides linked by an inert carrier. The allergy peptides are derived
CC	from Immunoglobulin E (IgE) or IgE receptor. The present peptide is one
CC	such peptide from IgE. The composition is useful as a vaccine or for
CC	manufacturing a medicament for the prophylaxis or treatment of allergy.
CC	In particular, for boosting an anti-allergy immune response in an
CC	individual susceptible to an allergic response.
XX	
SQ	Sequence    13 AA;
	Query Match                 87.7%; Score 64; DB 22; Length 13;
	Best Local Similarity 100.0%; Pred. No. 0.0015;
	Matches    12; Conservative    0; Mismatches    0; Gaps    0;
QY	1 IEGGQWQVDEL 12 
D6	1 IEGGQWQVDEL 12

```

RESULT 10
AB000224
ID AR000224 standard; Peptide; 13 AA.
XX AC
XX AB000224
XX
XX 02 SEP 2000 (first entry)
XX
XX Human IgE immunogenic peptide SEQ ID NO: 10.
XX
XX Immunogen; human; IgE; immunoglobulin E; allergy; food allergy; linkage;
XX vaccine; antiallergic.
XX
XX Homo sapiens.
XX
XX WO200216403 A2
XX
XX 28 FEB 2000.
XX
XX 17-AUG-2000; 2001WO-EP09596.
XX
XX 22-AUG-2000; 2000GB-0026717.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS
XX (PEPT-1) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC.
XX
XX WPI; 2000-489648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy; comprises
XX disulfide bridge cyclized peptide and immunogenic carrier.
XX
XX Claim 4; Page 9; 45pp; English.
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX where the conjugate comprises a disulfide bridge cyclized peptide and an
XX immunogenic carrier. The vaccines can be used in the treatment of
XX allergies. The present sequence is a peptide immunogen derived from human
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 97.7%; Score 64; D5 23; Length 13.
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CLEGGQWMDVL 12
XX I 1 CLEGGQWMDVL 12
XX
XX RESULT 11
AB000226
ID AR000226 standard; Peptide; 13 AA.
XX AC
XX AB000226
XX
XX 02 SEP 2000 (first entry)
XX
XX Human IgE immunogenic peptide SEQ ID NO: 10.
XX
XX Immunogen; human; IgE; immunoglobulin E; allergy; food allergy; linkage;
XX vaccine; antiallergic.
XX
XX Homo sapiens.
XX
XX WO200216403 A2
XX
XX 28 FEB 2000.
XX
XX 17-AUG-2000; 2001WO-EP09596.

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XX
XX 22-AUG-2000; 2000GB-0026717.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-1) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC.
XX
XX WPI; 2000-489648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy; comprises
XX disulfide bridge cyclized peptide and immunogenic carrier.
XX
XX Claim 4; Page 9; 45pp; English.
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX where the conjugate comprises a disulfide bridge cyclized peptide and an
XX immunogenic carrier. The vaccines can be used in the treatment of
XX allergies. The present sequence is a peptide immunogen derived from human
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 87.7%; Score 64; D5 23; Length 13.
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 LEDGGQWMDVL 13
XX D 2 LEDGGQWMDVL 13
XX
XX RESULT 12
AB025929
ID AAR05929 standard; Peptide; 10 AA.
XX AC
XX AAR05929.
XX
XX 05 JAN-2001 (first entry)
XX
XX PI mimotope peptide P1st SEQ ID NO:23.
XX
XX Epitope; mimotope; human; immunoglobulin E; IgE; C-peptide-2 domain;
XX allergic disease; immunophy-axis; immunotherapy; antiallergic;
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX allergy; atopy
XX
XX Homo sapiens.
XX
XX WO2000050400 A1
XX
XX 31-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-EP01455.
XX
XX 25-FEB-1999; 99GB-0004405.
XX 29-MAR-1999; 99GB-0007151.
XX 07-MAY-1999; 99GB-0010537.
XX 07-MAY-1999; 99GB-0010538.
XX 07-AUG-1999; 99GB-0018594.
XX 07-AUG-1999; 99GB-0018603.
XX 07-SEP-1999; 99GB-0021046.
XX 07-SEP-1999; 99GB-0021047.
XX 29-OCT-1999; 99GB-0025619.
XX 23 NOV-1999; 99GB-0027698.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-1) PEPTIDE THERAPEUTICS LTD.
XX
XX Dwyer M, Fildes M, Greenwood C, Hewitt E, Lamont A, Mason S,
XX Sandall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC.
XX
XX WPI; 2000-520000/01.

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XX Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.  
XX  
XX Disclosure: Page 9; 129pp; English.  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (II) of C epsilon-2 domain (I) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are (i) an  
XX immunogen (II) for treating allergy comprising (II), (i) a vaccine (III)  
XX for treating allergies comprising (II), (ii) a ligand (IV) capable of  
XX recognising E1; (4) a pharmaceutical composition (V) comprising (IV);  
XX (5) a peptide (IIa) capable of being recognised by (IV); (6) an immunogen  
XX (IIb) comprising (IIa); and (7) producing (IIb) by producing (IIa). (I)  
XX can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (II), (II) and (III) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (5) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (I), (II) and (II) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (IV) is also useful in diagnosing atopy. AA05997 to AA02699 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.  
SQ Sequence 10 AA;

Query Match 69.9%; Score 51; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDGQWVVD 11  
DB 1 LEDGQWVVD 10  
RESULT 13  
AAU16654  
TF AAU16654 standard; Peptide: 10 AA.  
XX AAU16654  
XX  
XX CV N/A; entry.  
XX Peptide P58 derived as epitope of domain 2 of human IgE.  
XX Human; linkage technology; conjugated compounds; carrier vehicles;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.  
XX Homo sapiens.  
XX Synthesis.  
XX WC000145745-A2.  
XX 28 JUN 2001.  
XX  
XX 21-DEC-2000; 2000WO-GB04935.  
XX  
XX 21-DEC-1999; 99GB-0030233.  
XX 22-FEB-2000; 2000GB-0004096.  
XX 22-AUG-2000; 2000GB-0020707.  
XX 22-AUG-2000; 2000GB-0020708.  
XX  
XX JACAY; ACAMBI; RES LTD.  
XX (SMIX); SMITHKLINE BEECHAM BIOLOGICALS  
XX  
XX Eliam N; Johnson T;  
XX  
XX WPI; 2001 501367/57.

PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases.  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
XX conjugation of compounds (e.g. peptides) to carrier vehicles  
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
XX biological and immunological constructs. The invention provides a  
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
XX protein) for use in a pharmaceutical composition or a vaccine. The  
XX invention describes peptides derived from or mimotopes of the  
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
XX (IgE) which are used to produce conjugated compounds. The compounds or  
XX compositions of the invention are useful in the manufacture of a  
XX medicament for the treatment of IgE mediated diseases. The invention  
XX allows for controlled conjugation of a peptide epitope (antigen) to a  
XX protein so as to form an immunogenic conjugate which may be able to  
XX raise a protective antibody response in an animal or human patient.  
XX AAU16632-AAU1691 represent peptides derived from or mimotopes of  
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

QY Sequence 10 AA.  
Query Match 69.9%; Score 51; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDGQWVVD 11  
DB 1 LEDGQWVVD 10  
RESULT 14  
AB000226  
ID ABC00228 standard; Peptide: 10 AA.  
XX  
XX AB000228;  
XX  
XX 02-SEP-2002 (first entry)  
XX Human IgE immunogenic peptide SEQ ID NO: 12.  
XX  
XX Immunogen; Human IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic  
XX Homo sapiens.  
XX  
XX WC000216459-A2.  
XX  
XX 29-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EF09576.  
XX  
XX 22-AUG-2000; 2000GB-0020717.  
XX  
XX (SMIX); SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT); PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede N; Mason S; Turnell WG; Vinals Bassols YC;  
XX  
XX WPI; 2002-489645/52.  
XX  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX  
XX Claim 4; Page 9; 4pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulphide bridge cyclised peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a peptide immunogen derived from human  
XX immunoglobulin E IgE suitable to be cyclised and used in the invention.



```

XX
SQ Sequence 13 AA:
Query Match 68.8%, Score 50, 13 AA, Identical 1
Best Local Similarity 100.0%, Pref Max 100, 13 AA
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LQEDQVNDV 11
   1 11
DB 1 LQEDQVNDV 13

RESULT 5
ABJ00541
10 AR00541 standard; Peptide; 13 AA.
XX
AC AR00541:
XX
DT 02 SEP 2002 (first entry)
XX
DE Human IgE cyclic immunogen.c peptide SEQ ID NO: 13.
XX
KW Immunogen; human; IgE; immunoglobulin; B; allergic; anti-venom; venom;
XX
KW vaccine; antitoxenic; cyclic
XX
FS Homo sapiens.
XX
FN K026016409-ALL
XX
PD 28 FEB 2002
XX
PF 17-JUN 2001; 17-JUN-EP05516.
XX
PP 22-AUG-2001; 2003G5-0020712.
XX
QA SMITHKLINE BEECHAM BIOLOGICALS
XX
QA (SEPT) PEPTIDE THERAPEUTICS LTD
XX
PI Fries, V, Mason S, Turbell WG, Vaccine Research YL
XX
PI WI: 2-02-443-49/52.
XX
PT Candidate for use in vaccine for treatment of allergy or asthma
XX
PT disulfide bridge cyclized peptide and immunogen
XX
PS Claim 4: page 16; 45pp; English.
XX
XX The present invention relates to a vaccine, and to a method of
XX where the vaccine comprises a modified protein, a cyclic peptide, and an
XX immunogenic carrier. The vaccine can be used for the treatment of
XX allergies. The present sequence is a cyclic peptide, and is derived
XX from human immunoglobulin G (IgG) variable region. The invention.
XX
SQ Sequence 13 AA:
Query Match 68.8%, Score 50, 13 AA, Identical 13
Best Local Similarity 100.0%, Pref Max 100, 13 AA
Matches 9; Conservative 0; Mismatches 4; Gaps 0;

QY 1 LQEDQVNDV 9
   1 11
DB 1 LQEDQVNDV 9

Search completed: November 5, 2003, 14:01:00
CPU time: 1.543 secs

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GenCore version 3.1.6  
Copyright (c) 1993-2003 Computer Inc.

CV protein - protein search, using sw -de1

Run on: November 5, 2003, 18:53:44 Search time: 20 seconds  
Without alignment  
101,486 Million pairs of residues

Title: US-09-914-088-11

Perfect score: 73

Sequence: MEDGOWMDVLC 13

Scoring table: BLOSUM62

Gap: 10.0, Gapex: 0.5

Sequences: 44479 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 392

Minimum DB seq length: 0

Maximum DB seq length: 13

List processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:

1. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
2. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
3. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
4. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
5. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
6. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
7. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
8. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
9. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
10. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
11. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
12. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
13. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
14. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
15. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
16. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
17. /cgn2\_6/pdata/2/pbpa/US09-914-088-11
18. /cgn2\_6/pdata/2/pbpa/US09-914-088-11

Pred. No. is the number of results predicted for the query. The score is the number of hits greater than or equal to the score of the query. The results are printed, and is derived by analysis of the total score data table.

Summary

Result	Seq	Score	Match	Length	DB	ID	Description
1	49	67.1	10	12	US-10-092-014-282	252	App
2	49	67.1	10	12	US-10-092-014-282	135	App
3	47	64.4	9	12	US-10-092-014-282	273	App
4	47	64.4	9	12	US-10-092-014-282	127	App
5	45	61.6	10	12	US-10-092-014-282	55	App
6	74	46.6	10	12	US-10-092-014-282	1084	App
7	39	39.7	10	12	US-10-092-014-282	1086	App
8	28	38.4	7	10	US-09-932-165-102	12	App
9	28	38.4	7	10	US-09-932-165-102	12	App
10	28	38.4	7	10	US-09-932-165-102	12	App
11	27	37.6	10	11	US-09-932-165-102	12	App
12	26	36.6	10	11	US-09-932-165-102	12	App
13	25	35.6	10	11	US-09-932-165-102	12	App
14	25	35.6	10	11	US-09-932-165-102	12	App
15	25	35.6	10	11	US-09-932-165-102	12	App

16	25	34.2	13	11	US-09-932-165-102	Sequence 34, Appl
17	24	32.9	8	14	US-10-095-450-10	Sequence 2, Appl
18	24	32.9	8	14	US-10-095-450-10	Sequence 6, Appl
19	24	32.9	8	14	US-10-095-450-10	Sequence 10, Appl
20	24	32.9	8	14	US-10-095-450-10	Sequence 14, Appl
21	24	32.9	8	14	US-10-095-450-10	Sequence 18, Appl
22	24	32.9	8	14	US-10-095-450-10	Sequence 22, Appl
23	24	32.9	8	14	US-10-095-450-10	Sequence 26, Appl
24	24	32.9	8	14	US-10-095-450-10	Sequence 30, Appl
25	24	32.9	8	14	US-09-780-053-434	Sequence 434, Appl
26	24	32.9	12	10	US-09-780-053-434	Sequence 556, Appl
27	24	32.9	12	10	US-09-766-353A-8	Sequence 8, Appl
28	24	32.9	12	10	US-10-345-764-22	Sequence 22, Appl
29	24	32.9	12	10	US-10-006-869-2346	Sequence 2346, Appl
30	24	32.9	16	15	US-09-932-165-102	Sequence 1418, Appl
31	23	31.5	8	12	US-10-147-140-47	Sequence 47, Appl
32	23	31.5	9	8	US-05-464-363-55	Sequence 55, Appl
33	23	31.5	9	12	US-09-932-165-102	Sequence 20, Appl
34	23	31.5	9	12	US-09-932-165-102	Sequence 118, Appl
35	23	31.5	9	12	US-09-935-384-535	Sequence 535, Appl
36	23	31.5	9	12	US-09-935-384-533	Sequence 633, Appl
37	23	31.5	9	12	US-10-277-292-458	Sequence 458, Appl
38	23	31.5	9	12	US-10-277-292-458	Sequence 591, Appl
39	23	31.5	10	12	US-09-932-165-102	Sequence 102, Appl
40	23	31.5	10	12	US-09-932-165-102	Sequence 196, Appl
41	23	31.5	10	12	US-09-932-165-102	Sequence 504, Appl
42	23	31.5	10	12	US-09-935-384-163	Sequence 163, Appl
43	23	31.5	10	12	US-09-935-384-289	Sequence 289, Appl
44	23	31.5	10	12	US-09-935-384-587	Sequence 587, Appl
45	23	31.5	10	12	US-10-353-929-174	Sequence 174, Appl
46	23	31.5	10	12	US-09-765-330A-23	Sequence 23, Appl
47	23	31.5	10	12	US-10-777-292-64	Sequence 64, Appl

FILE REFERENCE: 4564787179  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2003-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/082,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 1.2  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

Query Match: 64.43% Score 45; IP 12; Length 10;  
 Best Local Similarity: 100.00; Pct. No. 0.00;  
 Matches: 9; Conservative: 1; Mismatches: 0; Gaps: 0;

QV 1 YEDCGQVMDV 11  
 ||| |||  
 DE 1 YEDCGQVMDV 10

RESULT 4  
 US-10-144-188-55  
 Sequence 55, Application US/10/82016  
 Publication No. US2003/019858A1  
 GENERAL INFORMATION  
 APPLICANT: Biorad, Ashby, CA  
 TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS VACCINES, INCLUDING WITH AN N-TERMINAL CY  
 FILE REFERENCE: PCT/US 01/04564/789124  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 190  
 SOFTWARE: Patent in version 1.1  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

Query Match: 64.43% Score 45; IP 12; Length 10;  
 Best Local Similarity: 100.00; Pct. No. 0.00;  
 Matches: 9; Conservative: 1; Mismatches: 0; Gaps: 0;

QV 1 YEDCGQVMDV 11  
 ||| |||  
 DE 1 YEDCGQVMDV 10

RESULT 4  
 US-10-144-188-55  
 Sequence 55, Application US/10/82016  
 Publication No. US2003/019858A1  
 GENERAL INFORMATION  
 APPLICANT: Biorad, Ashby, CA  
 TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS VACCINES, INCLUDING WITH AN N-TERMINAL CY  
 FILE REFERENCE: PCT/US 01/04564/789124  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 190  
 SOFTWARE: Patent in version 1.1  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

FILE REFERENCE: 4564787179  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2003-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/082,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 1.2  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

Query Match: 64.43% Score 45; IP 12; Length 10;  
 Best Local Similarity: 100.00; Pct. No. 0.00;  
 Matches: 9; Conservative: 1; Mismatches: 0; Gaps: 0;

QV 1 YEDCGQVMDV 11  
 ||| |||  
 DE 1 YEDCGQVMDV 10

RESULT 5  
 US-10-144-188-55  
 Sequence 55, Application US/10/82016  
 Publication No. US2003/019858A1  
 GENERAL INFORMATION  
 APPLICANT: Biorad, Ashby, CA  
 TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS VACCINES, INCLUDING WITH AN N-TERMINAL CY  
 FILE REFERENCE: PCT/US 01/04564/789124  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 190  
 SOFTWARE: Patent in version 1.1  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

Query Match: 64.43% Score 45; IP 12; Length 10;  
 Best Local Similarity: 100.00; Pct. No. 0.00;  
 Matches: 9; Conservative: 1; Mismatches: 0; Gaps: 0;

QV 1 YEDCGQVMDV 11  
 ||| |||  
 DE 1 YEDCGQVMDV 10

RESULT 6  
 US-10-144-188-55  
 Sequence 55, Application US/10/82016  
 Publication No. US2003/019858A1  
 GENERAL INFORMATION  
 APPLICANT: Biorad, Ashby, CA  
 TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS VACCINES, INCLUDING WITH AN N-TERMINAL CY  
 FILE REFERENCE: PCT/US 01/04564/789124  
 CURRENT APPLICATION NUMBER: US/10/572,016  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/080,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 190  
 SOFTWARE: Patent in version 1.1  
 SEQ ID NO 136  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10 572 016 136

Query Match: 64.43% Score 45; IP 12; Length 10;  
 Best Local Similarity: 100.00; Pct. No. 0.00;  
 Matches: 9; Conservative: 1; Mismatches: 0; Gaps: 0;

QV 1 YEDCGQVMDV 11  
 ||| |||  
 DE 1 YEDCGQVMDV 10

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide antigen  
US-10-144 189-60

Query Match 46.6%; Score 34; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QGVMDV 12  
DB 1 QGVMDV 7

## RESULT 7

US-09-572-270A-1084

Sequence 1094; Application US/09572270A

Publication No. US2003014836A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Inter-complementary peptide (18-104)

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/572,270A

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 1144

SOFTWARE: Pro-Patent version 1.0

SEQ ID NO 1084

LENGTH: 10

TYPE: PRT

ORGANISM: Arabidopsis Thaliana

OTHER INFORMATION: Sequence located in (AVA-P) OR TABLE 1084 AND AVA-P2

US-09-572-270A-1084

Query Match 39.7%; Score 29; DB 12; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1; 1;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGVMDV 11  
DB 2 QGVMDV 8

## RESULT 8

US-09-572-270A-1086

Sequence 1086; Application US/09572270A

Publication No. US2003014836A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Inter-complementary peptide (108-1086)

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/572,270A

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 1144

SOFTWARE: Pro-Patent version 1.0

SEQ ID NO 1086

LENGTH: 10

TYPE: PRT

ORGANISM: Arabidopsis Thaliana

OTHER INFORMATION: Sequence located in (AVA-P) OR TABLE 1086 AND AVA-P2

US-09-572-270A-1086

Query Match 39.7%; Score 29; DB 12; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1; 1;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGVMDV 11  
DB 3 QGVMDV 9

## RESULT 9

US-09-842-164-12

Sequence 12; Application US/09842164

Patent No. US20020102687A)  
GENERAL INFORMATION:  
APPLICANT: INCOVE, Satoshi  
TITLE OF INVENTION: Luciferase and Photoprotein  
FILE REFERENCE: 206497US9  
CURRENT APPLICATION NUMBER: US/09/842,164  
CURRENT FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: JAPAN 2000 125053  
PRIOR FILING DATE: 2000 04 26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 12  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Oplophorus gracilirostris  
NAME/KEY: MISC FEATURE  
LOCATION: 113-173  
OTHER INFORMATION: PRT, 35 kDa protein, partial  
US-09-842-164-12

Query Match 39.4%; Score 28; DB 10; Length 7;  
Best Local Similarity 71.4%; Pred. No. 5.8e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QGVMDV 11  
DB 1 QGVMDV 7

## RESULT 10

US-09-925 442-3

Sequence 3; Application US/09925442

Patent No. US20020103346A1

GENERAL INFORMATION:

APPLICANT: VOGEL, CARL WILHELM

BRODEHCHST, REINHOLDST

KOCK, MICHAEL

FRITZINGER, DAVID

TITLE OF INVENTION: RECOMBINANT PROCVF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22212

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/925,442

FILING DATE: 10-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/017,947

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-0107-CX

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

```

1  TOPOLOGY: linear
2  MOLECULE TYPE: peptide
3  SEQUENCE DESCRIPTION: SEQ ID NOS: 3
4  US 09-925-442 3

Query Match: 38.4%; Score 28; DB 10; Length 10;
Best Local Similarity: 50.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EAGQVMQVD 12
   |||||
DB 1 EAGQVMQVD 10

RESULT 11
US-09-562-151 1
1 Sequence 1; Application US/09562151
2 Publication No. US2003092746A1
3 GENERAL INFORMATION:
4 APPLICANT: Hagmann, William K.
5 APPLICANT: Delasalle, Stephen E.
6 APPLICANT: Kameoka, Theodore
7 APPLICANT: MacCoss, Malcolm
8 TITLE OF INVENTION: SUBSTITUTED AMIDINE DERIVATIVES AND
9 INHIBITORS OF CELL ADHESION
10 FILE REFERENCE: 20698
11 CURRENT APPLICATION NUMBER: US/09/562-151
12 CURRENT FILING DATE: 2002-11-14
13 PRIOR APPLICATION NUMBER: 50/206-181
14 PRIOR FILING DATE: 2000-05-22
15 NUMBER OF SEQ ID NOS: 4
16 SOFTWARE: FASTSEQ for Windows Version 4.0
17 SEQ ID NO 1
18 LENGTH: 10
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US 09-562-151 1

Query Match: 37.0%; Score 27; DB 10; Length 10;
Best Local Similarity: 40.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAGQVMQVD 10
   |||||
DB 1 EAGQVMQVD 10

RESULT 12
US-09-572-454-298 1
1 Sequence 1; Application US/09572454-298
2 Publication No. US2003028374A1
3 GENERAL INFORMATION:
4 APPLICANT: Pfluum Ltd.
5 TITLE OF INVENTION: Complementary peptide-oligos for RNA human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572-454-298
8 CURRENT FILING DATE: 2002-05-17
9 NUMBER OF SEQ ID NOS: 4203
10 SOFTWARE: ProParent version 1.0
11 SEQ ID NO 2983
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 FEATURE:
16 OTHER INFORMATION: sequence located in 3' UTR of human mRNA for RETGC OR GUC14A
17 OTHER INFORMATION: CORD6 at 314-321 and may interact with Sequence 2984 in this patent
18 US 09-572-454-298 3

Query Match: 35.6%; Score 26; DB 10; Length 10;
Best Local Similarity: 44.4%; Pred. No. 3; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAGQVMQVD 9

```

```

DB 2 CPSEGSVD 10

RESULT 13
US-10-155-922-72 1
1 Sequence 1; Application US/10/155922
2 Publication No. US2003086893A1
3 GENERAL INFORMATION:
4 APPLICANT: Hata, Yoko
5 APPLICANT: Oka, Yutiko
6 APPLICANT: Takeba, Kyoko
7 APPLICANT: Tsuda, Eikari
8 APPLICANT: Teshigi, Keiko
9 APPLICANT: Shinagawa, Toko
10 APPLICANT: Murakami, Kayoko
11 APPLICANT: Koshida, Shogo
12 TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
13 FILE REFERENCE: 46792000220
14 CURRENT APPLICATION NUMBER: US/10/155,922
15 CURRENT FILING DATE: 2002-05-23
16 PRIOR APPLICATION NUMBER: PCT/GP/04691
17 PRIOR FILING DATE: 2001-06-14
18 PRIOR APPLICATION NUMBER: JP 2000-166903
19 PRIOR FILING DATE: 2000-06-05
20 PRIOR APPLICATION NUMBER: JP 2001-347340
21 PRIOR FILING DATE: 2001-11-13
22 PRIOR APPLICATION NUMBER: JP 2001-347338
23 PRIOR FILING DATE: 2001-11-13
24 PRIOR APPLICATION NUMBER: JP 2001-371175
25 PRIOR FILING DATE: 2001-12-05
26 PRIOR APPLICATION NUMBER: JP 2001-371166
27 PRIOR FILING DATE: 2001-12-05
28 NUMBER OF SEQ ID NOS: 156
29 SOFTWARE: FastSeq for Windows Version 4.0
30 SEQ ID NO 72
31 LENGTH: 10
32 TYPE: PRT
33 ORGANISM: Artificial Sequence
34 FEATURE:
35 OTHER INFORMATION: Synthetic Construct
36 FEATURE:
37 NAME/KEY: VARIANT
38 LOCATION: 7
39 OTHER INFORMATION: Xaa = Any Amino Acid
40 US-10-155-922-72 1

Query Match: 34.2%; Score 26; DB 10; Length 10;
Best Local Similarity: 80.0%; Pred. No. 5; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLEDS 9
   |||
DB 5 CLEDS 10

RESULT 14
US-09-863-043A-77 1
1 Sequence 1; Application US/09863043A
2 Publication No. US2003032055A1
3 GENERAL INFORMATION:
4 APPLICANT: Kenwick, Sue J.
5 APPLICANT: Nelson, David L.
6 APPLICANT: Aradhye, Swaroop
7 APPLICANT: D'Urso, Michele
8 APPLICANT: Wofford, Hayley
9 APPLICANT: Murnigh, Arnold
10 APPLICANT: Smith, Asaee
11 APPLICANT: Israel, Alain
12 APPLICANT: Foustka, Annetarie
13 APPLICANT: Lewis, Richard A.
14 APPLICANT: Levy, Wase
15 APPLICANT: Reiss, Nina

```

1 TITLE OF INVENTION: Diagnosis and Treatment of Medial and Lateral Ankle Sprains Associated with Def

2 FILE REFERENCE: NFKAPPA B (NF-2B) Activation  
 3 CURRENT APPLICATION NUMBER: US/09/963,043A  
 4 PRIOR APPLICATION NUMBER: US/09/963,043A  
 5 PRIOR FILING DATE: 2001-05-22  
 6 PRIOR APPLICATION NUMBER: US/09/963,043A  
 7 PRIOR FILING DATE: 2001-05-22  
 8 NUMBER OF SEQ ID NOS: 77  
 9 SOFTWARE: Patent in version 3.1  
 10 SEQ ID NO: 77  
 11 LENGTH: 11  
 12 TYPE: PRT  
 13 ORGANISM: Human  
 14 (US-09-914-088-11)

Query Match: 14.2% Score 25: 14.2% Length 11  
 Best local similarity: 56.3% Pred. No. Gaps: 0  
 Matches: 4: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

CV 1: CLEGG 6  
 1b 1: 1  
 1c 4: CLEGG 9

# RESULT 15

1 US-09-914-088-11  
 2 Sequence 34: Application US/99/9854  
 3 Patent No. US/2002/076739A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Gelb, Michael H.  
 6 APPLICANT: Gysi, Steven  
 7 APPLICANT: Scott, C.R.  
 8 APPLICANT: Turcotte, Frantisek  
 9 APPLICANT: Gerber, Scott A.  
 10 APPLICANT: Riss, Beate  
 11 TITLE OF INVENTION: Rapid Quantitative Analysis of Protein  
 12 FILE REFERENCE: 98A  
 13 CURRENT APPLICATION NUMBER: US/09/914-088-11  
 14 CURRENT FILING DATE: 2001-04-20  
 15 PRIOR APPLICATION NUMBER: 02/383,552  
 16 PRIOR FILING DATE: 1999-08-25  
 17 PRIOR APPLICATION NUMBER: 62/099,328  
 18 PRIOR FILING DATE: 1998-08-26  
 19 NUMBER OF SEQ ID NOS: 64  
 20 SOFTWARE: Patent in Ver. 2.0  
 21 SEQ ID NO: 34  
 22 LENGTH: 11  
 23 TYPE: PRT  
 24 ORGANISM: Yeast  
 25 FEATURE:  
 26 NAME/KEY: VARIANT  
 27 LOCATION: (1)  
 28 OTHER INFORMATION: Cat position 11 is not used (position 11 is not used)  
 29 OTHER INFORMATION: residue  
 30 (US-09-914-088-11)

Query Match: 14.2% Score 25: 14.2% Length 11  
 Best local similarity: 80.0% Pred. No. Gaps: 0  
 Matches: 4: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

CV 9: DVALC 13  
 1b 1: 1  
 1c 7: DVALC 11

Search completed: November 5, 2003, 14:11:14  
 Job time: 1:22 secs

GenCore version 1.1.6  
Copyright (c) 1993 GenPage, Inc.

CM protein - protein search, using sw -old

Received: November 5, 2003; 18:00:30; Search: 19.74 seconds  
without attachments.

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title; US-99-914 089-11  
perfect score; 73  
sequence; 1 CLEGGCGVGVGVL 13
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DATE: 08/19/2016

Gapex 10.5, Gapext 0.5

Searched: 128317 seqs, 42110856 residues

Total number of hits satisfying chosen parameters: 1,149.

**Maria Teresa**

max: num 23 seq 13

Test processing: Minimum Match 0.8  
Maximum Match 1.0  
Distance first 45

Released Pursuant to E.O. 14176

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6: /cgn2_6/ptodata/1/aa/5B_0MS.jpg

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itted. No. is the number of results predicted by chance; have is a score greater than or equal to the score of the result to be placed, and is derived by analysis of the total score distribution.

## SUMMARY

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30	34	32	8	4	US-93-127-815D-14	Sequence 14, Appl.
31	34	32	8	4	US-93-127-815D-18	Sequence 18, Appl.
32	34	32	8	4	US-93-127-815D-22	Sequence 22, Appl.
33	34	32	9	3	US-93-127-710-25	Sequence 25, Appl.
34	34	32	9	3	US-93-148-186-24	Sequence 25, Appl.
35	34	32	9	11	US-04-126-106A-134	Sequence 134, App
36	34	32	9	11	US-06-336-483-38	Sequence 38, Appl.
37	34	32	9	11	US-00-162-897-38	Sequence 38, Appl.
38	34	32	9	12	US-06-142-884-26	Sequence 38, Appl.
39	34	32	9	12	US-08-117-929-53	Sequence 32, Appl.
40	34	32	9	13	US-07-142-089B-13	Sequence 13, Appl.
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85	34	32	9	13	US-08-364-485-19	Sequence 19, Appl.
86	34	32	9			

## ALIGNMENTS

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1  RESULT: 1
2  US-CG-057-897 13
3  Sequence 13, Application: US/C9057993
4  Patent No. 630476
5  GENERAL INFORMATION:
6  APPLICANT:  L.J. Anthony Y.H.
7  APPLICANT:  Wang, Regina W.
8  TITLE OF INVENTION:  Anti Peptide Antibody Against Human
9  TITLE OF INVENTION:  Cyclochrome P450 1A7
10 NUMBER OF SEQUENCES: 16
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE:  Verck & Co., Inc.
13 STREET:  P.O. Box 2000
14 CITY:  Rahway
15 STATE:  NJ
16 COUNTRY:  US
17 ZIP:  07066-0970
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE:  Floppy disk
20 COMPUTER:  IBM PC compatible
21 OPERATING SYSTEM:  PC-DOS/MS-DOS
22 SOFTWARE:  Patented in Release #1.0, Version #1.30
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER:  US-CG-057-897
25 FIELDS DATA:
26 CLASSIFICATION:
27 ATTCREY/AGENT INFORMATION:
28 NAME:  Rand, J. V. &
29 REGISTRATION NUMBER:  16,545
30 REFERENCE/DOCNO NUMBER:  19902
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  7321594-3905
33 TELEFAX:  7321594-4720
34 INFORMATION FOR SEQ ID NO: 13:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 11 amino acids
37 TYPE:  amino acid
38 STRANDNESS:  single
39 TOPOLOGY:  linear
40 MOLECULE TYPE:  polypeptide
41 US-CG-057-897 13

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Query Match	42.54	Scores 11	DB 4	Length 11
Best Match Similarity	63.64			
Matches	0	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0





12 1 EDGFIADSDI 10

## RESULT 6

US-08-162-081B-13  
Sequence 3, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROOF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBAUER, P.C.  
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,227  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-162-081B-13

Query Match 38.4%, Score 28, DB 4, Length 10,  
Best Local Similarity 50.0%, Pred. No. 78,  
Matches 5, Conservative 2, Mismatches 3, Gaps 0,

QY 3 EDGQVMDVLD 12

DB 1 EDGFIADSDI 10

## RESULT 7

US-09-017-947-3  
Sequence 3, Application US/09017947  
Patent No. 6303754  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROOF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBAUER, P.C.  
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,947  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/162,227  
FILING DATE: 14-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-017-947-3

Query Match 38.4%, Score 28, DB 4, Length 10,  
Best Local Similarity 50.0%, Pred. No. 78,  
Matches 5, Conservative 2, Mismatches 3, Gaps 0,

QY 3 EDGQVMDVLD 12

DB 1 EDGFIADSDI 10

## RESULT 8

US-08-162-081B-13  
Sequence 3, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael; Dhand, Ritu  
APPLICANT: Bald, Watfield, Michael; Derek, Parker, Peter  
APPLICANT: Joseph, Oishi, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefania, West, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualucci, Patricia A.

REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US 08-162-081B 13

Query Match 38.4% Score 28; DB 2; Length 13;  
 Best Local Similarity 44.4% Pred. No. Leu:0;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
 Db : DDGQLEHD 9

RESULT 9  
 US-09-780-972-13

Sequence 13, Application US/05780872  
 Patent No. 646924  
 GENERAL INFORMATION:  
 APPLICANT: Hiles, Ian Donald; Fyfe, Michael; Cohen, Chard, Ritu  
 APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter;  
 APPLICANT: Joseph, Oleg, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Stefana, Gout, Ivac Parasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY.  
 TITLE OF INVENTION: THEIR PREPARATION AND USE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/05780872  
 FILING DATE: 09 JAN 1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/780,872  
 FILING DATE: 09 JAN 1997  
 APPLICATION NUMBER: 08/162,081  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: PCT/GB93/00761  
 FILING DATE: 13 April 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884

INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US 08-162-081B 13

Query Match 38.4% Score 28; DB 2; Length 13;  
 Best Local Similarity 44.4% Pred. No. Leu:0;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
 Db : DDGQLEHD 9

RESULT 15  
 US-09-057-897-15

Sequence 15, Application US/09057897  
 Patent No. 636476  
 GENERAL INFORMATION:  
 APPLICANT: Liu, Anthony Y.H.  
 APPLICANT: Wang, Peihua W.  
 TITLE OF INVENTION: Anti-Influenza Antibody Against Human

QY 3 EDGQWMDV 11  
 Db : DDGQLEHD 9

RESULT 10  
 US-09-085-957-13

Sequence 13, Application US/09085957  
 Patent No. 6274127  
 GENERAL INFORMATION:  
 APPLICANT: Hiles, Ian Donald; Fyfe, Michael; Cohen, Chard, Ritu  
 APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter;  
 APPLICANT: Joseph, Oleg, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Stefana, Gout, Ivac Parasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY.  
 TITLE OF INVENTION: THEIR PREPARATION AND USE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/085,957  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/780,872  
 FILING DATE: 09 JAN 1997  
 APPLICATION NUMBER: 08/162,081  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: PCT/GB93/00761  
 FILING DATE: 13 April 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884

INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-085-957-13

Query Match 38.4% Score 28; DB 3; Length 13;  
 Best Local Similarity 44.4% Pred. No. Leu:0;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDV 11  
 Db : DDGQLEHD 9

TITLE OF INVENTION: Cytochrome P450 3A4  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000  
 CITY: Rahway  
 STATE: NJ  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patent in Release #1.1, Version #1.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/057,877  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hurd, C. Mark  
 REGISTRATION NUMBER: 36,545  
 REFERENCE/DOCKET NUMBER: 19902  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (732)594-3305  
 TELEFAX: (732)594-4720  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-914-088-11

Query Match: 37.8% Score 27 DB 47 Length 47  
 Best Local Similarity: 81.3% Pred No: 2 Seq-Id:  
 Matches: 5; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY : CLEOTQ 6  
 DB : CLEOTQ 6

RESULT 12  
 US-09-914-088-11  
 Sequence ID: Application US/09/057,877  
 Patent No: 593530  
 GENERAL INFORMATION:  
 APPLICANT: Frank, Ronald  
 TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
 TITLE OF INVENTION: SUPPORT BOUND OR FREE PEPTIDES OF  
 TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
 TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
 TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Joseph T. Eisele  
 ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
 ADDRESSEE: Levy, Eisele and Richard  
 STREET: 711 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10017-4259  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3-1/2" DISKETTE  
 COMPUTER: IBM-XT COMPATIBLE  
 OPERATING SYSTEM: DOS 3.3  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/724,544

FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/928,624  
 FILING DATE: 03/22/93  
 ATTORNEY/AGENT INFORMATION:  
 NAME: EISELE, JOSEPH T.  
 REGISTRATION NUMBER: 25,312  
 REFERENCE/DOCKET NUMBER: 2729 68 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 487-6800  
 TELEFAX: (212) 482-3485  
 TELEEX: (212) 487-7777  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 residues  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE: Internal fragment  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLER:  
 IMMEDIATE SOURCE:  
 US-08-724-544 26

Query Match: 37.8% Score 27 DB 27 Length 13  
 Best Local Similarity: 50.0% Pred No: 118-02:  
 Matches: 2; Conservative: 2; Mismatches: 3; Indels: 0; Gaps: 0;

QY : EDGQWVVEL 12  
 DB : DDGICLXKL 13

RESULT 13  
 US-09-914-088-11  
 Sequence ID: Application US/09/057,877  
 Patent No: 6045423  
 GENERAL INFORMATION:  
 APPLICANT: Frank, Ronald  
 TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
 TITLE OF INVENTION: SUPPORT BOUND OR FREE PEPTIDES OF  
 TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
 TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
 TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Joseph T. Eisele  
 ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
 ADDRESSEE: Levy, Eisele and Richard  
 STREET: 711 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10017-4259  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3-1/2" DISKETTE  
 COMPUTER: IBM-XT COMPATIBLE  
 OPERATING SYSTEM: DOS 3.3  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/724,544

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/978,674E  
FILING DATE: 03/22/93  
CLASSIFICATION: 435  
EPICR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,332  
REFERENCE/DOCKET NUMBER: 2727 FR 90T  
TELEPHONE: (212) 687-6600  
TELEFAX: (212) 682 3485  
TELEX: (212) 426767  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: Internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLER:  
INTERMEDIATE SOURCE:  
US-07-978-674E-28

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 50.03; Pred No. 1,5e-02;  
Matches 4; Conservative 4; M.matches 3; Indels 0; Gaps 0;

QY ? EDGQVMDL 12  
|||  
DB 1 EDGQVMDL 10

RESULT 14  
US-09-914-435-57  
Sequence No. Application US/09/341,435  
Patent No. 631,961  
GENERAL INFORMATION:  
APPLICANT: TAKAHASHI, YUSHIYA  
TITLE OF INVENTION: Method for Determining Likelihood of Immunogenicity  
FILE REFERENCE: US 100  
CURRENT FILING DATE: 1999-01-28  
EARLIER APPLICATION NUMBER: 50/073,333  
FILING DATE: 1998-01-30  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Cyclic peptide  
US-09-914-435-57

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 50.03; Pred No. 1,5e-02;  
Matches 4; Conservative 4; M.matches 3; Indels 0; Gaps 0;

QY 3 EDGQVMDL 12  
|||  
DB 5 EDGQVMDL 10

RESULT 15  
US-09-914-435-57  
Sequence No. Application US/09/341,435  
Patent No. 631,961  
GENERAL INFORMATION:  
APPLICANT: TAKAHASHI, YUSHIYA  
TITLE OF INVENTION: Method for Determining Likelihood of Immunogenicity  
FILE REFERENCE: US 100  
CURRENT FILING DATE: 1999-01-28  
EARLIER APPLICATION NUMBER: 50/073,333  
FILING DATE: 1998-01-30  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Cyclic peptide  
US-09-914-435-57

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 50.03; Pred No. 1,5e-02;  
Matches 4; Conservative 4; M.matches 3; Indels 0; Gaps 0;

QY 1 CLEDSQVMDL 10  
|||  
DB 1 CLEDSQVMDL 10

Search completed: November 5, 2003, 16:04:57  
Job time: 14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2001 Compaq Inc

OM Protein - protein search, using sw model

Run on: November 5, 2003, 18:11:25 / Search time 17.6 seconds  
(without alignment)  
76,935 Million cell updates/sec

Title: US-09-914-088-13  
Perfect score: 89  
Sequence: 1 CFMKQLADLELPPE 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 2.5

Searched: 283308 seqs, 9616892 residues

Total number of hits satisfying chosen parameters: 279

Minimum DP seq length: 0  
Maximum DP seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 76\*  
1: PIR1\*  
2: PIR2\*  
3: PIR3\*  
4: PIR4\*

Prod. No. is the number of results predicted by chain to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	17.0	12	2	S7034	potB protein - Salmonella typhimurium (fragment)
2	23	25.8	10	2	S7034	potB protein - Salmonella typhimurium
3	22	24.9	9	2	S7034	potB protein - Salmonella typhimurium
4	22	24.9	9	2	S7034	potB protein - Salmonella typhimurium
5	22	24.9	10	2	A31435	adherence lectin h
6	22	24.7	12	2	A31435	adherence lectin h
7	22	24.7	15	2	A31435	adherence lectin h
8	21	23.6	9	2	B28495	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
9	21	23.6	9	2	A29477	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
10	21	23.6	15	2	S62671	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
11	20.5	23.0	9	2	A28495	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
12	20.5	23.0	9	2	S2902	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
13	20	22.5	10	2	A21195	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
14	20	22.5	12	2	G92125	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
15	20	22.5	14	2	A35377	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
16	20	22.5	14	2	I49514	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
17	20	22.5	15	2	S10891	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
18	20	22.5	15	2	P20093	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
19	19	21.3	8	2	A32593	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
20	19	21.3	9	2	P10119	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
21	19	21.3	9	2	I52974	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
22	19	21.3	12	2	J02308	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
23	19	21.3	15	2	C82318	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
24	19	21.3	15	2	S36990	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
25	19	21.3	16	2	S29631	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
26	18.5	20.8	9	2	P20241	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
27	18	20.2	11	2	B39504	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
28	18	20.2	11	2	S66636	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii
29	18	20.2	12	2	S23168	glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii

ALIGNMENTS

RESULT 1

S7034  
potB protein - Salmonella typhimurium (fragment)  
C:Species: Salmonella typhimurium  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999  
C:Accession: S7034  
Mol. Microbiol.: 20, 151-164, 1996  
A:Title: Identification of a Salmonella virulence gene required for formation of filamentous phage  
A:Reference number: S7034; MIMD:97014378; PMID:8861213  
A:Accession: S7034  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-12 <STX>  
A:Cross-references: EMBL:U51867; NID:91272352; PIDN:AAA97466.1; PID:91272352  
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1996  
C:Genetics:  
A:Gene: potB

Query Match: 27.0%; Score 24; DB 2; Length 12;  
Best Local Similarity: 37.5%; Pred. No. 9,8e-02;  
Matches: 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKQLADLELPPE 10  
DB 1 MKKQLADLELPPE 10

RESULT 2

B39308  
glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii  
C:Species: Clostridium sticklandii  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997  
C:Accession: B39308  
R:Stadman, T. C.; Davis, J. N.  
J. Biol. Chem. 266, 22147-22153, 1991  
A:Title: Glycine reductase protein C: Properties and characterization of its role in the  
A:Reference number: A39308; MIMD:92342141; PMID:1919235  
A:Accession: B39308  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <STX>  
C:Function:  
A:Description: glycine reductase complex catalyzes the reductive deamination of glycine  
C:Keywords: ATP; oxidoreductase

Query Match: 25.8%; Score 23; DB 2; Length 10;  
Best Local Similarity: 57.1%; Pred. No. 1.2e-03;  
Matches: 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKQLADLELPPE 10  
DB 1 MKKQLADLELPPE 10

```

Db          3  MNKQIAD 9

RESULT 3
Sat175
  Arginine vasotocin, sea lamprey
  C:Species: Petromyzon marinus [sea lamprey]
  C:Date: 29-Feb-1993 #sequence_revision 29-Jan-1993 #text_change 31-Mar-1993
  C:Accession: S06175
  P:Lang, Z.F.; Sower, S.A.; Kawachi, H.
  Gen. Comp. Endocrinol. 70, 152-157, 1994
  A:Title: Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus)
  A:Reference number: S06175; MUID:98228296; PMID:1311649
  A:Accession: S06175
  A:Molecule type: protein
  A:Residues: 1-9 <LAN>
  C:Keywords: amidated carboxyl end; hormone; neuropeptide; pituitary
  F1/Modified site: amidated carboxyl end; Gly; status experimental
  F1/Modified site: amidated carboxyl end; Gly; status experimental

  Query Match      24.7%  Score 22; DB 2; Length 9;
  Best Local Similarity 50.0%  Pred. No. 2.8e-05;
  Matches      3;  Conservative 2; Mismatches 1; Gaps 0;

  QY      10  MNKQIAD 9
  DB          3  MNKQIAD 9

RESULT 4
H61364
  Vasotocin, common carp
  C:Species: Cyprinus carpio [common carp]
  C:Date: 05-Sep-1994 #sequence_revision 04-Sep-1994 #text_change 23-Jun-2000
  C:Accession: B61364
  A:Chauvet, J.; Chauvet, M.T.; Chauvet, J.; Acher, R.
  Comp. Biochem. Physiol. A 14, 245-254, 1983
  A:Title: Characterization des hormones neurohypophysaires chez le poisson osseux d'eau douce
  A:Reference number: A61364
  A:Accession: B61364
  A:Status: preliminary
  A:Molecule type: protein
  A:Residues: 1-9 <CB>
  C:Keywords: amidated carboxyl end; neuropeptide; posterior pituitary

  Query Match      24.7%  Score 22; DB 2; Length 9;
  Best Local Similarity 50.0%  Pred. No. 2.8e-05;
  Matches      3;  Conservative 2; Mismatches 1; Gaps 0;

  QY      10  MNKQIAD 9
  DB          3  MNKQIAD 9

RESULT 5
A61131
  Hydrin 2, bullfrog
  N:Alternate names: AVT-related peptide
  C:Species: Rana catesbeiana [bullfrog]
  C:Date: 12-Mar-1994 #sequence_revision 04-Mar-1994 #text_change 11-Jul-1997
  C:Accession: A61131
  P:Warner, S.; Hayashi, H.; Yatabuchi, K.; Kikuyama, S.
  Gen. Comp. Endocrinol. 84, 412-418, 1993
  A:Title: Arginine vasotocin (AVT) and AVT related peptide in the pituitary gland of the bullfrog
  A:Reference number: A61131; MUID:92224411; PMID:1383420
  A:Accession: A61131
  A:Molecule type: protein
  A:Residues: 1-15 <CB>
  C:Comment: With the decapeptide hydrin 2 and the undecapeptide hydrin 3, Arg vasotocin
  C:Superfamily: oxytocin-neurophysin
  C:Keywords: amidated carboxyl end; neuropeptide; pituitary
  F1/9/Product: Arg vasotocin #status experimental; AVTAS

  Query Match      24.7%  Score 22; DB 2; Length 15;
  Best Local Similarity 50.0%  Pred. No. 2.7e-03;
  Matches      5;  Conservative 2; Mismatches 5; Indels 0; Gaps 0;

  QY      10  MNKQIAD 15
  DB          3  MNKQIAD 9

RESULT 6
A33900
  Hydrin 1, African clawed frog
  N:Alternate names: arginine-vasotocin-related peptide; vasotocinyl-Gly Lys
  C:Species: Xenopus laevis [African clawed frog]
  C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 31-Mar-1997
  C:Accession: A33900; S30176
  P:Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
  Proc. Natl. Acad. Sci. U.S.A. 86, 5272-5275, 1989
  A:Title: Hydrins, hydroelectric neurohypophysial peptides: osmoregulatory adaptation in
  A:Reference number: A33900; MUID:69315739; PMID:2787509
  A:Accession: A33900
  A:Status: preliminary
  A:Molecule type: protein
  A:Residues: 1-12 <RC>
  P:Wamide, S.; Hayashi, H.; Kikuyama, S.
  Biochim. Biophys. Acta 1176, 143-147, 1993
  A:Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly Lys, in Xenopus
  A:Reference number: S30176; MUID:93200145; PMID:8452872
  A:Accession: S30176
  A:Molecule type: protein
  A:Residues: 1-12 <IWA>
  C:Keywords: neuropeptide

  Query Match      24.7%  Score 22; DB 2; Length 12;
  Best Local Similarity 50.0%  Pred. No. 2.1e-03;
  Matches      3;  Conservative 2; Mismatches 1; Indels 0; Gaps 0;

  QY      10  MNKQIAD 12
  DB          3  MNKQIAD 9

RESULT 7
PA0092
  Protein Q100011, fusarium (Fusarium sporotrichoides) (fragment)
  C:Species: Fusarium sporotrichoides
  C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
  C:Accession: PA0092
  P:Chow, L.F.; Fukaya, M.; Sugita, Y.; Jeno, Y.; Tabuchi, K.; Tsugita, A.
  Submitted to JBC, October 1994
  A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides
  A:Reference number: PA0092
  A:Accession: PA0092
  A:Molecule type: protein
  A:Residues: 1-15 <CB>
  C:Keywords: pyroglutamic acid
  F1/Modified site: pyroglutamic acid (Gln) #status experimental

  Query Match      24.7%  Score 22; DB 2; Length 15;
  Best Local Similarity 41.7%  Pred. No. 2.7e-03;
  Matches      5;  Conservative 2; Mismatches 5; Indels 0; Gaps 0;

  QY      3  MNKQIAD 15
  DB          2  MNKQIAD 13

RESULT 8
B28495
  Compensin S, cone snail (Conus striatus)
  N:Alternate names: A1 vasopressin

```

F1/Modified site: amidated carboxyl end (Gly; lamide in mature form from following gly

C:Species: Conus striatus (striated cone)  
 C:Date: 30 Jun-1989 #sequence\_revision 10 Jun-1989 #text\_change 20 Apr-1997  
 C:Accession: B28495  
 R:Cruz, L.J., de Santos, V., Zafaralla, G.C., Ramilo, C.A., Zeikus, R., Gray, W.R., Oliv  
 J. Biol. Chem. 262, 15821-15824, 1987  
 A:Title: Invertebrate vasopressin/oxytocin homologs: characterization of peptides from C  
 A:Reference number: A32617; MUID:8805932; PMID:3682228  
 A:Accession: B28495  
 A:Molecule type: protein  
 A:Residues: 1-9 <CPU>  
 C:Superfamily: oxytocin/neurophysin  
 C:Keywords: amidated carboxyl end; venom  
 F1-6/Disulfide bonds: #status experimental  
 F19/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.64; Score 20.5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 3  
 A29477  
 C:Species: Locusta migratoria (migratory locust)  
 C:Date: 31 Dec-1988 #sequence\_revision 11 Dec-1988 #text\_change 31 Dec 1993  
 C:Accession: A29477  
 R:Proulx, J.P., Miller, C.A., Jr., J.P., Curney, P., G. Girardier, A., Delage, M., Schooley  
 Biochem. Biophys. Res. Commun. 149, 186-196, 1987  
 A:Title: Identification of an arginine vasopressin like diuretic hormone from Locusta mi  
 A:Reference number: A29477; MUID:8807907; PMID:3682228  
 A:Accession: A29477  
 A:Molecule type: protein  
 A:Residues: 1-9 <PEP>  
 A:Note: two neurophysins, F1 and F2, were identified. F2 is an antiparallel dimer of F1  
 C:Keywords: neuropeptide

Query Match 23.64; Score 20.5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 10  
 S62641  
 C:Title: porthobilinogen synthase (EC 4.2.1.24): a green alga, S. viridis, and fungus (fragment)  
 N:Alternate names: 5-aminolevulinic acid dehydratase  
 C:Species: Scolecismus obliquus  
 C:Date: 14 Feb-1997 #sequence\_revision 11-Mar-1997 #text\_change 08 May 1999  
 C:Accession: S62641  
 R:Stolz, M., Doornemann, D.  
 Eur. J. Biochem. 236, 600-608, 1996  
 A:Title: Purification, metal cofactor, N-terminal sequence, and subunit composition of a  
 A:Reference number: S62641; MUID:96195600; PMID:8810164  
 A:Accession: S62641  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <STO>  
 C:Keywords: carbon-oxygen lyase; hydrolase

Query Match 23.64; Score 20.5; DB 2; Length 9;  
 Best Local Similarity 30.8%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 NKKQLAQLLELQPR 15  
 Db 3 VQSKNDIVSPR 15

RESULT 11  
 A28495  
 C:Species: Conus geographus (cone shell) (Conus geographus)  
 N:Alternate names: lys conopressin-G  
 C:Species: Conus geographus (geography cone)  
 C:Date: 30 Jun-1989 #sequence\_revision 10 Jun-1989 #text\_change 25-Apr-1997  
 C:Accession: A28495  
 R:Cruz, L.J., de Santos, V., Zafaralla, G.C., Ramilo, C.A., Zeikus, R., Gray, W.R., Oliv  
 J. Biol. Chem. 262, 15821-15824, 1987  
 A:Title: Invertebrate vasopressin/oxytocin homologs: Characterization of peptides from C  
 A:Reference number: A32617; MUID:8805932; PMID:3682228  
 A:Accession: A28495  
 A:Molecule type: protein  
 A:Residues: 1-9 <CPU>  
 C:Superfamily: oxytocin/neurophysin  
 C:Keywords: amidated carboxyl end; venom  
 F1-6/Disulfide bonds: #status experimental  
 F19/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.64; Score 20.5; DB 2; Length 9;  
 Best Local Similarity 26.7%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 1 CFMKQLAQLLELQPR 15  
 Db 1 CFIRK--- -CPR 8

RESULT 12  
 S39040  
 C:Species: Epibdella octoculata  
 C:Date: 19 Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999  
 C:Accession: S39040  
 R:Salzet, M., Bilet, P., van Dorsselaer, A., Majecka, Z.  
 Eur. J. Biochem. 217, 897-903, 1993  
 A:Title: Isolation, structural characterization and biological function of a lysine-cont  
 A:Reference number: S39040; MUID:94039146; PMID:8223646  
 A:Accession: S39040  
 A:Molecule type: protein  
 A:Residues: 1-9 <SAL>

Query Match 23.64; Score 20.5; DB 2; Length 9;  
 Best Local Similarity 26.7%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 1 CFMKQLAQLLELQPR 15  
 Db 1 CFIRK--- -CPR 8

RESULT 13  
 A32195  
 N:K-exchanging ATPase (EC 3.6.3.9): alpha chain - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 20 Oct-1989 #sequence\_revision 20 Oct-1989 #text\_change 19-Apr-2002  
 C:Accession: A32195  
 R:Tyson, P.A., Steinberg, M., Walluck, E.T., Kirley, T.L.  
 J. Biol. Chem. 264, 726-734, 1989  
 A:Title: Identification of the S-iodoacetamidofluorescein reporter site on the Na,K-ATP  
 A:Reference number: A32195; MUID:89093137; PMID:2536022  
 A:Accession: A32195  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <TYS>  
 C:Keywords: hydrolase

Query Match 22.54; Score 20.5; DB 2; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 3.9e+03;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 QPAC 13

DB 2 HRC 5

## RESULT 14

G49215  
 Disease: BC virus, small subunit (GenBank) Helicobacter fetus (GenBank)  
 CSpecies: Helicobacter fetus  
 CDate: 19-Nov-1993 #sequence revision to Nov 1994 #next release 10 May 1995  
 CAccession: G49215  
 Ruffebert, G.R., Hsu, P.B., Horne, R. & Van, P.C.  
 Infect. Immun. 60, 5259-5266, 1992  
 ATitle: Purification and characterization of the disease-causing Helicobacter species  
 AReference number: A49215; MUID:93084178; PMID:1452159  
 AAccession: G49215  
 AStatus: preliminary  
 A-Molecule type: protein  
 AResidues: 1-12 cDNA  
 AExperimental source: ATCC 49179  
 ANote: sequence extracted from NCBI database (NCBIRefSeq)  
 CKeywords: hydrolase

Query Match 22.5% Score 100 DB 27 Length 120  
 Post local similarity 42.5% Pref DB 42.5%  
 Matches 3; Conservative 3; Mismatches 17 Indels 0 Gaps 0

QY 11 DELCPE 16

PB 1 NKLTPKE 9

## RESULT 15

A45377  
 GTP binding protein, Galphai1 chain, rat (GenBank)  
 CSpecies: Rattus norvegicus (Norway rat)  
 CDate: 17-Aug-1992 #sequence revision to Aug 1995 #next release 10 May 1997  
 CAccession: A45377  
 Rindler, M.E., Ewald, D.A., Miller, R. & Gilman, A.G.  
 J. Biol. Chem. 265, 8243-8251, 1990  
 ATitle: Purification and characterization of G proteins and their  $\gamma$ -subunits of Galphai1 after  
 AReference number: A45377; MUID:90344079; PMID:1615446  
 AAccession: A45377  
 AStatus: preliminary  
 A-Molecule type: protein  
 AResidues: 1-14 cDNA  
 CKeywords: GTP binding, regulatory protein, G protein

Query Match 42.1% Score 100 DB 27 Length 120  
 Post local similarity 50.1% Pref DB 50.1%  
 Matches 4; Conservative 1; Mismatches 17 Indels 0 Gaps 0

QY 7 PNMKCLA 8

DB 11 111

DB 8 PNTARLA 14

Search completed: November 5, 2003, 13:04:10  
 Job time: 120 secs



GenCore version 5.1.6  
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OX protein protein search, using sw model

Run on: November 5, 2003, 18:05:10 / Search time: 11 seconds  
without alignment  
68,472 Million cell updates/sec

Title: US-09-914-088-13

Perfect score: 89

Sequence: 1 CFMKRQACLETPRE 16

Scoring table: Gapop 10.0, Supext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 632

Minimum DB seq length: 0

Maximum DB seq length: 16

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID
1	22	24	9	1 OXYT_CYPCA
2	21.5	24.2	9	1 OXYA_SAVCA
3	21.5	24.2	9	1 OXYA_SQVAC
4	21	23.6	9	1 CONG_CKST
5	21	23.6	9	1 DNEP_DWVY
6	20.5	23.0	9	1 CONG_SHP
7	20.5	23.0	9	1 OXYF_SVYA
8	20	22.5	12	1 LICH_PABT
9	20	22.5	12	1 NC4I_SQVAC
10	20	22.5	15	1 UBL1_X_HYD
11	19	21.3	15	1 OX1A_CKST
12	18.5	20.8	9	1 OXYT_EHFO
13	18	20.2	9	1 OXYT_BURE
14	18	20.2	11	1 O2CA_CWTE
15	18	20.2	15	1 ALLS_MAXSE
16	18	20.2	16	1 KTRC_ASZYA
17	18	20.2	16	1 LESC_PICED
18	17.5	19.7	9	1 OXYT_PABT
19	17	19.1	9	1 OXYT_PABT
20	17	19.1	9	1 OXYV_SQVAC
21	17	19.1	9	1 SAP_STVA
22	17	19.1	13	1 UPE3_MBYVC
23	17	19.1	15	1 COX1_THRUB
24	17	19.1	16	1 OXAL_CKST
25	17	19.1	16	1 UVSX_RPT5
26	16.5	18.5	9	1 ISOT_CVYA
27	16	18.0	7	1 LANC_CASZ
28	16	18.0	9	1 CON_CWVE
29	16	18.0	9	1 OXYT_CVYA
30	16	18.0	10	1 XTRP_PABT
31	16	18.0	11	1 CX5A_CKST
32	16	18.0	11	1 CX5B_CKST
33	16	18.0	12	1 NC40_CKST

34	16	18.0	12	1 PR16_GINBI
35	16	18.0	13	1 ACT7_SOYBN
36	16	18.0	14	1 ATP6_SPIOL
37	16	18.0	15	1 CAX_WHEAT
38	16	18.0	15	1 CX38_CONQU
39	16	18.0	15	1 CX38_DDMA
40	16	18.0	15	1 KLCM_LVTE
41	16	18.0	15	1 ONC1_ORCWY
42	16	18.0	15	1 PH2_PRRAY
43	16	18.0	15	1 UC28_MAIZE
44	16	18.0	16	1 DBH3_RRICE
45	15	16.9	9	1 UAH_HUMAN

## ALIGNMENTS

RESULT 1  
OXYT\_CYPCA STANDARD; PRT; 9 AA.  
ID P23879;  
DT 01-NOV-1991 (Rel. 20, Created;  
DT 01-NOV-1991 (Rel. 20, Last sequence update;  
DT 01-NOV-1995 (Rel. 12, Last annotation update;  
DE Vasotocin.

OS Cyprinus carpio (Common carp), and  
OS Petromyzon marinus (Sea lamprey);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus  
CX NCBI\_TaxID:7962, 7757;  
RN 1;  
RP SEQUENCE.

RC SPECIES: C. carpio, TISSUE: Pituitary;  
RA Acher R., Chalvet J., Chalvet M., Crepy D.  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp, Cyprinus carpio". Comparison with hormones from sea  
RT water bony fishes.  
RC Comp. Biochem. Physiol. 14:245-254(1965).  
RN 1;  
RP SEQUENCE.

RC SPECIES: P. marinus, TISSUE: Pituitary;  
RX MEDLINE:80225976, PubMed:371648;  
RA Kane T.F., Sower S.A., Kawachi H.;  
RT "Antigenic vasotocin from the pituitary gland of the lamprey  
RT (Petromyzon marinus): isolation and amino acid sequence."  
RC Gen. Comp. Endocrinol. 70:152-157(1989).  
CC 1- FUNCTION: ANTI-DIURETIC HORMONE.  
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR: S61364; S61364.  
DR PIR: S65375; S65375.  
DR InterPro: IPR000581; Neurohyp\_horm.  
DR Pfam: PF0220; Hormone4.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID  
FT MOD\_RES  
SQ SEQUENCE 9 AA; 10-3 WW; 17EB176B5456D045 CRC64;  
1 2 3 4 5 6 7 8 9  
AMIDATION

Query Match: 24.71; Score 22; DB 1; Length 9;  
Best Local Similarity: 50.08; Pred. No. 1.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 HELCPR 15  
DB 3 TONGPR 6

RESULT 2  
OXYA\_SQVCA STANDARD; PRT; 9 AA.  
ID P42596;  
DT 01-NOV-1991 (Rel. 20, Created;  
DT 01-NOV-1991 (Rel. 20, Last sequence update;  
DT 01-NOV-1995 (Rel. 12, Last annotation update;  
DE Vasotocin.







KW toxin, hydroxylation; Amidation.  
 FT DISULFID 1 9 PROBABLE.  
 FT DISULFID 2 12 PROBABLE.  
 FT DISULFID 6 13 PROBABLE.  
 FT DISULFID 11 11 HYDROXYLATION.  
 FT MOD RES 15 15 AMIDATION.  
 SQ SEQUENCE 15 AA; 1601 MW; 447894648040 ID (R0644)  
 Query Match 21.3%; Score 19; DB 1; Length 15;  
 Best Local Similarity 28.6%; Pred. No. 2.9e-03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY : CFMKQLADLELCP 14  
 |  
 DB : CCSQDCVCLPCCP 14  
 |  
 RESULT 12  
 QOXT\_EISEN STANDARD; PRT: 9 AA;  
 AC P4939;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Anetoxin.  
 OS Eisenia foetida (Common branding worm) (Common flatworm  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplocladia;  
 CC Lumbricidae; Eisenidae; Eisenia  
 CC NCBI\_TaxID:6196;  
 RN 1;  
 RP SEQUENCE.  
 RC TISSUE: Pituitary;  
 RX MEDLINE:84121660; PubMed:8292046;  
 RA Qurt T, Ukena K, Matsushima G, Ikeda T, Fujita T, Minakawa H,  
 BA Kuroki K,  
 FT "Anetoxin: an oxytocin-related peptide isolated from the earthworm,  
 FT Eisenia foetida";  
 PI Biochem Biophys Res Commun. 1993;193:399-1994;  
 CC 1; FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
 CC RELAXATORY CONTRACTIONS AND BLADDER SHAKING MOVEMENT OF THE  
 CC NEPHRIDIA. MAY BE INVOLVED IN "SNOOZEGUATION" OF THE ANIMAL THROUGH  
 CC NEPHRIDIAL FUNCTION.  
 CC 1; SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 ER PIR; P0021; P02021.  
 DE Interact: IP0000981; Neutryp\_horm.  
 DE Pfam: PF00220; hormone4; 1.  
 DE PROSITE: PS02264; NEUROHYPOPHYS\_H\_42; FALSE NEG  
 KW Hormonal; Amidation  
 FT DISULFID 1 5  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 996 MW; 3468394110 ID (R0644)  
 Query Match 20.8%; Score 18; DB 1; Length 9;  
 Best Local Similarity 28.6%; Pred. No. 1.4e-05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 1;  
 QY : CFMKQLADLELCP 14  
 |  
 DB : ICFVRN -----CP 7  
 |  
 RESULT 13  
 QOXT\_EISEN STANDARD; PRT: 9 AA;  
 AC P4939;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15 SEP 2003 (Rel. 42, Last annotation update)  
 DE Seritoxin ([Ser5,11leu]-oxytocin).  
 OS Bufa beryllaris (leopard toad).  
 CC Eukaryota; Metazoa; Chordata; Clamata; Bufonidae; Bufoninae; Bufonini;  
 CC Amphibia; Bufonidae; Anura; Neobatrachia; Bufonidae; Bufoninae; Bufonini;  
 CC Bufa

OX NCBI\_TaxID:8390;  
 RN 1;  
 RP SEQUENCE.  
 RC TISSUE: Pituitary; Neurointermediate lobe;  
 RX MEDLINE:96059113; PubMed:7591488;  
 RA Chauvet J, Michel G, Ouedraogo Y, Chou J, Chait B.T, Acher P;  
 RT "A new neurohypophyseal peptide, seritoxin ([Ser5,11leu]-oxytocin),  
 RT identified in a dry-season-resistant African toad, Bufo regularis";  
 RL Int J Pept Protein Res. 45:482-487(1995).  
 CC 1; FUNCTION: Peptide of oxytocic activity.  
 CC 1; SUBCELLULAR LOCATION: Secreted.  
 CC 1; SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DE Interact: IP000391; Neutryp\_horm.  
 DE Pfam: PF00220; hormone4; 1.  
 DR PROSITE: PS02264; NEUROHYPOPHYS\_HORM; FALSE NEG.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 983 MW; 17749169456040B CRC64;  
 Query Match 20.2%; Score 18; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY : IQLSLCP 14  
 |  
 DB : IQLSLCP 7  
 |  
 RESULT 14  
 QOXT\_EISEN STANDARD; PRT: 11 AA;  
 AC P80464;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-NOV-2003 (Rel. 45, Last annotation update)  
 DE Quinolone 2-oxidoreductase, alpha chain (EC 1.3.99.17) (fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Comamonadaceae; Comamonas.  
 CC NCBI\_TaxID:285;  
 RN 1;  
 RP SEQUENCE.  
 RC STRAIN:63;  
 RX MEDLINE:9603589; PubMed:7556404;  
 RA Schach S, Ishizuka P, Fetzner S, Lingens F;  
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation";  
 RL Eur J Biochem. 232:535-544(1995).  
 CC 1; FUNCTION: CONVERTS 3-METHYL-1-QUINOLINE TO (3-METHYL-1)-2-OXO-  
 CC 1,2-DIHYDROQUINOLINE.  
 CC 1; CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isooquinolin-  
 CC 1(2H) one + reduced acceptor.  
 CC 1; COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC 1; PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first  
 CC step.  
 CC 1; SUBUNIT: PETERHEXAMER (OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND  
 CC TWO GAMMA CHAINS (PROBABLE)).  
 DR PIR: S66506; S66506.  
 DR Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON-TER 11 11  
 SQ SEQUENCE 11 AA; 1213 MW; 460994322B1DC2CA CRC64;  
 Query Match 20.2%; Score 18; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 2.9e-03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY : IQLSLCP 14  
 |  
 DB : IQLSLCP 11  
 |

```

RHSID: 15
ID: ALLS MANSE STANDARD; PRT: 15 AA.
AC 2425591
PT 01 NOV 1996 Rel. 32. Created.
DT 01 NOV 1996 Rel. 32. Last sequence update.
DE 28 FEB 2003 Rel. 41. Last annotation update.
DE Allotmentation (Mas-AS).
OS Manduca sexta (Tobacco hawkmoth) (Lepidoptera:
OC Eukaryota; Metazoa; Arthropoda; Insecta; Lepidoptera;
OC Neoptera; Euclyptera; Lepidoptera; Glossata; Papilionoidea;
OC Spiliptera; Spiliptera; Manduca.
CX NCBI TaxID: 7130;
RN 11.
RP SEQUENCE.
RC TISSUE Head;
RX MEDLINE: 92050112; PubMed: 1946159;
RA Kravitz S.G., Toschi A., Miller C.A., Karsaka H., Quastad D.B.,
RA Li J.P., Carney R.L., Schooley D.A.;
RT "Identification of an allatostatin from the tobacco hornworm Manduca
RT sexta."
R1 Proc. Natl. Acad. Sci. U.S.A. 86:9438-9442(1989)
CC 1 FUNCTION: STRONGLY INHIBITS GONADOTROPIN RELEASE IN VITRO
CC BY THE CORPORA ALLATA FROM FIFTH-STADIUM LARVAE AND ADULT FEMALES.
CC 1 SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CR FIP; A61612; A61612.
KW Neuropeptide; Pyroglutamate; Carboxyl; Acid.
PT MAP RES 1 1 PVP: LDONE CAP: XY110 A 100.
SO SEQUENCE 15 AA: 1909 MW: 1634 PCD: DRE: DRE: CFC64.

Query Match 20.2%; Score 15; EB 17; Length 15;
Post. Local Similarity 50.0%; Prob. No. 40.0%;
Matches 2; Conservative 1; Mismatch 1; 100.0% 1; 100.0% 0;

CY 1 CPM 4
BL 2 CYP 10

Search completed: November 5, 2003, 12:13:10
Job time: 12 secs

```

GenCore version 5.1.6  
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QW protein protein search, using sw model

Run on: November 5, 2003, 18:10:25 : Search time: 13 Seconds

With local alignment

Title: US-09-914-088-13

Perfect score: 89

Sequence: 1 QWKKQLADLECHRE 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 81025 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4 21

Minimum CB seq length: 3

Maximum CB seq length: 16

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SPTREMS, 23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_humans:\*

5: sp\_invertebrate:\*

6: sp\_mammals:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phages:\*

10: sp\_plants:\*

11: sp\_protein:\*

12: sp\_virus:\*

13: sp Vertebrate:\*

14: sp Unclassified:\*

15: sp\_virus:\*

16: sp\_bacteria:\*

17: sp\_archaea:\*

Pred. No. is the number of results identified by the search engine  
score greater than or equal to the score of the best hit found,  
and is derived by analysis of the data set.

# SUMMARIES

Result	Ref	Score	Query	Length	DB	ID
1	27	30.3	15	5	Q9TW99	
2	25	28.1	14	4	O15222	
3	24	28.0	15	2	O9R407	
4	23	25.8	13	6	Q9TUB1	
5	23	25.8	15	10	Q8WAX4	
6	23	25.4	15	11	O91XV4	
7	23	25.4	16	2	O937K1	
8	22	24.7	11	4	O75811	
9	22	24.7	11	4	O9H3V2	
10	22	24.7	11	13	Q9R582	
11	22	24.7	14	4	Q8TCE4	
12	22	24.7	15	4	Q9UCB3	
13	22	24.7	15	4	Q9XKX3	
14	21	23.6	11	7	O76131	
15	21	23.6	13	13	Q8R2S5	
16	21	23.6	14	1	Q8TUB1	

17	21	23.6	14	6	Q9V131	Q8TUB1 sus scrofa
18	21	23.6	15	2	Q47892	Q47892 trematode
19	21	23.6	15	10	Q9S631	Q9S631 scenedesmus
20	21	23.6	16	3	P79014	P79014 emericella
21	20	22.5	10	2	Q9RSU2	Q9RSU2 heliobacter
22	20	22.5	10	9	Q17103	Q17103 saccharomyc
23	20	22.5	11	10	Q9T029	Q9T029 brassica ol
24	20	22.5	12	2	Q9S5F7	Q9S5F7 heliobacter
25	20	22.5	12	2	Q9S5F5	Q9S5F5 heliobacter
26	20	22.5	13	4	Q9H4C1	Q9H4C1 homo sapien
27	20	22.5	14	11	Q921H4	Q921H4 mus musculu
28	20	22.5	14	5	Q9PYL3	Q9PYL3 human t cell
29	20	22.5	15	9	Q8C277	Q8C277 lactococcus
30	20	22.5	16	4	Q16731	Q16731 homo sapien
31	19	21.3	13	4	Q9H454	Q9H454 homo sapien
32	19	21.3	12	12	Q8S577	Q8S577 theiler's e
33	19	21.3	12	12	Q8S578	Q8S578 theiler's e
34	19	21.3	12	12	Q8S579	Q8S579 theiler's e
35	19	21.3	12	12	Q8S575	Q8S575 theiler's e
36	19	21.3	12	12	Q8S580	Q8S580 theiler's e
37	19	21.3	12	12	Q8S582	Q8S582 theiler's e
38	19	21.3	12	12	Q8S581	Q8S581 theiler's e
39	19	21.3	12	12	Q8S576	Q8S576 theiler's e
40	19	21.3	13	2	Q9XBYC	Q9XBYC nitrogen fi
41	19	21.3	15	2	Q9R542	Q9R542 mycobacteri
42	19	21.3	15	4	P78482	P78482 homo sapien
43	19	21.3	15	6	P82665	P82665 bos taurus
44	19	21.3	16	4	Q9DP51	Q9DP51 homo sapien
45	18	20.2	9	4	Q16276	Q16276 homo sapien

## ALIGNMENTS

RESULT 1  
Q9TW99 PRELIMINARY; PRT: 15 AA.

AC Q9TW99  
CT Q1-MAY 2003 (TEMPREL: 13, Created)  
DT Q1-MAY 2003 (TEMPREL: 13, Last sequence update)  
DT Q1-JUN 2003 (TEMPREL: 14, Last annotation update)  
DE G39 antigen (fragment)  
OS Hirudo medicinalis (Medicinal leech)  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinidae; Hirudo.  
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI TaxID:6421.  
BN 111  
BB SEQUENCE  
RA MEDLINE: 94195315 [EMBL-BL13084]  
RA Luthi, L E.; Froehner, G.; Jentsch, P.  
RT "Identification of a 70 kD protein with sequence homology to squid  
RT neurofilament protein in glial cells of the leech CNS."  
RL C. Neurobiol. 25:821-821(1994).  
SQ SEQUENCE 15 AA: 1717 MW: 1535H4984A11C95E CRC64;

Query Match: 30.3%, Score 27; DB 5; Length 15;  
Best Local Similarity: 62.5%; Pred.No. 7.1e+02;  
Matches: 5; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

QY 4 NKQLADLE 11  
DB 2 NCQUSQVE 9

RESULT 2  
O15222 PRELIMINARY; PRT: 14 AA.

AC O15222  
CT Q1-JAN 1998 (TEMPREL: 15, Created)  
DT Q1-JAN 1998 (TEMPREL: 15, Last sequence update)  
DT Q1-DEC-2001 (TEMPREL: 19, Last annotation update)  
DE BOXC9 protein (insect)  
OX NCBI TaxID:6421.

```

CE Homo sapiens Human
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
CC NCBI_TaxID=9606;
CN 1;
EN
FX SEQUENCE FROM N.A.
FX XREF:ENR019011; PubMed=9357979;
GA FLAG:Oligo E.C. Gibaud A.; Durrillaux R.; Poupon M.F.; Mallat Y.B.;
RT Distinct patterns of all-trans retinoic acid dependent expression of
RT the HcXB and HcXC homologues in human embryonal and small-cell lung
RT carcinoma cell lines";
PL PERS Lett. 415:263-267;1997);
PL EVEL X99642; CAA67998.1;
DR TRANSFAC; T03327;
FT NON-TER
FT
SQ SEQUENCE 14 AA; 10725 MW; 6C5D727255499A18 CR664;
Query Match 58.1%; Score 35; DB 4; Length 14;
Best Local Similarity 25.6%; Pred. No. 1 be-04;
Matches 5; Conservative 1; Mismatches 4; Indels 3; Gaps 0;
CY 3 MKKQTADLE 11
DB 111; 11
DB 4 MKKERTDKE 12
RESULT 3
CQ3477 PRELIMINARY; PRT; 15 AA;
CC Q09437
CC Q09437
CT 01-MAY-2000 (TEMBREL); 13; Created;
CT 01-MAY-2000 (TEMBREL); 13; Last sequence update;
CT 01-JUN-2000 (TEMBREL); 14; Last annotation update;
DE Malonate decarboxylase gamma subunit; Fragment;
DS Acinetobacter calcoaceticus;
DS Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteria;
DS Moraxellaceae; Acinetobacter;
DS NCBI_TaxID=471;
EN 1;
EN SEQUENCE
RX MELINE-95050612; PubMed=7761952;
RA Kinyas, Pyon H.S.;
RA Functionalization and properties of a novel type of "calixarene"
RA from Acinetobacter calcoaceticus";
RE J. Polym. Chem. 269:29616-29641(1994);
SQ SEQUENCE 15 AA; 1816 MW; 4514F1E49F4F0A 5434;
Query Match 24.2%; Score 14; DB 4; Length 15;
Best Local Similarity 15.7%; Pred. No. 2 be-04;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
CY 1 MNKQLADCELPRE 16
DB 111; 11
DB 1 MNTELLKQLEFPKQ 14
RESULT 4
CQ3477 PRELIMINARY; PRT; 14 AA;
AC Q09437
CT 01-MAY-2000 (TEMBREL); 13; Created;
CT 01-MAY-2000 (TEMBREL); 13; Last sequence update;
CT 01-MAY-2000 (TEMBREL); 13; Last annotation update;
DE Tia-2/tek receptor tyrosine kinase; Fragment;
DS Bos taurus; Bovine;
DS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bos;
DS NCBI_TaxID=9913;
EN 1;
EN SEQUENCE FROM N.A
FX XREF:ENR019011; PubMed=9357979;
GA FLAG:Oligo E.C. Gibaud A.; Durrillaux R.; Poupon M.F.; Mallat Y.B.;
RT Distinct patterns of all-trans retinoic acid dependent expression of
RT the HcXB and HcXC homologues in human embryonal and small-cell lung
RT carcinoma cell lines";
PL PERS Lett. 415:263-267;1997);
PL EVEL X99642; CAA67998.1;
DR TRANSFAC; T03327;
FT NON-TER
FT
SQ SEQUENCE 14 AA; 10725 MW; 6C5D727255499A18 CR664;
Query Match 58.1%; Score 35; DB 4; Length 14;
Best Local Similarity 25.6%; Pred. No. 1 be-04;
Matches 5; Conservative 1; Mismatches 4; Indels 3; Gaps 0;
CY 3 MKKQTADLE 11
DB 111; 11
DB 4 MKKERTDKE 12

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RT "Cloning and characterization of human tie-2/-ek promoter."
RL Submitted (JUL-1998) to the FvBL/GenBank/DBSJ databases.
DR EMBL: AF077857; AAF01566.1;
KW Kinase; Receptor;
FT NON_TER 13
SQ SEQUENCE 13 AA: 1295 MW: 8AF0F2F5RCBCQ735 CRC64;

Query Match 25.8%; Score 23; DB 6; Length 13;
Best Local Similarity 71.4%; Pred No. 3.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 7 LADLEUC 13
DB 4 LADLEUC 10

RESULT 5
ID Q8W4X5 PRELIMINARY; PRT; 15 AA.
AC Q8W4X5;
DT 01-MAR-2002 (TREVELLRE); 20; Created;
DT 01-MAR-2002 (TREVELLRE); 20; Last sequence update;
DT 01-MAR-2002 (TREVELLRE); 20; Last annotation update;
DE Chl3/nitrate reductase structural protein (Fragment).
GN NIA2.
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID:3702;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE:93005711; PubMed:1840922;
RA Wilkinson J.Q.; Crawford N.M.;
RT Identification of the Arabidopsis Chl3 gene as the nitrate reductase
RT structural gene NIA2.
RJ Plant Cell 14:461-471 (1991);
DR EMBL: S45394; AAC32722.1;
FT NON_TER 15
SQ SEQUENCE 15 AA: 1721 MW: V1C9G1F0829ELQFD CRC64;

Query Match 25.8%; Score 23; DB 10; Length 15;
Best Local Similarity 62.5%; Pred No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 4 NKQJLAME 15
DB 4 NKQJLAME 14

RESULT 6
ID Q91XV8 PRELIMINARY; PRT; 15 AA.
AC Q91XV8;
DT 01-DEC-2001 (TEMSHORE); 19; Created;
DT 01-DEC-2001 (TEMSHORE); 19; Last sequence update;
DT 01-DEC-2001 (TEMSHORE); 19; Last annotation update;
DE 2alpha hydroxysteroid dehydrogenase (Fragment).
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID:10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE:Liver;
RA Nakaiwa T.; Yasuda K.; Okada H.; Sanezum M.; Osaki T.; Kanzaki H.;
RA Nishizawa, N. Ito S.;
RT Expression of 2alpha-HSD (hydroxysteroid dehydrogenase) in
RT endometrium.
PL Fertilization and Implantation 17:186-197 (2000).
DR EMBL: AB028566; BAF4203.1;
FT NON_TER 15
SQ SEQUENCE 15 AA: 1792 MW: B45DE7CF45C4822F CRC64;

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Query Match 25.8% Score 23 DB 11 Length 16  
 Best Local Similarity 40.0% Pred. No. 3.7e+03;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 MKKQADLEL 12  
 DB 1 MNSKIQKXEL 10

RESULT 9  
 Q95811 PRELIMINARY; PRT: 11 AA.  
 ID Q95811  
 AC Q95811  
 DT 01-DEC-2001 (TRENDSrel. 13, Created;  
 DT 01-DEC-2001 (TRENDSrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TRENDSrel. 23, Last annotation update)  
 DE Putative metcuroic reductase (Fragment)  
 GN NEPA.  
 OS Escherichia coli.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
 CC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID:562  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=HE13; TRANSPOSON-TN5057;  
 EX MEDLINE=1694134; PubMed=11763247  
 PA Mindlin S.Z., Khododil G.V., Gorienko Z.M., Vinadkina S.V.,  
 PA Minakshin L.S., Kalyaeva E.S., Kopteva A.V., Petiova M.A.,  
 RA Yurlova O.V., Nikiforov V.G.  
 RT "Vesicular resistance transposons of Gram-negative enteric bacteria.  
 RT bacteria and their classification".  
 RL Rss. Microbiol. 152:811-822(2001).  
 DE EMBL: AF162764; CAC83555.1;  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1713 MW; 5AD764652956E12664;

Query Match 25.8% Score 23 DB 21 Length 16;  
 Best Local Similarity 40.0% Pred. No. 3.9e+03;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 NKQADLEL 13  
 DB 5 NKQKQSCC 14

RESULT 9  
 Q95811 PRELIMINARY; PRT: 11 AA.  
 ID Q95811  
 AC Q95811  
 DT 01-NOV-1998 (TRENDSrel. 08, Created;  
 DT 01-NOV-1998 (TRENDSrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TRENDSrel. 08, Last annotation update)  
 DE Pdb3 R2 (Fragment)  
 CC ERBB3-3.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TRANSUR=Ovarian carcinoma;  
 EX MEDLINE=98345147; PubMed=9681822;  
 PA Lee H., Mathie N.J.,  
 RT "Isolation and characterization of four alternative 5'UTR? transcripts  
 RT expressed in ovarian carcinoma-derived cell lines and normal human  
 RT tissues".  
 RL Oncogene 16:3243-3252(1998).  
 DE EXPL: U88358; AAC39858.1;  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1017 MW; 218234166E87C7979 97647;

Query Match 24.7% Score 22 DB 4 Length 11;  
 Best Local Similarity 50.0% Pred. No. 4.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 75.0% Pred. No. 4.1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LCPK 15  
 DB 6 LCPK 9

RESULT 9  
 Q9H3V7 PRELIMINARY; PRT: 11 AA.  
 ID Q9H3V7  
 AC Q9H3V7  
 DT 01-MAR-2001 (TRENDSrel. 16, Created;  
 DT 01-MAR-2001 (TRENDSrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENDSrel. 16, Last annotation update)  
 DE Aquaporin-4 (Fragment)  
 GN AQP4.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97008105; PubMed=8855281;  
 RA Lu M., Lee M.D., Smith B.L., Jung J.S., Agre P., Verkijk M.A.J.,  
 RA Merks G., Ripps J.P.L., Beer P.M.,  
 RT "The human AQP4 gene: definition of the locus encoding two water  
 RT channel polypeptides in brain".  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:15908-15912(1996).  
 DE EMBL: J63613; AAC17964.1;  
 KW Potn.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1233 MW; 37959CA111AER737 CRC64;

Query Match 24.7% Score 22 DB 4 Length 11;  
 Best Local Similarity 80.0% Pred. No. 4.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LCPK 16  
 DB 5 LCPK 9

RESULT 10  
 Q9PS22 PRELIMINARY; PRT: 11 AA.  
 ID Q9PS22  
 AC Q9PS22  
 DT 01-MAY-2000 (TRENDSrel. 13, Created;  
 DT 01-MAY-2000 (TRENDSrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENDSrel. 20, Last annotation update)  
 DE Hydrin 1, VASOTOCINYL G2Y-LYS.  
 OS Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=91200145; PubMed=8452872;  
 RA Iwamuro S., Hayashi H., Kikuyama S.,  
 RT "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-  
 RT Lys, in Xenopus neurohypophysis".  
 RL Biochem. Biophys. Acta 1176:143-147(1993).  
 DR InterPro: IPR000991; Neutryp\_horm.  
 DR Pfam: PF0220; hormone4.1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 SQ SEQUENCE 11 AA; 1238 MW; CC5B57EB176B9456 CRC64;

Query Match 24.7% Score 22 DB 13 Length 11;  
 Best Local Similarity 50.0% Pred. No. 4.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 10 Q9BCP5 15
FB 1 Q9BCP5 8

RESULT 11
Q9BCP5
ID Q9BCP5 PRELIMINARY: PRT: 14 AA
AC Q9BCP5
DT 01-JUN-2003 (TRENDS) 21, Created
DT 01-JUN-2003 (TRENDS) 21, Last sequence update
DT 01-JUN-2003 (TRENDS) 21, Last annotation update
DE CDS beta chain (Fragment)
GN CDS
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Kuster I.J., Grealis M.M., Landres L., Naj S., Nakatani Y.,
RA Kopal Shigamatsu T., Kavathas P.B.
RT Identification of a Candidate Regulatory Region in the Human CDS Beta
RT Complex by Colocalization of Orase I Hypersensitive Sites and Matrix
RT Attraction Regions Which Bind SAGE and GATA 3
RC J. Immunol. 168:1915-1924(2002)
DR EMBL: AY037223; AAK91556 1;
FT NON_TER 1
SQ SEQUENCE 14 AA: 1761 MW; 6463EDR22EAC1B CRC64;

Query Match 24.7%; Score 22; CR 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.0e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 Q9ADLE5BP 15
FB 1 Q9ADLE5BP 15

RESULT 12
Q9ADLE5BP
ID Q9ADLE5BP PRELIMINARY: PRT: 15 AA
AC Q9ADLE5BP
DT 01-MAY-2003 (TRENDS) 14, Created
DT 01-MAY-2003 (TRENDS) 14, Last sequence update
DT 01-MAY-2003 (TRENDS) 14, Last annotation update
DE Insulin like growth factor receptor alpha (Fragment)
GN IGF1R
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Mellgren J., Paz I.B., Maddux B.A., Substone L.F., Bell G.A.,
RA Fujita Y., Yaguchi Y.
RT Characterization of human placental insulin like growth factor
RT I/Insulin hybrid receptors by protein microsequencing and
RT purification
RC Biochemistry 42:1351-1356(1993)
DR Biochemistry 42:1351-1356(1993)
SQ SEQUENCE 15 AA: 1761 MW; 896F444E4E4E4E4E CRC64;

Query Match 24.7%; Score 22; CR 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 5.0e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 Q9BCP5 15
FB 1 Q9BCP5 8

RESULT 13
Q9BCP5
ID Q9BCP5 PRELIMINARY: PRT: 14 AA
AC Q9BCP5
DT 01-JUN-2003 (TRENDS) 21, Created
DT 01-JUN-2003 (TRENDS) 21, Last sequence update
DT 01-JUN-2003 (TRENDS) 21, Last annotation update
DE CDS beta chain (Fragment)
GN CDS
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Kuster I.J., Grealis M.M., Landres L., Naj S., Nakatani Y.,
RA Kopal Shigamatsu T., Kavathas P.B.
RT Identification of a Candidate Regulatory Region in the Human CDS Beta
RT Complex by Colocalization of Orase I Hypersensitive Sites and Matrix
RT Attraction Regions Which Bind SAGE and GATA 3
RC J. Immunol. 168:1915-1924(2002)
DR EMBL: AY037223; AAK91556 1;
FT NON_TER 1
SQ SEQUENCE 14 AA: 1761 MW; 6463EDR22EAC1B CRC64;

Query Match 24.7%; Score 22; CR 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.0e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Q9BCP5
ID Q9BCP5 PRELIMINARY: PRT: 15 AA
AC Q9BCP5
DT 01-JUN-2003 (TRENDS) 17, Created
DT 01-JUN-2003 (TRENDS) 17, Last sequence update
DT 01-MAR-2002 (TRENDS) 20, Last annotation update
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment)
GN TGM2
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Pestoff R.W.
RT Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease
RC J. Biol. Chem. 276:32001-32005(2001)
DR EMBL: AF311286; AAK15272 1;
FT NON_TER 1
SQ SEQUENCE 15 AA: 1641 MW; 0345982AF8F8F851 CRC64;

Query Match 24.7%; Score 22; CR 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 FVWQQLA 13
FB 1 FVWQQLA 13

RESULT 14
FVWQQLA
ID FVWQQLA PRELIMINARY: PRT: 11 AA
AC FVWQQLA
DT 01-NOV-1998 (TRENDS) 08, Created
DT 01-NOV-1998 (TRENDS) 08, Last sequence update
DT 01-DEC-2001 (TRENDS) 19, Last annotation update
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Cichlidae;
CC Cichlidae; Oreochromis
CX NCBI_TaxID:6128;
RN 1;
RP SEQUENCE FROM N.A.
RX VEDJN858131.1; PubMed:9648339;
RA Valasek-Kutyznska Z., McAndrew H., Vincek V.,
RA Figueroa F., Sultman H., Klein G.
RT Linkage relationships and haplotype polymorphism among cichlid the
RT class II B loci
RC Genetics 149:1527-1537(1998)
DR EMBL: AF050527; AAC41866 1;
FT NON_TER 1
SQ SEQUENCE 11 AA: 1362 MW; 03C12C8EB7341B54 CRC64;

Query Match 25.6%; Score 21; CR 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 1; Gaps 0;

QY 2 FVWQQLA 13
FB 1 FVWQQLA 13

RESULT 15
FVWQQLA
ID FVWQQLA PRELIMINARY: PRT: 11 AA
AC FVWQQLA
DT 01-NOV-1998 (TRENDS) 08, Created
DT 01-NOV-1998 (TRENDS) 08, Last sequence update
DT 01-DEC-2001 (TRENDS) 19, Last annotation update
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Cichlidae;
CC Cichlidae; Oreochromis
CX NCBI_TaxID:6128;
RN 1;
RP SEQUENCE FROM N.A.
RX VEDJN858131.1; PubMed:9648339;
RA Valasek-Kutyznska Z., McAndrew H., Vincek V.,
RA Figueroa F., Sultman H., Klein G.
RT Linkage relationships and haplotype polymorphism among cichlid the
RT class II B loci
RC Genetics 149:1527-1537(1998)
DR EMBL: AF050527; AAC41866 1;
FT NON_TER 1
SQ SEQUENCE 11 AA: 1362 MW; 03C12C8EB7341B54 CRC64;

Query Match 25.6%; Score 21; CR 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 1; Gaps 0;

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DT C1-MAR-2003 (TREMBSrel. 23, Created)  
 DT C1-MAR-2003 (TREMBSrel. 23, Last sequence update)  
 DT C1-MAR-2003 (TREMBSrel. 23, Last annotation update)  
 DE Gill urea transporter (fragment)  
 CN EUT  
 OS Anguilla japonica (Japanese eel)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Atherinomorpha; Atherinidae;  
 CC Anguilla  
 OX NCBI TaxID:5347  
 EN Eel  
 EN SEQUENCE FROM N.A.  
 SC TISSUE: Liver,  
 RA Hirose S., Mistry A.C.,  
 RA "eel gill urea transporter (eut) gene",  
 RL Submitted (Oct 2000) to the EMBL/GenBank/CCPC databases.  
 DR EMBL: AB049727; BAC51977.1; ...  
 FT NCN TSS 13  
 SC SEQUENCE 13 AA; 1536 MW; 4F367086488AA07 CRC64,  
 Query Match 23.6%; Score 11; CP 13; Length 19  
 Best local Similarity 33.3%; Pred. No 7.1e+03;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPXNKQLAD 9  
 |||:  
 Sb 4 CPDDEWPD 12

Search completed: November 5, 2003, 18:14:02  
 Job time: 1:45 secs

GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 18:04:19 Search time 41 seconds  
Without alignments  
61,942 Million cell updates/sec

Title: US 09-914 088-13

Perfect score: 89

Sequence: CPWKQACHELOPRE 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107963 seqs, 158726571 residues

Total number of hits satisfying chosen parameters: 16014

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Listing first 45 summaries

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Prod. No. is the number of results predicted by database to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	21	AA025935
2	89	100.0	16	22	AAU16660
3	89	100.0	16	23	AAU16660
4	81	93.3	16	21	AA025918
5	81	93.3	16	22	AAU16642
6	83	93.3	16	23	AAU00112
7	72	80.9	13	21	AA025918
8	72	80.9	13	22	AAU16661
9	72	80.9	13	23	AAU00114

10	66	74.2	13	21	AA025935	P1 mimotop SEQ ID
11	66	74.2	13	22	AAU16660	Peptide #1 derived
12	66	74.2	13	23	AAU00112	Human IgE cyclic
13	33	37.1	13	21	AA025918	P1 mimotop Peptide
14	33	37.1	13	22	AAU16642	Peptide P15g deriv
15	33	37.1	13	23	AAU00112	Human IgE cyclic
16	33	37.1	16	23	AAU00542	Human IgE cyclic
17	32	36.0	15	23	ABP0122	Human F10.01 N10
18	31	34.9	9	23	ABG34937	Human bone marrow
19	31	34.9	15	24	ABP08677	Human dihydrogenase
20	30	33.7	9	22	ABP16414	HIV A24 super moti
21	30	33.7	9	22	ABP4330	HIV A24 motif tat
22	30	33.7	11	22	ABP16416	HIV A24 super moti
23	30	33.7	11	22	ABP1937	HIV A03 motif tat
24	30	33.7	11	22	ABP21769	HIV A11 motif tat
25	30	33.7	14	22	AA096762	Human peptide #37
26	30	33.7	15	22	ABP4821	HIV DR Super-delf
27	29	32.6	9	22	AA09500	PRAME derived HLA-
28	29	32.6	10	23	ABP4863	CTL epitope HLA pe
29	29	32.6	10	23	ABP4959	CTL epitope HLA pe
30	29	32.6	10	23	ABP5030	CTL epitope HLA pe
31	29	32.6	10	23	ABP5145	CTL epitope HLA pe
32	29	32.6	12	14	AA030479	Synthetic sequence
33	29	32.6	12	14	AA030464	Synthetic sequence
34	29	32.6	12	14	AA030370	Human glycoalbumin
35	29	32.6	12	22	AA098053	Human peptide #132
36	28	31.5	10	24	ABP19082	Human cancer-relat
37	28	31.5	10	24	ABP19538	Human cancer-relat
38	28	31.5	10	24	ABP19685	Human cancer-relat
39	28	31.5	10	24	ABP19871	Human cancer-relat
40	28	31.5	10	24	ABP2136	Human cancer-relat
41	28	31.5	11	23	AA027463	Sequence of glycop
42	28	31.5	13	19	AA076566	Cyclic-UPA peptide
43	28	31.5	13	19	AA076570	Cyclic-UPA peptide
44	28	31.5	13	23	ABG60452	Selective target in
45	28	31.5	14	23	ABG61658	Human Hsp90XX? asp

# ALIGNMENTS

RESULT 1  
AAB25919 standard: Peptide: 16 AA

XX AAB25919  
XX AC AAB25919  
XX UT 05-JAN-2001 (first entry)  
XX DE P1 mimotop peptide P15g9 SEQ ID NO:13  
XX KW Epitope/ mimotop, Human, immunoglobulin E, IgE, C-epsilon-2 domain;  
KW allergic disease; immunophy-axis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.

XX OS Homo sapiens.  
XX XX  
XX PN W0000050460-01  
XX PD 31-AUG-2000  
XX PF 22 FEB 2003; 2003W; EP01455  
XX PR 25-FEB-1999; 99GB 0004405  
XX PR 29-MAY 1999; 99GB 0007151  
XX PR 07-MAY 1999; 99GB 0010537  
XX PR 07-MAY 1999; 99GB 0015538  
XX PR 07-AUG 1999; 99GB 0015594  
XX PR 07-AUG 1999; 99GB 0015603  
XX PR 07-SEP 1999; 99GB 0021046  
XX PR 07-SEP 1999; 99GB 0021047  
XX PR 09-OCT 1999; 99GB 0026619

PP 21-NOV 1999; 99GB-0027698.  
XX (SMK) SWITKLINE BEECHAM BIOLOGICALS.  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamm A, Martin S,  
TI Randall R, Turrell WG, Van Mechelen WF, Vinals B, Bassols YC.  
XX WPI: 2000-52003/53.  
XX  
XX Peptide useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed fragment of a specific  
PT domain from immunoglobulin E.  
XX  
XX Claim 14; Page 49; 129pp; English  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E) of Cεpsilon-2 domain (II) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are (III) an  
CC immunogen (III) for treating allergy comprising (I) or (II) a vaccine (III)  
CC protein for use in a pharmaceutical composition or a vaccine. The  
CC protein for use in a pharmaceutical composition or a vaccine (III)  
CC recognising EII (4), a pharmaceutical composition (IV) comprising (I),  
CC (II) a peptide (Ia), capable of being recognised by EII, (4) an immunogen  
CC (IIa) comprising (Ia), and (V) producing (Ia) by producing (IIa) (I)  
CC can have antiallergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor (I), (II) and (III) are  
CC used in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies (IV) is useful for identifying mimotopes of PI,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies (V) is useful in diagnosing and in the affinity purification  
CC of circulating anti IgE antibodies from blood (I), (II) and (III) are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. Analogs to AA016644 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.  
XX  
XX Sequence 16 AA;  
SQ

Query Match 100.0%; Score 89; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : CPNNKQACLELCPE 16  
DB : CPNNKQACLELCPE 16  
AC : CPNNKQACLELCPE 16  
CT 01-SEP 2002 (first entry)  
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 94.  
XX Immunogen: human IgE immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic, cyclic.  
XX Homo sapiens.  
XX WO200216403-A2.  
XX 28-FEB 2003.  
XX 17-AUG-2003; 2003WO-EP04576.  
XX 22-AUG-2000; 2000US-0023717.  
XX (SMK) SWITKLINE BEECHAM BIOLOGICALS.  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX Friede M, Mason S, Turrell WG, Vinals Bassols YC;  
XX WPI: 2001-449644/42.  
XX  
XX Technology used in vaccine for treatment of allergy, comprises

PP 22-AUG-2000; 2000GB-0020705.  
XX (ACAM) ACAMBIS RES LTD.  
PA (SMK) SWITKLINE BEECHAM BIOLOGICALS.  
XX  
PI Flynn M, Johnson T;  
XX WPI: 2001-521967/51.  
XX  
XX A linkage comprising an immunogenic conjugate useful treatment of IGE  
PT mediated diseases  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
CC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimotopes of the  
CC Cεpsilon2, Cεpsilon3 or Cεpsilon4 regions of human immunoglobulin E  
CC (IgE) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IGE mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope (antigen) to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AA016642-AA016913 represent peptides derived from or mimotopes of  
CC the Cεpsilon2/Cεpsilon3/Cεpsilon4 region of human IgE.  
XX  
XX Sequence 16 AA;  
SQ

Query Match 100.0%; Score 89; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : CPNNKQACLELCPE 16  
DB : CPNNKQACLELCPE 16  
AC : CPNNKQACLELCPE 16  
CT 01-SEP 2002 (first entry)  
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 94.  
XX Immunogen: human IgE immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic, cyclic.  
XX Homo sapiens.  
XX WO200216403-A2.  
XX 28-FEB 2003.  
XX 17-AUG-2003; 2003WO-EP04576.  
XX 22-AUG-2000; 2000US-0023717.  
XX (SMK) SWITKLINE BEECHAM BIOLOGICALS.  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX Friede M, Mason S, Turrell WG, Vinals Bassols YC;  
XX WPI: 2001-449644/42.  
XX  
XX Technology used in vaccine for treatment of allergy, comprises

PT disulfide bridge cyclized peptide and immunogenic carrier -  
 PS Claim 4; Page 11; 45pp; English.  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 89; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFNKKQLADLELCPE 16  
 DB 1 CFNKKQLADLELCPE 16  
 AC AAU16643;  
 DT 05 JAN 2001 (first entry)  
 DE P1 mimotope peptide C67/8 SEQ ID NO:12.  
 KW Epitope; mimotope; human; immunoglobulin E (IgE); Cepsilon2 domain;  
 KW allergic disease; immunotherapy; immunotherapy; allergic  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX Homo sapiens.  
 OS Synthetic.  
 PN WQ26014574-A2.  
 XX 31-AUG 2000.  
 XX 22 FEB 2000; 2000WQ-EP01455.  
 XX 25 FEB 1999; 99GB-0024405.  
 XX 29 MAR 1999; 99GB-0024405.  
 XX 07 MAY 1999; 99GB-0010537.  
 XX 07 MAY 1999; 99GB-0010537.  
 XX 07 AUG 1999; 99GB-0018534.  
 XX 07 AUG 1999; 99GB-0018534.  
 XX 07 SEP 1999; 99GB-0021046.  
 XX 07 SEP 1999; 99GB-0021047.  
 XX 29-OCT 1999; 99GB-0025619.  
 XX 23-NOV-1999; 99GB-0027699.  
 XX  
 XX (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX (SPR) : PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Cyson N, Friede M, Greenwood J, Hewitt B, Lambert A, Mason J,  
 XX Randall P, Turner WG, Van Mechelen WP, Vinals D, Westhead R.  
 XX WPI; 2001-572973/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 XX diseases, comprising an isolated surface exposed group of a specific  
 XX domain from immunoglobulin E -  
 XX Example 6; Page 12; 129pp; English  
 XX The present invention describes a peptide (1) comprising an isolated  
 XX surface exposed group/epitope (E) of Cepsilon2 domain (2) of  
 XX immunoglobulin E (IgE), or its mimotope. Also described is (3) an  
 XX immunogen (11) for treating allergy comprising (1) (2) a vaccine (111)

CC for treating allergies comprising (11); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (1a) capable of being recognised by (IV); (6) an immunogen  
 CC (12a) comprising (2a); and (7) producing (11) by producing (11); (11)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (1), (11) and (11) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (1) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (1), (11) and (11) are  
 CC useful for treating a patient susceptible to it suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AA25907 to AA26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 99.3%; Score 83; DB 21; Length 16;  
 Best Local Similarity 97.5%; Pred. No. 1,2e-06;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFNKKQLADLELCPE 16  
 DB 1 CFNKKQLADLELCPE 16  
 AC AAU16643;  
 DT 07-NOV 2001 (first entry)  
 DE Peptide C67/8 derived as mimotope of Cepsilon2 region of human IgE.  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 PN WQ26014574-A2.  
 XX 28-NOV 2001.  
 XX 21-FEB 2000; 2000WQ-0904935.  
 XX 21-DEC 1999; 99GB-0031233.  
 XX 22-FEB 2000; 2000GB-0004396.  
 XX 22-AUG-2000; 2000GB-0025707.  
 XX 22-AUG 2000; 2000GB-0025708.  
 XX  
 XX (ACAM) : ACAMRIS RES LTD.  
 XX (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Flint N, Johnson T;  
 XX WPI; 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 XX mediated diseases  
 XX Example 4; Page 21; 46pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. (111)

invention describes peptides derived from or mimotopes of the C-peptide, C-peptide or C-peptide regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds, the compounds or compositions of the invention are used in the manufacture of a medicament for the treatment of IgE mediated diseases, the invention allows for controlled conjugation of a peptide epitope, antigen to a protein as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient.

AA016912-AD016913 represent peptides derived from or mimotopes of the C-peptide/C-peptide/C-peptide region of human IgE

Sequence 16 AA:  
 Query Match 93.1% Score 43; E-Value 1e-08; Length 16  
 Best Local Similarity 87.5% Pref No. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 CFMKKQAULELCPE 16  
 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  
 1 CFMKKQAULELCPE 16

RESULT 6  
 AB016913  
 ID AB016913 standard; Peptide: 16 AA  
 AC AB016913  
 DT 22 SEP 2003 (first entry)  
 XX Human IgE cyclic immunogenic peptide SEQ ID NO. 16  
 LE Human IgE cyclic immunogenic peptide SEQ ID NO. 16  
 XX Immunogen; human IgE; immunoglobulin E; allergy; the C-peptide region  
 KW vaccine; anti-allergic; cyclic  
 XX Homo sapiens  
 CS WO2000050460 A2  
 PR 29-FEB-1999; 98GB 0007152  
 PR 07-MAY-1999; 98GB 0015337  
 PR 07-MAY-1999; 98GB 0015338  
 PR 07-AUG-1999; 98GB 0015594  
 PR 27-AUG-1999; 98GB 0015603  
 PR 27-SEP-1999; 98GB 0021046  
 PR 27-SEP-1999; 98GB 0021047  
 PR 29-OCT-1999; 98GB 0025619  
 PR 23-NOV-1999; 98GB 0027698  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD  
 XX Lyson M, Fricke M, Greenwood J, Hewitt E, Lamont A, Mason S, Randall P, Turnell W, Van Vechelen MP, Vinals De Bassols YC, WFI: 2000 51273753  
 DR Peptides useful for treating, preventing and ameliorating allergic diseases, comprising an isolated surface exposed group of a specific domain from immunoglobulin E  
 XX Description: Page 11; 45pp; English  
 CC The present invention describes a peptide (I) comprising an isolated surface exposed epitope (E) of C-peptide 2 domain (C) of immunoglobulin E (IgE), or its mimotope. Also described are: (i) an immunogen (II) for treating allergy comprising (i); (2) a vaccine (III) for treating allergies comprising (i); (3) a ligand (IV) capable of recognising E; (4) a pharmaceutical composition (V) comprising (IV); (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen (Ia) comprising (Ia); and (7) producing (Ia) by producing (Ia). (I) can have anti-allergic and immunosuppressive activities, and can be used as a vaccine and histamine release inhibitor (II), (III) and (IV) are useful in medicine and in the manufacture of medicaments for treating and preventing allergies. (IV) is useful for identifying mimotopes of E, in medicine and also in manufacturing medicaments for treating allergies. (I) is useful in diagnostics and in the affinity purification of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are useful for treating a patient susceptible to or suffering from allergies. (IV) is also useful in diagnosing allergy. AB016912 to AB016913 represent peptide sequences which are used in the exemplification of the present invention.

QY 1 CFMKKQAULELCPE 16  
 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  
 1 CFMKKQAULELCPE 16

Query Match 93.1% Score 43; E-Value 1e-08; Length 16  
 Best Local Similarity 87.5% Pref No. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0

RESJUL7  
 AAB25336  
 ID AAB25336 standard; Peptide: 16 AA  
 XX AAB25336  
 AC AAB25336  
 DT 05-JAN 2001 (first entry)  
 XX E1 mimotope SEQ ID NO. 30  
 CE E1 mimotope SEQ ID NO. 30

XX Epitope; mimotope; human; immunoglobulin E; IgE; C-peptide-2 domain; allergic diseases; immunopathology; immunotherapy; anti-allergic; immunosuppressive; vaccine; histamine release inhibitor; immunogen; allergy; atopy  
 OS Homo sapiens  
 XX WO2000050460 A2  
 XX 11-AUG-2000  
 XX 22-FEB-2000; 2000WO-EPC:455

XX 25-FEB-1999; 98GB 0004405  
 PR 29-MAR-1999; 98GB 0007152  
 PR 07-MAY-1999; 98GB 0015337  
 PR 07-MAY-1999; 98GB 0015338  
 PR 07-AUG-1999; 98GB 0015594  
 PR 27-AUG-1999; 98GB 0015603  
 PR 27-SEP-1999; 98GB 0021046  
 PR 27-SEP-1999; 98GB 0021047  
 PR 29-OCT-1999; 98GB 0025619  
 PR 23-NOV-1999; 98GB 0027698

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD

XX Lyson M, Fricke M, Greenwood J, Hewitt E, Lamont A, Mason S, Randall P, Turnell W, Van Vechelen MP, Vinals De Bassols YC, WFI: 2000 51273753

XX Peptides useful for treating, preventing and ameliorating allergic diseases, comprising an isolated surface exposed group of a specific domain from immunoglobulin E

XX Description: Page 11; 45pp; English  
 CC The present invention describes a peptide (I) comprising an isolated surface exposed epitope (E) of C-peptide 2 domain (C) of immunoglobulin E (IgE), or its mimotope. Also described are: (i) an immunogen (II) for treating allergy comprising (i); (2) a vaccine (III) for treating allergies comprising (i); (3) a ligand (IV) capable of recognising E; (4) a pharmaceutical composition (V) comprising (IV); (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen (Ia) comprising (Ia); and (7) producing (Ia) by producing (Ia). (I) can have anti-allergic and immunosuppressive activities, and can be used as a vaccine and histamine release inhibitor (II), (III) and (IV) are useful in medicine and in the manufacture of medicaments for treating and preventing allergies. (IV) is useful for identifying mimotopes of E, in medicine and also in manufacturing medicaments for treating allergies. (I) is useful in diagnostics and in the affinity purification of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are useful for treating a patient susceptible to or suffering from allergies. (IV) is also useful in diagnosing allergy. AB016912 to AAB25336 represent peptide sequences which are used in the exemplification of the present invention.

XX Sequence 16 AA:  
 Query Match 93.1% Score 43; E-Value 1e-08; Length 16  
 Best Local Similarity 87.5% Pref No. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CFVNKGADLELC 13  
 DB 13  
 : CFVNKGADLELC 13

RESULT 9  
 AAU16661  
 ID AAU16661 standard; Peptide; 13 AA  
 XX AC AAU16661  
 XX DT 07-NOV-2001 (first entry)  
 XX DE Peptide #2 derived from Cepsilon2 region of human IgE  
 XX KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW C-peptide; C-peptide; C-peptide; C-peptide; C-peptide; C-peptide;  
 KW IgE mediated disease; antibody response  
 XX OS Homo sapiens  
 XX OS Synthesis  
 XX PN WC200145745-A2  
 XX PD 28 JUN 2001  
 XX PF 21 DEC 2000; 2003KG-GB04915  
 XX PP 21-DEC-1999; 900R-00102331  
 XX PR 22-FEB-2000; 2000GS-0004096  
 XX PR 22-AUG-2000; 2000GS-0020707  
 XX PR 22-AUG-2000; 2000GS-0020708  
 XX RA (S) : ACAPUS PER LTD  
 RA (S) : SMITHKLINE BEECHAM BIOLOGI  
 XX PI F. Mann M. Johnson T  
 XX PT WPI: 2001-521967/57  
 XX PS A linkage comprising an immunogenically conjugate used in treatment of IgE  
 PT mediated diseases  
 XX PS Example 4; Page 11; 45pp; English  
 XX CC The present invention relates to linkages which are used in the  
 CC conjugation of compounds (e.g. peptides, polymers, nucleic acids, lipids, etc.)  
 CC to 3, macrophages, polymers, dendritic cells, etc.) for the treatment of  
 CC biological and immunological conditions. The invention provides a method  
 CC method for linking an epitope to a peptide, the method comprising a  
 CC protein for use in a pharmaceutical composition and a carrier for  
 CC invention describes peptides derived from C-peptides of the  
 CC C-peptide2, C-peptide3 or C-peptide4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the treatment of  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope, antigenic or a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal of the invention  
 CC AAU16661-AAU16613 represent peptides derived from C-peptides of  
 CC the C-peptide2/C-peptide3/C-peptide4 region of human IgE  
 XX Sequence 13 AA:  
 QY 1 CFVNKGADLELC 13  
 DB 13  
 : CFVNKGADLELC 13

RESULT 9  
 ABJ00324  
 ID ABJ00324 standard; Peptide; 13 AA  
 XX AC ABJ00324  
 XX DT 02-SEP-2002 (first entry)  
 XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 108  
 XX KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; antiallergic; cyclic  
 XX OS Homo sapiens  
 XX PN WC200216409-A2  
 XX PD 28-FEB-2002  
 XX PF 17-AUG-2001; 2001WG-EP09576  
 XX PR 22-AUG-2000; 2003GB-000917  
 XX RA (S) : SMITHKLINE BEECHAM BIOLOGICALS  
 RA (S) : PEPTIDE THERAPEUTICS LTD  
 XX PI Friede M, Mason S, Turner J W, Virals Bassols VC  
 XX PP WPI: 2002 489648/52  
 XX PT Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier  
 XX PS Claim 4; Page 11; 45pp; English  
 XX CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 XX Sequence 13 AA:  
 QY 1 CFVNKGADLELC 13  
 DB 13  
 : CFVNKGADLELC 13

RESULT 10  
 AA25935  
 ID AA25935 standard; Peptide; 13 AA  
 XX AC AA25935  
 XX DT 05-JAN-2001 (first entry)  
 XX DE P1 -imotope SEQ ID NO:109  
 XX KW Epitope; imotope; human; immunoglobulin E; IgE; C-peptide-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX OS Homo sapiens  
 XX PN WC20001440-A2  
 XX



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FD 11-AUG-2000;
XX
XX 22-FEB-2000; 2000MC-RPC1455;
XX
XX 26-FEB-1999; 99GB-C004405;
XX 23-MAR-1999; 99GB-C007151;
XX 02-MAY-1999; 99GB-0010537;
XX 03-MAY-1999; 99GB-0010538;
XX 07-AUG-1999; 99GB-0018594;
XX 07-AUG-1999; 99GB-0018623;
XX 07-SEP-1999; 99GB-0021346;
XX 07-SEP-1999; 99GB-0021647;
XX 24-OCT-1999; 99GB-0025619;
XX 23-NOV-1999; 99GB-C027658;
XX
XX (SMK) : SYNTHELINE BEECHAM BIOLOGICALS;
XX (SEPT) : PEPTIDE THERAPEUTICS LTD;
XX
XX Flynn M, Friede M, Greenwood J, Hewitt E, Johnson A, Mason G;
XX Randall R, Turner WG, Van Mechelen VL, Vinals De Bassols Y;
XX WPI: 2000-02071/53;
XX
XX Peptides useful for treating, preventing and ameliorating allergic
XX diseases, comprising an isolated surface exposed group of a specific
XX domain from immunoglobulin E;
XX
XX Disclosed: Page 11; 12pp; English;
XX
XX The present invention describes a peptide (I) comprising an isolated
XX surface exposed group/epitope (E) of Cε3 region 2 domain D of
XX immunoglobulin E (IgE), or its mimope. Also described are (II) an
XX immunogen (II) for treating allergic comprising (I); (II) A vaccine (III)
XX for treating allergies comprising (I); (IV) a ligand (IV) capable of
XX recognising E; (V) a pharmaceutical composition for comprising (IV);
XX (VI) a peptide (VI) capable of being recognised by (IV); and an immunogen
XX that comprising (VI) and (V) producing (VI) by producing (VI); (II)
XX can have anti-allergic and immunosuppressive activities, and can be used
XX as a vaccine and histamine release inhibitor; (III), (IV) and (VI) are
XX useful in medicine and in the manufacture of medicaments for treating
XX and preventing allergies; (IV) is useful for identifying mimotopes of (I),
XX in medicine and also in manufacturing antibodies for treating
XX allergies; (II) is useful in diagnostics and in the affinity purification
XX of circulating anti-IgE antibodies from blood; (I), (II) and (VI) are
XX useful for treating a patient susceptible to or suffering from allergies;
XX (VI) is also useful in diagnosing of (I); (V), (VI) and (IV) represent
XX peptide sequences which are used in the experiments of the present
XX invention;
XX
XX Query Match 74.23; Score 66; DA 12; Length 13;
XX Best Local Similarity 74.23; Pred No. 0.00004;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX Sequence 13 AA;
XX
XX 1 CHINKQVADLELC 13
XX 1 CHINKQVADLELC 13
XX
XX RESULT 11
XX AAU0662
XX ID AAU0662 standard; Peptide; 13 AA;
XX AC AAU0662;
XX
XX 07-SEP-2000 first entry;
XX
XX Peptide #1 derived from Cε3 region 2 domain D;
XX
XX Human linkage technology; contained specific antigenic
XX epitopes; Cε3 region 2; Cε3 region 3; Cε3 region 4; Cε3 region 5;
XX IgE-related disease; antibody ref 100;
XX

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XX Homc sapiens;
XX Synthetic;
XX WC200145745 A2;
XX 28 JUN-2001;
XX
XX 21-DEC-2000; 2000MC-RB04935;
XX
XX 21-DEC-1999; 99GB-C010233;
XX 22-FEB-2000; 2000GB-C004036;
XX 22-AUG-2000; 2000GB-C020307;
XX 22-AUG-2000; 2000GB-C020708;
XX
XX (ACAM) : ACAM'S RES LTD;
XX (SMK) : SMITHKLINE BEECHAM BIOLOGICALS;
XX
XX Flynn M, Johnson T;
XX WPI: 2001-521967/57;
XX
XX A linkage comprising an immunogenic conjugate useful treatment of IgE
XX mediated diseases;
XX
XX Example 4; Page 21; 4pp; English;
XX
XX The present invention relates to linkage methodology for use in the
XX conjugation of compounds (e.g. peptides) to carrier vehicles
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX biological and immunological constructs. The invention provides a
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX protein) for use in a pharmaceutical composition or a vaccine. The
XX invention describes peptides derived from Cε3 region 2 domain D of
XX Cε3 region 2, Cε3 region 3, Cε3 region 4 regions of human immunoglobulin E
XX (IgE) which are used to produce conjugated compounds. The compounds or
XX compositions of the invention are useful in the manufacture of a
XX reagent for the treatment of IgE-mediated diseases. The invention
XX allows for controlled conjugation of a peptide epitope (antigen) to a
XX protein so as to form an immunogenic conjugate which may be able to
XX raise a protective antibody response in an animal or human patient.
XX AAU0662; AAU0662 represent peptides derived from Cε3 region 2 domain D of
XX the Cε3 region 2/region 3/region 4 region of human IgE;
XX
XX Sequence 13 AA;
XX
XX Query Match 74.23; Score 66; DA 12; Length 13;
XX Best Local Similarity 74.23; Pred No. 0.00004;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CHINKQVADLELC 13
XX 1 CHINKQVADLELC 13
XX
XX RESULT 12
XX AB000323
XX ID AB000323 standard; Peptide; 13 AA;
XX AC AB000323;
XX
XX 02-SEP-2000 first entry;
XX
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 107;
XX
XX Immunogen; human IgE; immunoglobulin E; allergy; thio-ether linkage;
XX vaccine; anti-allergic; cyclic
XX
XX Homc sapiens;
XX WC200145745 A2;
XX 28 JUN-2001;
XX

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XX 17-AUG-2001; 2001WG-EP09576.  
XX  
XX  
XX 22-AUG-2000; 2000GP-0020717.  
XX  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT) PEPTIDE THERAPEUTICS LTD

XX Friede M., Mason S., Turnbull W.G., Vidal's Bassols YC.

XX WPI; 2002-48964a/50.

XX Conjugate for use in vaccine for treatment of allergy; comprising  
XX disulfide bridge cyclized peptide and immunogenic carrier

XX (Claim 4; Page 11; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulfide bridge cyclized peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a cyclic peptide immunogen derived  
XX from human immunoglobulin E (Ige) suitable for use in the invention.

XX Sequence 13 AA.

Query Match 74.2% Score 66; DB 23; Length 13;  
Best Local Similarity 84.6% Pred. No. 0.00034;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFVNKQLADLELC 13

Db : CFVNKQLADLELC 13

RESULT 14

AAU16642  
ID AAB25913 standard; Peptide; 13 AA.

AC AAB25917

DT 05 JAN 2001 (first entry)

DE P1 minotope peptide P15q SEQ ID NO:11.

XX Epitope; minotope; human; immunoglobulin E (Ige); Cepsilon2 domain;  
XX allergic disease; immunophylaxis; immunotherapy; antiallergic;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy

OS Homo sapiens.

XX WO20000460-A1.

PN 31 AUG-2000.

XX 22 FEB 2000; 2000WO-EP01455.

XX 25-FEB-1999; 99GB-0004405.

XX 23 MAR 1999; 99GB-0007151.

XX 03-MAY-1999; 99GB-0010537.

XX 04-MAY-1999; 99GB-0010538.

XX 07 AUG 1999; 99GB-0018594.

XX 07 AUG 1999; 99GB-0018601.

XX 07-SEP 1999; 99GB-0021046.

XX 07-SEP 1999; 99GB-0021047.

XX 23-OCT 1999; 99GB-0025619.

XX 23-NOV 1999; 99GB-0027698.

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

XX (PEPT) PEPTIDE THERAPEUTICS LTD.

XX Dyson M., Friede M., Greenwood M., Hewitt E., Landon A., Van der  
XX Randall M., Turnbull W.G., Van Mechelen MP., Vidal's Bassols YC.

XX WPI; 2000-592073/53

XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.

XX Claim 14; Page 9; 12pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (EI) of Cepsilon2 domain (D) of  
XX immunoglobulin E (Ige), or its minotope. Also described are: (i) an  
XX immunogen (II) for treating allergy comprising (iii) (2) a vaccine (Iiii)  
XX for treating allergies comprising (iii) (3) a ligand (IV) capable of  
XX recognising (ii) (4) a pharmaceutical composition (PC) comprising (iv),  
XX (5) a peptide (Ia) capable of being recognised by (iv); (6) an immunogen  
XX (Iia) comprising (Ia) and (7) producing (Iii) by producing (Iii) (i)  
XX can have antiallergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (ii) (i) and (iii) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (iv) is useful for identifying minotopes of E1,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (ii) is useful in diagnostics and in the affinity purification  
XX of circulating anti-Ige antibodies from blood. (i) (iii) and PC are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (iv) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.

XX Sequence 13 AA.

Query Match 37.1% Score 33; DB 21; Length 13;

Best Local Similarity 38.5% Pred. No. 0.02402;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFVNKQLADLELC 13

Db 1 CLEGGQWQVDEL 13

RESULT 14

AAU16642  
ID AAU16642 standard; Peptide; 13 AA.

XX AAU16642;

XX 07-NOV 2001 (first entry)

XX Peptide (Iii) derived as minotope of Cepsilon2 region of human Ige.

XX Human linkage technology; conjugated compound; carrier vehicle;

XX epitope; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2; immunoglobulin E;

XX Ige mediated disease; antibody response.

XX Homo sapiens.

XX Synthetic.

XX WO200145745 A2.

XX 28-JUN 2001.

XX 21-DEC-2000; 2000WO-GB04935.

XX 21-DEC 1999; 99GB-0030233.

XX 22-FEB-2000; 2000GB-0034096.

XX 22-AUG-2000; 2000GB-002707.

XX 22-AUG-2000; 2000GB-002708.

XX (ACAM) ACAMBIOS RES LTD.

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Flinn K., Johnson T.

DR WPI: 2001: 521967/52.  
XX A linkage comprising an immunogenic conjugate useful treatment of ipe  
PT -mediated diseases  
XX  
XX Example 4: Page 21; 49pp; English.  
XX  
CC The present invention relates to linkage with biology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, fluorescent probes,  
CC biological and immunological constructs). The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier in a  
CC preferred for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimetics of the  
CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human IgG1, IgG2, IgG3 and  
CC (IgG4) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IgE-mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope, conjugate to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AAU15632-AAU16913 represent peptides derived from or mimetics of  
CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgG.  
XX  
XX Sequence 13 AA:  
SC  
Query Match 37.1%; Score 33; DB 23; Length 13;  
Best Local Similarity 38.5%; Pred. No. 1,2,4+02;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CPNKKQLAULELC 13  
DB 1 CLEDSQVWVSLC 13  
RESULT 15  
ARCESTE  
CC ARCESTE standard; Peptide; 13 AA  
XX  
XX AC ARCESTE  
XX  
XX DT 02 SEP 2003 (first entry)  
XX  
XX CE Human IgE cyclic immunogenic peptide- SEQ ID NO: 36.  
XX  
XX KW Intravenous; human; IgE; immunoglobulin E allergy; anti-IgE linkage;  
XX vaccine; anti-allergic; cyclic.  
XX  
XX OS Homo sapiens.  
XX  
XX FN W0200216459 A2.  
XX  
XX PD 28-FEB-2002.  
XX  
XX EF 17 AUG 2001; 2001WO-EP039576.  
XX  
XX PR 22-AUG-2000; 2000GR-CC20717.  
XX  
XX PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
XX PI Friede X, Mason S, Turner W, Vinals R, Busby V.  
XX  
XX DR WPI: 2002-489648/52.  
XX  
XX PT Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX  
XX CLAI- 4; Page 11; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulfide bridge cyclized peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of

CC allergies. The present sequence is a cyclic peptide immunogen derived  
CC from human immunoglobulin E (IgE) suitable for use in the invention.  
XX  
XX SQ Sequence 13 AA:  
Query Match 37.1%; Score 33; DB 23; Length 13;  
Best Local Similarity 38.5%; Pred. No. 1,2,4+02;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CPNKKQLAULELC 13  
DB 1 CLEDSQVWVSLC 13  
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Job time: 42 secs

GenCore version 5.1.6  
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OM protein: protein search, using sw tool

Run on: November 5, 2003, 12:14:56 Search time 15 seconds

without alignment  
59,142 Million full queries/sec

Title: US-09-914-088-13

Perfect score: 89

Sequence: 1 GGVNQACILCPRE 16

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 64479 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 1169

Minimum DB seq length: 3

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA

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- 3: /cgn2\_6/prodata/2/pub/paa/US91 PUBINTP pep.
- 4: /cgn2\_6/prodata/2/pub/paa/US91 PUBINTP pep.
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- 17: /cgn2\_6/prodata/2/pub/paa/US91 PUBINTP pep.
- 18: /cgn2\_6/prodata/2/pub/paa/US91 PUBINTP pep.

Pred. No. is the number of result. Prediction is based on the  
score greater than or equal to the prediction score and is printed,  
and is derived by analysis of the result.

SUMMARIES

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3	29	32.6	10	12	US-09-914-088-13
4	29	32.6	10	12	US-09-914-088-13
5	29	32.6	10	12	US-09-914-088-13
6	29	32.6	10	12	US-09-914-088-13
7	29	32.6	10	12	US-09-914-088-13
8	29	32.6	10	12	US-09-914-088-13
9	29	32.6	10	12	US-09-914-088-13
10	29	32.6	10	12	US-09-914-088-13
11	29	32.6	10	12	US-09-914-088-13
12	29	32.6	10	12	US-09-914-088-13
13	29	32.6	10	12	US-09-914-088-13
14	29	32.6	10	12	US-09-914-088-13
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16	26	29.2	12	15	US-10-235-483-67
17	26	29.2	12	15	US-10-211-088-157
18	26	29.2	13	11	US-09-327-750-37
19	26	29.2	13	11	US-09-965-876A-19
20	26	29.2	13	11	US-09-965-876A-20
21	26	29.2	13	15	US-10-100-957A-140
22	26	29.2	13	15	US-10-100-957A-148
23	26	29.2	13	15	US-10-211-088-17
24	26	29.2	13	15	US-10-211-088-316
25	26	29.2	13	15	US-10-211-088-316
26	26	29.2	14	11	US-09-932-613-53
27	26	29.2	14	12	US-09-932-613-53
28	26	29.2	15	8	US-09-927-939-63
29	26	29.2	16	12	US-10-098-108-10
30	26	29.2	16	12	US-10-158-825-61
31	26	29.2	16	15	US-10-158-847-61
32	26	29.2	17	15	US-10-006-869-302
33	26	29.2	17	15	US-10-006-869-303
34	26	29.2	17	15	US-10-006-869-308
35	26	29.2	17	15	US-10-006-869-308
36	26	29.2	17	15	US-10-006-869-3104
37	26	29.2	17	15	US-10-006-869-3104
38	26	29.2	17	15	US-10-006-869-3104
39	26	29.2	17	15	US-10-006-869-3104
40	26	29.2	17	15	US-10-006-869-3104
41	26	29.2	17	15	US-10-006-869-3104
42	26	29.2	17	15	US-10-006-869-3104
43	26	29.2	17	15	US-10-006-869-3104
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ALIGNMENTS

RESULT: 1

US-09-935-394-392

Sequence 392, Application US/09/935394

Publication No. US2003016526A1

GENERAL INFORMATION:

APPLICANT: CHALLITA-ETD, P.A.

APPLICANT: HUBERT, PENE

APPLICANT: RAUTANO, ARTHUR

APPLICANT: APAR, DANIEL

APPLICANT: DEVIR, EUGEN

APPLICANT: FARIS, MARY

APPLICANT: GE, WANGMAO

APPLICANT: KAPKOVITZ, AYA

TITLE OF INVENTION: NOVEL ACIDS AND CORRESPONDING PROTEIN NAMED 14EPH4

TITLE OF INVENTION: NOVEL ACIDS AND CORRESPONDING PROTEIN NAMED 14EPH4

TITLE OF INVENTION: NOVEL ACIDS AND CORRESPONDING PROTEIN NAMED 14EPH4

TITLE OF INVENTION: NOVEL ACIDS AND CORRESPONDING PROTEIN NAMED 14EPH4

FILE REFERENCE: 51154-1039-00

CURRENT APPLICATION NUMBER: US/09/935,394

CURRENT FILING DATE: 2001-09-22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ IDS: 743

SOFTWARE: Patcom ver 2.1

SEQ ID NO 392

LENGTH: 10

TYPE: EST

ORGANISM: Homo sapiens

US-09-935-394-392

Query Match: 32.6%

Best Local Similarity: 35.3%

Matches: 6; Conservative: 1; Mismatches: 1; Indels: 0; Gaps: 0

CY: 5 KACADE 12

DB: 3 RELATED 10

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RESULT 2
US-09-935-384-485
? Sequence 494, Application US/09935384
? Publication No. US20030166526A1
? GENERAL INFORMATION:
? APPLICANT: CHALLITA-BID, PIA
? APPLICANT: HUBERT, RENE
? APPLICANT: RAITANO, ARTHUR
? APPLICANT: AFAR, DANIEL
? APPLICANT: LEVIN, ELANA
? APPLICANT: FAPIS, MARY
? APPLICANT: GE, WANGMAO
? APPLICANT: JAKROVITZ, AVA
? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4
? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
? TITLE OF INVENTION: OTHER CANCERS
? FILE REFERENCE: 51158-20033-CC
? CURRENT APPLICATION NUMBER: US/09/935,384
? PRIOR FILING DATE: 2001-08-22
? PRIOR FILING DATE: 2002-08-22
? NUMBER OF SEQ ID NOS: 783
? SOFTWARE: Patent in Ver. 2.1
? SEQ ID NO 488
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-935-384-485

Query Match 32.6%, Score 29, DB 12, Length 10,
Best Local Similarity 75.0%, Pred. No. 2,2+02,
Matches 6, Conservative 1, Mismatches 1, Gaps 0,

QY 5 KKLAFEL 12
DB 3 KKLAFEL 10

RESULT 3
US-09-935-384-485
? Sequence 494, Application US/09935384
? Publication No. US20030166526A1
? GENERAL INFORMATION:
? APPLICANT: CHALLITA-BID, PIA
? APPLICANT: HUBERT, RENE
? APPLICANT: RAITANO, ARTHUR
? APPLICANT: AFAR, DANIEL
? APPLICANT: LEVIN, ELANA
? APPLICANT: FAPIS, MARY
? APPLICANT: GE, WANGMAO
? APPLICANT: JAKROVITZ, AVA
? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4
? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
? TITLE OF INVENTION: OTHER CANCERS
? FILE REFERENCE: 51158-20033-CC
? CURRENT APPLICATION NUMBER: US/09/935,384
? PRIOR FILING DATE: 2001-08-22
? PRIOR FILING DATE: 2002-08-22
? NUMBER OF SEQ ID NOS: 783
? SOFTWARE: Patent in Ver. 2.1
? SEQ ID NO 488
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-935-384-485

Query Match 32.6%, Score 29, DB 12, Length 10,
Best Local Similarity 75.0%, Pred. No. 2,2+02,
Matches 6, Conservative 1, Mismatches 1, Gaps 0,

QY 5 KKLAFEL 12
DB 3 KKLAFEL 10

```

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DB 3 KKLAFEL 10

RESULT 4
US-09-935-384-674
? Sequence 674, Application US/09935384
? Publication No. US20030166526A1
? GENERAL INFORMATION:
? APPLICANT: CHALLITA-BID, PIA
? APPLICANT: HUBERT, RENE
? APPLICANT: RAITANO, ARTHUR
? APPLICANT: AFAR, DANIEL
? APPLICANT: LEVIN, ELANA
? APPLICANT: FAPIS, MARY
? APPLICANT: GE, WANGMAO
? APPLICANT: JAKROVITZ, AVA
? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4
? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
? TITLE OF INVENTION: OTHER CANCERS
? FILE REFERENCE: 51158-20033-CC
? CURRENT APPLICATION NUMBER: US/09/935,384
? PRIOR FILING DATE: 2001-08-22
? PRIOR FILING DATE: 2002-08-22
? NUMBER OF SEQ ID NOS: 783
? SOFTWARE: Patent in Ver. 2.1
? SEQ ID NO 674
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-935-384-674

Query Match 32.6%, Score 29, DB 12, Length 10,
Best Local Similarity 75.0%, Pred. No. 2,2+02,
Matches 6, Conservative 1, Mismatches 1, Gaps 0,

QY 5 KKLAFEL 12
DB 3 KKLAFEL 10

RESULT 5
US-09-935-384-47
? Sequence 47, Application US/09935384
? Publication No. US20030166526A1
? GENERAL INFORMATION:
? APPLICANT: CHALLITA-BID, PIA
? APPLICANT: HUBERT, RENE
? APPLICANT: RAITANO, ARTHUR
? APPLICANT: AFAR, DANIEL
? APPLICANT: LEVIN, ELANA
? APPLICANT: FAPIS, MARY
? APPLICANT: GE, WANGMAO
? APPLICANT: JAKROVITZ, AVA
? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4
? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
? TITLE OF INVENTION: OTHER CANCERS
? FILE REFERENCE: 51158-20033-CC
? CURRENT APPLICATION NUMBER: US/09/935,384
? PRIOR FILING DATE: 2001-08-22
? PRIOR FILING DATE: 2002-08-22
? NUMBER OF SEQ ID NOS: 783
? SOFTWARE: Patent in Ver. 2.1
? SEQ ID NO 47
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-935-384-47

Query Match 32.6%, Score 29, DB 12, Length 10,
Best Local Similarity 75.0%, Pred. No. 2,2+02,
Matches 6, Conservative 1, Mismatches 1, Gaps 0,

QY 5 KKLAFEL 12
DB 3 KKLAFEL 10

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: polypeptide  
 US-09-966-782A-47

Query Match 31.5% Score 28; DP 11; Length 14;  
 Best Local Similarity 60.0%; Pred No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MNKQLADEL 12  
 : |||  
 DB 5 MNKQLADEL 14

RESULT 6

US-10-254-905-47  
 Sequence 47, Application US/10254905  
 Publication No. US2003018625A1

GENERAL INFORMATION:  
 APPLICANT: Bristol Myers Squibb Company  
 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, HGFBRNRY7, EXPRESSED HIGHLY IN SPINAL CORD

FILE REFERENCE: D0044 CIP  
 CURRENT APPLICATION NUMBER: US/10/254,905  
 CURRENT FILING DATE: 2002-09-25  
 NUMBER OF SEQ ID NOS: 75  
 SOFTWARE: Patent in version 3.1

SEQ ID NO 47  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-254-905-47

Query Match 31.5% Score 28; DP 12; Length 14;  
 Best Local Similarity 60.0%; Pred No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MNKQLADEL 12  
 : |||  
 DB 5 MNKQLADEL 14

RESULT 7

US-10-091-215-6  
 Sequence 61, Application US/10071275  
 Publication No. US2003013893A1

GENERAL INFORMATION:  
 APPLICANT: Meyers, Rachel E.  
 TITLE OF INVENTION: A NOVEL HUMAN HEMOPHILIN  
 FILE REFERENCE: 19448 117001  
 CURRENT APPLICATION NUMBER: US/10/117,001  
 CURRENT FILING DATE: 2002-02-07  
 PRIOR APPLICATION NUMBER: 60/267,654  
 PRIOR FILING DATE: 2001-02-07  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-091-215-6

Query Match 31.5% Score 14; DP 12; Length 14;  
 Best Local Similarity 57.1%; Pred No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFNKKQJ 7  
 : |||  
 DB 5 CFNKKQJ 14

RESULT 8

US-09-773-054-20

Sequence 20, Application US/0979054  
 Patent No. US20020123102A1

GENERAL INFORMATION:  
 APPLICANT: Lu, Xingjie  
 TITLE OF INVENTION: USE OF GENDRASPIN AS A SCAFFOLD FOR NON DENDROSPIN DOMAINS  
 FILE REFERENCE: A-75112/TAL/AMS  
 CURRENT APPLICATION NUMBER: US/09/773,054  
 CURRENT FILING DATE: 2001-12-05  
 PRIOR APPLICATION NUMBER: GB 0002425.2  
 PRIOR FILING DATE: 2000-02-05  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: Patent in version 3.0

SEQ ID NO 20  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial  
 US-09-773-054-20

Query Match 31.5% Score 28; DP 10; Length 16;  
 Best Local Similarity 50.0%; Pred No. 5.1e+02;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFYKQKQJADEL 10  
 : |||  
 DB 2 CFYKQKQJADEL 11

RESULT 9

US-09-966-782A-40  
 Sequence 40, Application US/09966782A  
 Publication No. US2003002183A1

GENERAL INFORMATION:  
 APPLICANT: Battaglin, F.  
 APPLICANT: Feder, G. N.  
 APPLICANT: Mintier, G.  
 APPLICANT: Ramanathan, G. S.  
 APPLICANT: Westphal, A.  
 APPLICANT: Hawken, D. B.  
 APPLICANT: Caracci, A.  
 APPLICANT: Barber, L.  
 APPLICANT: Kornacker, M. G.  
 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, HGFBRNRY7, EXPRESSED HIGHLY IN SPINAL CORD

FILE REFERENCE: D0044NP  
 CURRENT APPLICATION NUMBER: US/09/966,782A  
 CURRENT FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 60/235,731  
 PRIOR FILING DATE: 2000-03-27  
 PRIOR APPLICATION NUMBER: 60/204,480  
 PRIOR FILING DATE: 2001-02-14  
 PRIOR APPLICATION NUMBER: 60/115,420  
 PRIOR FILING DATE: 2001-01-28  
 NUMBER OF SEQ ID NOS: 64  
 SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 40  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Polypeptide  
 US-09-966-782A-40

Query Match 30.8% Score 27; DP 11; Length 14;  
 Best Local Similarity 60.0%; Pred No. 6.5e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 MNKQLADEL 12  
 : |||  
 DB 5 MNKQLADEL 14

```

RESULT 10
US-10-254-905-40
; Sequence 40, Application US/10254905
; Publication No. US20030196265A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COHESIN RELATED PROTEIN, EXPRESSED HIT
; FILE REFERENCE: 20044 CIP
; CURRENT APPLICATION NUMBER: US/10/254,905
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-254-905-40

Query Match: 30.3%, Score 27, DB 12, Length 14
Best Local Similarity: 60.0%, Pred. No. 6.9e+05
Matches: 6, Conservative 1, Mismatches 3, Indels 0, Gaps 0

CY 3 MNKQLADEL 12
Dc 3 MNKQLADEL 12

RESULT 11
US-10-029-075B-132
; Sequence 132, Application US/10029075B
; Publication No. US2003011733A1
; GENERAL INFORMATION:
; APPLICANT: Behner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/029,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 132
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: pdb/1BFA/1BFA
US-10-029-075B-132

Query Match: 29.2%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
Dc 4 CPRE 4

RESULT 12
US-10-029-206A-132
; Sequence 132, Application US/10029206A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Glucosylpeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 132
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: pdb/1BFA/1BFA
US-10-029-206A-132

Query Match: 29.2%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
Dc 4 CPRE 4

RESULT 13
US-10-028-075B-131
; Sequence 131, Application US/10028075B
; Publication No. US2003011733A1
; GENERAL INFORMATION:
; APPLICANT: Behner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/029,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 131
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: pdb/1BFA/1BFA
US-10-028-075B-131

Query Match: 29.2%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
Dc 4 CPRE 4

RESULT 14
US-10-029-206A-131
; Sequence 131, Application US/10029206A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Glucosylpeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 131
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: pdb/1BFA/1BFA
US-10-029-206A-131

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Query Match: 29.2% Score 26; DB 15; Length 97
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 13 CPSE 16
DB 4 CPSE 7

RESULT 15
US 10 211-049 337
: Sequence 497; Application US/0211049
: Publication No. US2003104479A1
: GENERAL INFORMATION:
: APPLICANT: Bright, Gary R.
: APPLICANT: Premkumar, D. David
: APPLICANT: Cheng, Yih-Tai
: TITLE OF INVENTION: NO. US20030104479A1: Fusion Proteins And Assays For Molecular Bi
: FILE REFERENCE: 01 1022-US
: CURRENT APPLICATION NUMBER: US/10/211-049
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 62/109,395
: PRIOR FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: 62/341,599
: PRIOR FILING DATE: 2001-12-13
: NUMBER OF SEQ ID NOS: 166
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 137
: LENGTH: 17
: TYPE: PFT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Nuclear export signal
US 10 211-049 337

Query Match: 29.2% Score 26; DB 15; Length 107
Best Local Similarity 50.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 3 MMSQLADDFL 12
DB 1 LQKAEHELE 10

Search completed: November 5, 2003, 18:19:14
Job time 1.74 secs

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GenCore version: 5.11.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein protein search, using sw model

Run on: November 5, 2003, 18:12:15 / Search time of 30 seconds  
(without alignment)  
32,737 million cells loaded/sec

Title: US-09-914-088-13

Perfect score: 89  
Sequence: 1 GEMKQLADDELTPSE 16

Scoring table: PLOSM62  
Gap: 12.0, Gapext: 6.0

Searched: 128717 seqs, 4231288 residues

Total number of hits satisfying chosen parameters: 1129.

Minimum DB seq length: 5  
Maximum DB seq length: 16

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA\*  
1: /seq2\_6/prodata1/1/aa/AA\_CXXA.pep\*  
2: /seq2\_6/prodata1/1/aa/AA\_CXXA.pep\*  
3: /seq2\_6/prodata1/1/aa/AA\_CXXA.pep\*  
4: /seq2\_6/prodata1/1/aa/6S\_CXXA.pep\*  
5: /seq2\_6/prodata1/1/aa/6S\_CXXA.pep\*  
6: /seq2\_6/prodata1/1/aa/6S\_CXXA.pep\*

Prod. No. is the number of results predicted by the search. It has a score greater than or equal to the score of the best hit being listed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Query Match	Length	DB ID	Prod. No.
1	81	84.8	16	5310729-5	1
2	80	83.7	8	5310729-13	2
3	80	83.7	9	US-09-914-088-13	3
4	80	83.7	9	5310729-13	4
5	80	83.7	10	5310729-13	5
6	80	83.7	11	5310729-13	6
7	80	83.7	9	5310729-13	7
8	80	83.7	9	5310729-13	8
9	80	83.7	11	US-07-543-413-14	9
10	80	83.7	11	US-07-543-413-14	10
11	80	83.7	11	US-08-530-530-13	11
12	80	83.7	11	US-08-530-530-13	12
13	80	83.7	13	US-09-914-088-13	13
14	80	83.7	15	US-09-914-088-13	14
15	80	83.7	14	US-08-530-530-13	15
16	80	83.7	8	US-08-530-530-13	16
17	80	83.7	12	US-09-914-088-13	17
18	80	83.7	12	US-08-530-530-13	18
19	80	83.7	12	US-08-530-530-13	19
20	80	83.7	13	US-09-914-088-13	20
21	80	83.7	13	US-09-914-088-13	21
22	80	83.7	14	US-08-530-530-13	22
23	80	83.7	15	US-08-530-530-13	23
24	80	83.7	15	US-08-530-530-13	24
25	80	83.7	16	US-08-530-530-13	25
26	80	83.7	16	US-08-530-530-13	26
27	80	83.7	16	US-08-530-530-13	27

28 29 2 26 5 PCT-US95-54567-14 Sequence 14, Appl.  
29 25.5 28.7 12 1 US-08-218-026-57 Sequence 17, Appl.  
30 25.5 28.7 12 2 US-08-653-632-57 Sequence 17, Appl.  
31 25 28.1 7 4 US-09-187-859-3102 Sequence 3102, Ap  
32 25 28.1 7 4 US-09-339-542B-3102 Sequence 3102, Ap  
33 25 28.1 8 2 US-06-811-492-110 Sequence 110, App  
34 25 28.1 8 4 US-09-187-859-3103 Sequence 1103, Ap  
35 25 28.1 8 4 US-09-339-542B-3103 Patent No. 5310729  
36 25 28.1 8 6 5310729-20 Sequence 3104, Ap  
37 25 28.1 9 4 US-09-187-859-3104 Sequence 80, Appl.  
38 25 28.1 9 4 US-09-344-040C-82 Sequence 3104, Ap  
39 25 28.1 9 6 5310729-21 Patent No. 5310729  
40 25 28.1 10 1 US-08-750-007-17 Sequence 17, Appl.  
41 25 28.1 10 4 US-09-344-040C-85 Sequence 85, Appl.  
42 25 28.1 10 4 US-09-341-992-43 Sequence 43, Appl.  
43 25 28.1 10 6 5310729-22 Patent No. 5310729  
44 25 28.1 10 6 5459046-17 Patent No. 5459046  
45 25 28.1 10 6 5459046-17

ALIGNMENTS

RESULT 1  
5310729-5  
Patent No. 5310729  
APPLICANT: LERNHARDT, WALDEMAR  
TITLE OF INVENTION: INTERFERON-RELATED POLYPEPTIDES AS CR2  
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS  
NUMBER OF SEQUENCES: 47  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/512,118  
FILING DATE: 20-APR 1990  
SEQ ID NO: 5  
LENGTH: 16  
5310729-5

Query Match 34.8% Score 31; DB 6; Length 16;  
Best Local Similarity 66.7% Pred. No. 65;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 5 KQLADDELTP 13  
DB 5 QQLNDLEAC 13

RESULT 2  
5310729-13  
Patent No. 5310729  
APPLICANT: LERNHARDT, WALDEMAR  
TITLE OF INVENTION: INTERFERON-RELATED POLYPEPTIDES AS CR2  
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS  
NUMBER OF SEQUENCES: 47  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/512,118  
FILING DATE: 20-APR 1990  
SEQ ID NO: 13  
LENGTH: 8  
5310729-13

Query Match 33.3% Score 30; DB 6; Length 9;  
Best Local Similarity 75.0% Pred. No. 2,550,05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 QQLADDELTP 13  
DB 1 QQLNDLEAC 8

RESULT 3  
US-07-720-202-47  
Sequence 47, Applicant US/07/202-47  
Patent No. 5,459,877



ANTIGENS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS

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Query Match 31.5% Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 6 QADLEUC 13  
Db 1 QADLEUC 8

US-07-663-413-13

Sequence 1, Application US/07663413

Patent No. 5240703

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/663.413

FILING DATE: 19910301

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 38720

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-3525

TELEX: 422523 COOP U

INFORMATION FOR SEQ ID NO: 13

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-663-413-13

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/663.413

FILING DATE: 19910301

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 38720

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-3525

TELEX: 422523 COOP U

INFORMATION FOR SEQ ID NO: 12

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-663-413-32

Query Match 31.5% Score 28, DB 1, Length 11,

Best Local Similarity 57.1%, Pred. No. 1.46+02,

Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCP 15

Db 1 EYDLCPR 7

US-08-055-510-13

Sequence 1, Application US/08055530

Patent No. 5451499

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/055.530

FILING DATE: 19910430

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.

REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39720-2/JEP/350  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELEX: 422523 COOP U  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-055-510 13

Query Match 31.5% Score 28; DB 13; Length 13;  
 Best Local Similarity 57.1% Pred No. 1.7e-02;  
 Matches 4; Conservative 2; Mismatches 1; Gaps 0;

QY 9 DLELPR 15  
 DE 1 EYDLCPR 7

RESULT 12  
 US-08-055-510 12  
 Sequence 32, Application US/08055530  
 Patent No. 5451499

GENERAL INFORMATION:  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: ATTENUATED, GENETICALLY ENGINEERED  
 TITLE OF INVENTION: PSEUDORABIES VIRUS STRV 155 AND USES  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John D. White, Esq.  
 STREET: 10 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10119

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.04  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/255,510  
 FILING DATE: 19940430  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White Esq., John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39720-2/JEP/350

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELEX: 422523 COOP U  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-055-510 32

Query Match 31.5% Score 28; DB 13; Length 13;  
 Best Local Similarity 57.1% Pred No. 1.7e-02;  
 Matches 4; Conservative 2; Mismatches 1; Gaps 0;

QY 9 DLELPR 15  
 DE 1 EYDLCPR 7

RESULT 13  
 US-09-402-641-1  
 Sequence 1, Application US/09402641  
 Patent No. 6528619  
 GENERAL INFORMATION:  
 APPLICANT: BURGESS, Markus  
 APPLICANT: GRAEFF, Heinrich  
 APPLICANT: KESSLER, Holst  
 APPLICANT: MAGDOLEN, Viktor Robert  
 APPLICANT: KOENIG, Bernhard  
 APPLICANT: KOPITZ, Marius  
 APPLICANT: RIEMER, Christoph  
 APPLICANT: SCHMITT, Manfred  
 APPLICANT: WEDDE, Ulrich  
 APPLICANT: WILHEIM, Olaf  
 TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR  
 FILE REFERENCE: Case 2036705  
 CURRENT APPLICATION NUMBER: US/09/402,641  
 CURRENT FILING DATE: 2000-01-10  
 PRIOR APPLICATION NUMBER: EP97106034.9  
 PRIOR FILING DATE: 1997-04-21  
 PRIOR APPLICATION NUMBER: PCT/EP98/02,728  
 PRIOR FILING DATE: 1998-04-24  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Peptide Psycho  
 OTHER INFORMATION: 19,31 UPA 19 31"; Figure 3A  
 US-09-402-641-1

Query Match 31.5% Score 28; DB 4; Length 13;  
 Best Local Similarity 30.8% Pred No. 1.7e-02;  
 Matches 4; Conservative 1; Mismatches 6; Gaps 0;

QY 1 CENKQKAGLEK 13  
 DE 1 CENKQKAGLEK 13

RESULT 14  
 US-08-142-590B-5  
 Sequence 5, Application US/08142590B  
 Patent No. 6100746

GENERAL INFORMATION:  
 APPLICANT: HIRATA, Toshihiko; TAKAHASHI, Tadashi; HORII, Izumi; and  
 TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/142,590B  
 FILING DATE: 25 OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/042,318  
 FILING DATE: 22 APR 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WYVIS, Paul L.  
 REGISTRATION NUMBER: 35,365

Search completed: November 5, 2003, 18:15:08  
Job time : 22 secs

1 REFERENCE/DOCKET NUMBER: MGP 6024P  
2 TELECOMMUNICATION INFORMATION:  
3 TELEPHONE: (617) 227-7400  
4 TELEFAX: (617) 227-5941  
5 INFORMATION FOR SEQ ID NO: 5:  
6 SEQUENCE CHARACTERISTICS:  
7 LENGTH: 15 amino acids  
8 TYPE: amino acid  
9 TOPOLOGY: linear  
10 MOLECULE TYPE: peptide  
11 FRAGMENT TYPE: internal  
12 US 09-142,091B 5

Query Match 31.5% Score 27, 18.1% Identical  
Best Local Similarity 30.0% Pident 19.4%  
Matches 4; Conservative 5; Mismatches 6; Gaps 0;

CY : CPNNKQLADLCL 13  
DB : 2 CYSKVFESNHC 14

RESULT 15  
US 09-248 6197-91  
1 Sequence 92, Application US/06248893  
2 Patent No. 5843702  
3 GENERAL INFORMATION:  
4 APPLICANT: McConnel, David  
5 APPLICANT: Devine, Kevin  
6 APPLICANT: O'Keefe, Charles  
7 TITLE OF INVENTION: A Gene Expression System  
8 NUMBER OF SEQUENCES: 185  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: No. 58437020 No. 58437020disk of No. 58437020 America, Inc.  
11 STREET: 405 Lexington Avenue  
12 CITY: New York  
13 STATE: New York  
14 COUNTRY: USA  
15 ZIP: 10174-6401  
16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Diskette  
18 COMPUTER: IBM Compatible  
19 OPERATING SYSTEM: DOS  
20 SOFTWARE: FastSeq for Windows Version 1.0  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/99/248,893  
23 FILING DATE: 25-MAY-1994  
24 CLASSIFICATION: 435  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: Gregg, Valinda A.  
27 REGISTRATION NUMBER: 15,127  
28 REFERENCE/DOCKET NUMBER: 3614, 214 US  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-867-0123  
31 TELEFAX: 212-978-9655  
32 INFORMATION FOR SEQ ID NO: 93:  
33 SEQUENCE CHARACTERISTICS:  
34 LENGTH: 14 amino acids  
35 TYPE: amino acid  
36 STRANDEDNESS: single  
37 TOPOLOGY: linear  
38 MOLECULE TYPE: Protein  
39 US-09 248 619C 93

Query Match 30.3% Score 27, 18.1% Identical  
Best Local Similarity 100.0% Pident 19.4%  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY : 2 FNKQ 6  
DB : 4 FVNKQ 8

GenCore version 3.1.6  
Copyright (c) 1993-2003 Computer Ltd.

CM protein: protein search, using sw match

Run on: November 5, 2003, 15:18:36 / Search time 23 seconds  
(without alignment)  
96,163 Million cell states/sec

Title: US-09-914-088-15

Perfect score: 112

Sequence: CLEMSQWMDVLCGSSGGP 20

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 28162 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1443

Minimum DB seq length: 7  
Maximum DB seq length: 20

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 26.6  
1: prot.  
2: para.  
3: para.  
4: para.

Prod. No. is the number of results predicted by chosen criteria. A score greater than or equal to the score of the result is then printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	PIR ID	Accession
1	35	31.2	15	2	S62609
2	34	30.4	12	2	S43170
3	30	26.8	13	2	S74110
4	30	26.8	16	2	S65410
5	28	25.0	14	2	P43241
6	27	24.1	10	2	A01110
7	27	24.1	11	2	P70214
8	27	24.1	15	2	S43170
9	27	24.1	22	2	R41269
10	26	23.3	12	2	A58374
11	26	23.3	15	2	P40024
12	26	23.3	17	2	S05671
13	25	22.3	10	2	P50787
14	25	22.3	10	2	P60780
15	25	22.3	10	2	D63786
16	25	22.3	10	2	B63788
17	25	22.3	10	2	A60788
18	25	22.3	10	2	C60549
19	25	22.3	10	2	D60549
20	25	22.3	10	2	P09125
21	25	22.3	12	2	J02108
22	25	22.3	13	2	J02018
23	25	22.3	18	2	B61110
24	25	22.3	18	2	S48839
25	24	21.4	5	2	PTC669
26	24	21.4	9	2	PTC225
27	24	21.4	10	2	P40344
28	24	21.4	13	1	SW031
29	24	21.4	13	2	S43170

30 24 21.4 14 2 S47366 T-cell antigen rec  
31 24 21.4 15 2 E56978 collagen alpha 2(I)  
32 24 21.4 16 2 A12729 glutamate dehydrog  
33 24 21.4 16 2 A44897 ferredoxin-NADP re  
34 24 21.4 20 2 P10192 Ig lambda 2 chain  
35 23 20.5 10 2 C60788 sperm-activating p  
36 23 20.5 10 2 A60787 sperm-activating p  
37 23 20.5 10 2 A60527 sperm-activating p  
38 23 20.5 10 2 D60527 sperm-activating p  
39 23 20.5 10 2 C39572 sperm-activating p  
40 23 20.5 10 2 T60527 sperm-activating p  
41 23 20.5 11 2 PTC302 Ig heavy chain CDR  
42 23 20.5 11 2 H3903 T-cell receptor be  
43 23 20.5 12 2 S26557 T-cell receptor be  
44 23 20.5 12 2 P41188 T-cell receptor al  
45 23 20.5 12 2 P41470 T-cell receptor be

## ALIGNMENTS

RESULT 1  
S62609  
glutathione-disulfide reductase (EC 1.8.1.7) - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1996 Sequence\_revision 13-Mar-1997 #text\_change 03-Jun 2002  
C:Accession: S62609  
R:Krauth Stegel, R L; MacLier, J G; Lottspeich, F; Schirmer, R H.  
Eur. J. Biochem. 235, 345-350, 1996  
A:Title: Glutathione reductase and glutamate dehydrogenase of Plasmodium falciparum, th  
A:Reference number: S62609; XUID:96202957; PMID:8631352  
A:Accession: S62609  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 «KRA»  
A:Keywords: FAD; flavoprotein; NADP; oxidoreductase  
Query Match: 31.2%; Score 35; DB 2; Length 15;  
Best Local Similarity: 53.8%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0

QY 7 WVDVLCGSSGG 19  
DB : WVDVLCGSSGG 19  
RESULT 2  
S43170  
Kinesin light chain - human (Hsacmori)  
C:Species: Homo sapiens (Hs)  
C:Date: 17-Jun-1995 Sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: S43170  
R:Chernatovsky, Y; Brown, A; Jones, T A; Sheer, D.  
submitted to the EMBL Data Library, December 1993  
A:Description: Promoter: first exon/intron characterization and chromosomal location of  
A:Reference number: S43170  
A:Accession: S43170  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-12 «CHE»  
A:Cross-references: EMBL:X65658; NID:9468786; PIR:CAA49349.1; PID:9468786  
Query Match: 30.4%; Score 34; DB 2; Length 12;  
Best Local Similarity: 57.8%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 12 LCGSSGGP 20  
DB : LCGSSGGP 20  
RESULT 3  
S74110

```

NADH oxidase Giardia duodenalis (fragment)
C:Species: Giardia duodenalis
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S74130
P:Brown, D.M.; Speciot, J.A.; Upcroft, P.
Eur J. Biochem. 241, 155-161, 1996
A:Title: A H120C producing NADH oxidase from the protozoan parasite Giardia duodenalis.
A:Reference numbers: S74130; MUID:97094-24; PMID:8748521
A:Accession: S74130
A:Molecule type: protein
A:Residues: 113 <BS>
A:Experimental source: strain: B913/83 Hapt 16
C:Keywords: Flavoprotein; monomer; NAD

Query Match 26.88; Score 27; DB 2; Length 10;
Best Local Similarity 50.08; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 MVVLCCGSSGG 19
DB 1 MKVILGGTHGG 12

RESULT 4
S654C
Tyrogallol, hydroxyltransferase (EC 1.9.1.12) large chain, beta-1,2-acidinnallic (frag
C:Species: Tyrogallol acidinnallic
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 07-May-1999
C:Accession: S65430
P:Reichenbacher, W.; Ruediger, A.; Kr. Lenz, F.M.H.; Schink, W.
Eur. J. Biochem. 237, 426-433, 1996
A:Title: Gene structure of polydopamine polymerase distributed in the sea slugs related with each sub
and mass spectrometry.
A:Reference numbers: S65429; MUID:962154-1; PMID:8643279
A:Accession: S65430
A:Molecule type: protein
A:Residues: 114 <PE>
C:Keywords: oxidoreductase

Query Match 26.88; Score 27; DB 2; Length 10;
Best Local Similarity 50.08; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 GVMDVLCGSSGG 20
DB 1 GGVVLSSTGG 14

RESULT 5
P626C
T-cell receptor alpha chain (V alpha 2) region (10-0.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Dec-1991 #sequence_revision 11-Dec-1991 #text_change 30-May-1997
C:Accession: P626C
P:Nakanishi, K.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restri
A:Reference numbers: P626C; MUID:912176-1; PMID:1902501
A:Accession: P626C
A:Molecule type: cDNA
A:Residues: 111 <NA>
C:Keywords: T cell receptor

Query Match 24.18; Score 27; DB 2; Length 11;
Best Local Similarity 57.18; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GVSASGG 14
DB 1 GVSASGG 14

RESULT 6
S473A7
T-cell antigen receptor VJ junction beta chain human
C:Species: Homo sapiens (human)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S473A7
P:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*01: restricted recognition of influenza A is dominated by T
A:Reference numbers: S473A5
A:Accession: S473A7
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 115 <LEH>
A:Cross references: EMBL:Z15692; NID:9527475; P:DN:CAA84761.1; P:ID:9527476
C:Keywords: T-cell receptor

Query Match 24.18; Score 27; DB 2; Length 15;
Best Local Similarity 57.18; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 10 GVSASGG 14
DB 1 GVSASGG 14

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RESULT 6
A32195
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 19-Apr-2002
C:Accession: A32195
P:Tyson, P.A.; Steinberg, M.; Wallack, E.T.; Kiley, T.L.
C. Biol. Open. 254, 126-134, 1999
A:Title: Identification of the 5'-untranslated region of the Na+/K+-ATP
A:Reference numbers: A32195; MUID:89091137; PMID:12536082
A:Accession: A32195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 110 <TYS>
C:Keywords: hydrolase

Query Match 24.18; Score 27; DB 2; Length 10;
Best Local Similarity 57.18; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 VDLGGS 16
DB 2 FDLXGS 8

RESULT 7
P70218
T-cell receptor beta chain V beta region (7.10-0.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 11-Dec-1991 #sequence_revision 11-Dec-1991 #text_change 30-May-1997
C:Accession: P70218
P:Nakanishi, K.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restri
A:Reference numbers: P70218; MUID:912176-1; PMID:1902501
A:Accession: P70218
A:Molecule type: cDNA
A:Residues: 111 <NA>
C:Keywords: T cell receptor

Query Match 24.18; Score 27; DB 2; Length 11;
Best Local Similarity 57.18; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GVSASGG 14
DB 1 GVSASGG 14

RESULT 8
S473A7
T-cell antigen receptor VJ junction beta chain human
C:Species: Homo sapiens (human)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S473A7
P:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*01: restricted recognition of influenza A is dominated by T
A:Reference numbers: S473A5
A:Accession: S473A7
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 115 <LEH>
A:Cross references: EMBL:Z15692; NID:9527475; P:DN:CAA84761.1; P:ID:9527476
C:Keywords: T-cell receptor

Query Match 24.18; Score 27; DB 2; Length 15;
Best Local Similarity 57.18; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 10 GVSASGG 14
DB 1 GVSASGG 14

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DB          8  MDVLCGGSSG 18
           1  EVLLGGGSSG 11

RESULT 9
B41259
C:Title: alpha chain precursor V region (B41259) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 28-May-1999
C:Accession: B41259
R:Kumatsu, Y., Waga, H., Straus, A., Oht, Y., Hamakawa, K., Inokubara, J., Panayi, G.,
Piro, Naci, Acad. Sci. U.S.A. 88, 5514-5518, 1991
A:Title: The T-cell receptor repertoire in the synovial fluid of a patient with rheumatoid
arthritis
A:Reference number: A41299; MUID:9220843; PMID:1656459
A:Accession: B41259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <OR>
A:Cross-references: GB:857436; NID:9236120; PDB:1A4P; PDB:1A4321
C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain
C:Keywords: T cell receptor

Query Match 24.1%; Score 20; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 1; Gaps 0;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1  MDVLCGGSSG 11
DB 3  EVLLGGGSSG 11

RESULT 10
A58375
C:Title: Escherichia coli (fragment)
C:Species: Escherichia coli (plasmid pPV11)
C:Date: 13-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 03-May-1999
C:Accession: A58375
R:Korogay, P., Lee, J., Koedel, C., Vivas, E., Warner, P., del Marham, D., Koller, R.,
Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A:Title: Posttranslational modifications in microvillar PIV define an additional class of
A:Reference number: A58375; MUID:94242167; PMID:8149191
A:Accession: A58375
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 1-12 <OR>

Query Match 21.2%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1  MDVLCGGSSG 19
DB 1  EVLLGGGSSG 10

RESULT 11
PAC038
C:Title: Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 04-Jun-1995 #text_change 04-Jun-1997
C:Accession: PAC038
R:Kato, M., Kawakami, T., Miyatake, N., Tsudzuki, A.,
submitted to JPEB, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PAC001
A:Accession: PAC038
A:Molecule type: Protein
A:Residues: 1-15 <KAW>
A:Experimental source: callus

Query Match 23.2%; Score 26; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1; Gaps 0;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 8  MDVLCGGSSG 18
DB 1  EVLLGGGSSG 11

RESULT 12
S05671
C:Title: medicinal leech (fragment)
C:Species: Hirudo medicinalis (medicinal leech)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Jun-1998
C:Accession: S05671
R:Scharf, M., Engels, J., Thipser, D.,
FEBS Lett. 256, 135-137, 1989
A:Title: Primary structures of new "iso-hirudins"
A:Reference number: S05671; MUID:9206545; PMID:2792365
A:Accession: S05671
A:Molecule type: protein
A:Residues: 1-17 <SCH>
C:Superfamily: thrombin inhibitor
C:Keywords: anticoagulant; serine proteinase inhibitor; sulfoprotein
F,6-14/disulfide bonds; #status: predicted

Query Match 23.2%; Score 26; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 1; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1  MDVLCGGSSG 13
DB 6  CTESGQ----NLC 14

RESULT 13
P6C787
C:Title: sperm-activating peptide (Se: 5 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: P6C787
R:Suzuki, N., Kajitani, H., Nomura, K., Garbers, D.L., Yoshino, K., Kurita, M., Tanaka, I.,
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, pseudocentric
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: P6C787
A:Molecule type: Protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction
C:Superfamily: unassigned animal peptides

Query Match 22.3%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1; Gaps 0;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1  MDVLCGGSSG 14
DB 3  DLGGGSSG 10

RESULT 14
H60787
C:Title: sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: H60787
R:Suzuki, N., Kajitani, H., Nomura, K., Garbers, D.L., Yoshino, K., Kurita, M., Tanaka, I.,
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, pseudocentric
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: H60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of

```



at shows some, but not absolute, species restriction  
C:Superfamily: unassigned animal peptides

Query Value 22.18; Score 25; E-2; Length 18,  
Best Local Similarity 62.61; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLGGSSG 18  
||  
LB 5 DTGGGQ 17

RESULT 15  
E60788  
sperm-activation peptide (Thy-5 speract) sea urchin Pseudocentrotus depressus  
C:Species: Pseudocentrotus depressus  
C:Date: 30-Sep-1991; sequence revision 1; Sep-1991 #text change in Aug-2000  
C:Accession: E60788  
C:Author: N. J. Kallala, H. J. Nomura, K. J. Garbars, D. J. Yeh, R. J. Kallala, M. J. Tanaka, H. J. Suzuki, N. J. Kallala, B. J. 89, 587-694, 1998  
C:Comp. Blochm. Physiol. B 89, 587-694, 1998  
A:Title: Some more speract derivatives associated with eggs of sea urchins. Pseudocentrotus depressus  
A:Reference number: A60787; MUID:86242184; PMID:3338493  
A:Accession: E60788  
A:Molecule type: protein  
A:Residues: 1-18 (SU7)  
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of which shows some, but not absolute, species restriction.  
C:Superfamily: unassigned animal peptides

Query Match 22.18; Score 25; E-2; Length 18,  
Best Local Similarity 62.61; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLGGSSG 18  
||  
LB 5 DTGGGQ 17

Search completed: November 5, 2003, 18:11:47  
Job file: 09-914-088

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

Query protein: protein search, using sw model

Run on: November 5, 2003, 18:15:11 / Search time 11 seconds  
(without alignment)  
35,503 Million cells of 100-aa/sec

Title: US-09-914-088-15

Perfect score: 112

Sequence: 1 GLEPGQWMDVCGSSGGP 20

Scoring table: BLOSUM62

Gapop 15.0, Gapext 0.5

Searched: 127823 seqs, 47026205 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 2

Maximum DB seq length: 20

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	10	26.8	16	1 PGTL_PELAC	Protein Pellicle
2	28	25.0	15	1 CHIL_PEA	Chitinase
3	26	23.2	15	1 TAL_TREX	Talipexin
4	24	23.2	17	1 TCHB_HIVE	Tchb
5	23	22.3	20	1 HGL1_PASHE	Hgl1
6	24	21.4	13	1 TAL3_TREVE	Tal3
7	24	21.4	16	1 EHEZ_TRECH	Ehez
8	24	21.4	16	1 ENRZ_STREP	Enrz
9	22	19.6	14	1 GRPS_PASPA	Grps
10	22	19.6	17	1 PPRF_PEPAY	Pprf
11	22	19.6	20	1 RIF_PEPAY	Rif
12	21	18.8	15	1 ACT1_PEPAY	Act1
13	21	18.8	15	1 CDK2_PEPAY	Cdk2
14	21	18.8	20	1 MAX6_PEPAY	Max6
15	21	18.8	20	1 MAX8_PEPAY	Max8
16	23	17.9	13	1 GAUC_HUMAN	Gauc
17	20	17.9	12	1 PVK2_PEPAY	Pvk2
18	20	17.9	15	1 CLOA_PAF	Cloa
19	20	17.9	15	1 KICM_LUYTE	Kicm
20	20	17.9	15	1 OKCL_TONAY	Okcl
21	20	17.9	15	1 TRPA_LEMDA	Trpa
22	20	17.9	17	1 FLAW_AZ_08	Flaw
23	20	17.9	17	1 PATS_ARABE	Pats
24	20	17.9	20	1 COG1_PASPE	Cog1
25	20	17.9	20	1 COG1_PASPE	Cog1
26	20	17.9	20	1 FLAW_AZ_08	Flaw
27	20	17.9	20	1 MAX1_PEPAY	Max1
28	20	17.9	20	1 POK1_CLOA	Pok1
29	20	17.9	20	1 RIFX_PEPAY	Rifx
30	19.5	17.4	19	1 FISA_SHEEP	Fisa
31	19	17.0	8	1 ALLE_CARMA	Alle
32	19	17.0	8	1 ALLE_CARMA	Alle
33	19	17.0	9	1 CSIP_RABIT	Csip

34	19	17.0	11	1 BPP4_ROTIN	Bpp4
35	19	17.0	12	1 V23K_WSSV	V23k
36	19	17.0	13	1 BOML_PSEGU	Boml
37	19	17.0	13	1 CHAL_HUMAN	Chal
38	19	17.0	14	1 UN46_CLOPA	Un46
39	19	17.0	15	1 DICH_PSESP	Dich
40	19	17.0	15	1 PLAS_MICAF	Plas
41	19	17.0	20	1 CD4_SHEEP	Cd4
42	19	17.0	20	1 T214_SPLIC	T214
43	18.5	16.5	20	1 T214_ALBUM	T214
44	18	16.1	8	1 ACT_CARMA	Act
45	18	16.1	12	1 CPS3_DROVI	Cps3

ALIGNMENTS

RESULT:	PGTL_PELAC	STANDARD:	FRT:	16 AA
ID	PGTL_PELAC	STANDARD:	FRT:	16 AA
AC	P80563			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)			
CS	Pelotactin acid (fragment)			
CC	Pelotactin acid (fragment)			
CC	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;			
CC	Pelobacteraceae; Pelobacter			
OX	NCBI_TaxID=35216;			
RN	[1]			
RP	SEQUENCE			
RC	STRAIN:DSM 2277 / Braunschwetzig;			
RX	MEDLINE=94215436; PubMed=8647079;			
RA	Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.			
RT	"One molecule of methylcobalamin-dependent dihydroxyacetone phosphate (DHAP) is associated with each subunit of the heterodimeric MoFe-S protein"			
RT	transhydroxylase of Pelobacter acidgallii as determined by SDS/PAGE and mass spectrometry."			
RL	Eur. J. Biochem. 237:436-443 (1996).			
CC	-1- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-tetrahydroxybenzene -> 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-tetrahydroxybenzene.			
CC	tetrahydroxybenzene.			
CC	-1- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-tetrahydroxybenzene -> 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-tetrahydroxybenzene.			
CC	-1- SURF: MOLECULAR WEIGHT (KDa) 16.5			
DR	PIR: S65430; S65430.			
KW	Oxidoreductase; Methylcobalamin; Iron-sulfur.			
FT	NCN_TER 16			
SQ	SEQUENCE 16 AA, 165.0 MW, 454853ACADEM3 (CR044);			
Query Match:	16.4%	Score 10	DB 17	Length 16
Best Local Similarity:	50.0%	Pred. No. 26-02		
Matches	W: Conservative	2; Mismatches	4; Indels	2; Gaps
CY	5 GGVNPDVCGSSGGP 20			
DB	1 GGVNPDVCGSSGGP 14			
RESULT 2	CHIL_PEA	STANDARD:	FRT:	15 AA
ID	CHIL_PEA	STANDARD:	FRT:	15 AA
AC	P21225			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Endochitinase A1 (EC 3.2.1.14; (Fragment))			
CS	Pisum sativum (garden pea)			
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	SpERMATOPHYTES; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;			
CC	eurostias 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.			
OX	NCBI_TaxID=4852;			
RN	[1]			



```

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 41.7%  Pred. No. 1.4e+03;
Matches      5;  Conservative      2;  Mismatches      5;  Indels      0;  Gaps      0;

QY      7 VMDVLCGSSG 18
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      3 VVDVFGGAKG 14
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 8
FNR STGR
ID FNR STGR STANDARD FRT 16 AA.
AC P24714:
DT 01-MAR-1992 (Rel. 21, Created:
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Ferredoxin-NAD(P)+ reductase (EC 1.18.1.3) (Fragment).
CS Streptomyces griseus.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Streptomyces; Streptomyetaceae; Streptomyces.
OX NCBI_TaxID:19117
RN (1)
RP SEQUENCE
RX MEDLINE:82041527; PubMed:193912;
RA Ramachandra M., Sentharam R., Emeage M.H., Sathasani P.S.;
RT "Purification and characterization of a soybean flour-inducible
RL J. Bacteriol. 173:7106-7112(1991).
CC (1) FUNCTION: COUPLE ELECTRON TRANSFER FROM NADH TO CYTOCHROME
CC P450(SOV) IN THE PRESENCE OF FERREDOXIN.
CC (1) CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(P)+ = oxidized
CC ferredoxin + NAD(P)+.
CC (1) COFACTOR: FAD; REQUIRES MAGNESIUM.
DR PIP; A41697; A44897
KW Oxidoreductase; Flavoprotein; NAD; FAD; Magnesium.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1485 MW; 27011AV37AC0510 CRC64;

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 52.0%  Pred. No. 1.4e+03;
Matches      4;  Conservative      1;  Mismatches      3;  Indels      0;  Gaps      0;

QY      12 ICGGSSGG 19
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      5 ICGGSGG 12
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 9
GRVS CANFA
ID GRVS CANFA STANDARD FRT 14 AA.
AC P99432:
DT 15-JUL-1998 (Rel. 46, Created:
DT 15-JUL-1998 (Rel. 46, Last sequence update)
DT 15-JUL-1998 (Rel. 46, Last annotation update)
DE Mitochondrial stress-70 protein (75 kDa glucose regulated protein;
DE GRP75) (Fragment).
GN HSPA9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN (1)
RP SEQUENCE
RC TISSUE=Heart;
RX MEDLINE:98163140; PubMed:9504412;
RA Dunn M.B., Corbett D.N., Wheeler C.H.;
RT "HSC 20PAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 14:275-282(1993).
CC (1) FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND
CC CELLULAR GROWTH. MAY ALSO ACT AS A CHAPERONE.
CC (1) SUBCELLULAR LOCATION: Mitochondrial.
CC (1) SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 57.1%  Pred. No. 1.1e+03;
Matches      4;  Conservative      1;  Mismatches      2;  Indels      0;  Gaps      0;

QY      14 GGSNGG 20
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      1 GGRGSP 9
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 7
DHF THUTH
ID DHF THUTH STANDARD FRT 16 AA.
AC P30576:
DT 01-FEB-1991 (Rel. 17, Created:
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NAD specific glutamate dehydrogenase (EC 1.4.1.3) (Fragment).
CS Thymus thymus (Bluefin tuna).
CC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euplatychthyes; Clupeiformes;
CC Acanthomorpha; Acanthopterygii; Delmonidae; Delmonidae; Clupeidae;
CC Scophthalmidae; Thunnini.
OX NCBI_TaxID:5437.
RN (1)
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE:76251947; PubMed:182270;
RA Veronow F.W., Bevilacqua R., Bacon E., Biwa D.Y.;
RT "Purification, characteristics and sequence of a protein containing
RT an essential lysine residue."
RL Biochim. Biophys. Acta 445:113-120(1975).
CC (1) CATALYTIC ACTIVITY: L-glutamate + H2O + NAD+ = L-glutamate
CC + NH3 + NADH.
CC (1) SIMILARITY: BELONGS TO THE GLUTAMATE DEHYDROGENASE FAMILY.
CC PIP; A12729; A12729.
DR InterPro; IPR026095; G5FV dehydrog
DR InterPro; IPR026097; G5FV dehydrog
DR Pfam; PF02812; G5FV dehydrog N; 1.
DR PROSITE; PS00074; GLUF_DEHYDROGENAS; PARTIAL.
KW Oxidoreductase; NAD.
FT NON_TER 1
FT ACT_SITE 12 12
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1518 MW; F527AAV37AC0510 CRC64

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DR HSP20PAGE; P99502; DOG.
DR InterPro; IPRO01023; HSP70.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS00336; HSP70_3; PARTIAL.
DR PROSITE; PS00336; HSP70_3; PARTIAL.
KW ATP binding; Mitochondrion.
FT NUP.REF 14
FT NUP.REF 14
SQ SEQUENCE 14 AA; 1439 MW; 2A5EDCAA PAEW8 IF 64.
Query Match 19.6%; Score 22; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 GQVNVVDL 12
DB 7 GAVVXLDL 14
RESULT 10
EPK0.PEAV
ID -PK0.PEAM STANDARD; PRT; 17 AA
AC P9267;
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Pyrokinin-5 (Pea-PK-5) (EXPRC antibi-
DE Pyroplasma americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Euryzoa;
CC Neoptera; Orthoptera; Dictyoptera; Blattella; Blattellidae;
CC Blattellidae; Blattellinae.
CX NCBI_TaxID:6974;
RN [1]
SQ SEQUENCE, FUNCTION, AND MASS SPECIFIC MERRY.
RP TISSUE:Adiponal perivascular (lipid).
RP MEDLINE 99212463; PubMed 10196716;
EX Pridel R., Keller R., Nachman R.D., Bahrman N., Kremer A.,
RP "Cellular distribution of pyrokinin in the perivascular
RP at abdominal neuroendocrine organs of the American cockroach."
RP Insect Biochem. Mol. Biol. 29:133-144 (1999).
RN [1]
RP TISSUE SPECIFICITY.
RX MEDLINE 20169844; PubMed 10723010;
RA Pridel R., Eckert M.;
RP "Plasma specific distribution of EXPRC antibodies in the perivascular
RP of the American cockroach."
RL J. Comp. Neurol. 459:352-363 (2003).
CC FUNCTION: MEDIATES VISCERAL MOTOR CONTRACTIONS ACTIVELY
CC MYOTROPIC ACTIVITY.
CC TISSUE SPECIFICITY: MAINLY IN ADIPONAL PERIVASCULAR SPACES AND
CC TO A LARGER EXTENT IN PERIVASCULAR SPACES
CC IN VARIOUS SPECIES: MW 1651.7, P I 1.1, MW 1.1.
UR EMBL:IP001494; Pyrokinin.
UR PROSITE; PS00336; PYROKININ; 1;
DR PROSITE; PS00336; PYROKININ; 1;
KW Neurotrophic; Amidation; Pyrokinin.
FT MCD RES 17
FT MCD RES 17
SQ SEQUENCE 17 AA; 1653 MW; 8527162BA45H954 IF 64.
Query Match 19.6%; Score 22; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GISSGSLH
DB 2 GISSGSLH
RESULT 11
BIP.PEAV
ID BIP.PEAV STANDARD; PRT; 17 AA
AC P9049;
DT 01-DEC-1991 (Rel. 24; Last annotation update)
DT 01-DEC-1991 (Rel. 24; Last annotation update)
DE "Water deficit-responsive proteins in maritime pine";
DE Plant Mol. Biol. 14:587-596 (1998).
RN [2]
RP TISSUE:Needle;
RP MEDLINE 99274388; PubMed 10144291;
RA Costa P., Bahrman N., Figueiro J.M., Kremer A., Plomion C.;
RA Figueiro J.M., Plomion C.;
RA "Separation and characterization of needle and xylem maritime pine
RP proteins."
RP Electrophoresis 20:1398 (1999).
CC FUNCTION: ACTING AS HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNICITOUSLY EXPRESSED
CC IN ALL EUPHYTIC CELLS BY SIMILARITY.

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DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Luminal binding protein (78 kDa glucose-regulated protein homolog)
DE (GRP 78) (Fragment).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OS Eucosids; Fabales; Paraceae; Papilionaceae; Phaseolidae; Phaseolus.
CX NCBI_TaxID:3885;
RN [1]
SQ SEQUENCE.
RP STRAIN:CV. Greensleeves; TISSUE:Cotyledon;
RX MEDLINE 94221964; PubMed 1344865;
RA D'Amico L., Valsesia S., Damiani M.G., Fabbri M.S., Nitti G.,
RA Bollini R., Ceriotti A., Vitale A.;
RT "Bean homologs of the mammalian glucose-regulated proteins: induction
RT by tunicamycin and interaction with newly synthesized seed storage
RT proteins in the endoplasmic reticulum."
RL Plant J. 2:443-450 (1992).
CC FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF
CC MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
CC SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC INDUCTION: By tunicamycin.
CC SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR InterPro; IPR01023; HSP70
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS00336; HSP70_3; PARTIAL.
KW ATP-binding; Endoplasmic reticulum.
FT UNSURE 4
FT UNSURE 4
FT UNSURE 18
FT NUP.REF 20
FT NUP.REF 20
SQ SEQUENCE 20 AA; 2147 MW; 8C9D43AF21A21476 CRC64;
Query Match 19.6%; Score 22; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 GQVNVVDL 12
DB 8 GTVIGIDL 15
RESULT 12
ACT.FINPS
ID ACT.FINPS STANDARD; PRT; 15 AA
AC P91085;
DT 15-JUL-1994 (Rel. 36; Created)
DT 15-JUL-1994 (Rel. 36; Last sequence update)
DT 10-MAY-2000 (Rel. 39; Last annotation update)
DE Actin: Water stress responsive protein 2 (fragment).
OS Phaseolus vulgaris (Kidney bean).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OS Spermatophyta; Coniferales; Pinaceae; Pinus.
CX NCBI_TaxID:31547;
RN [1]
SQ SEQUENCE.
RP TISSUE:Needle;
RP MEDLINE 99418576; PubMed 9747824;
RA Costa P., Bahrman N., Figueiro J.M., Kremer A., Plomion C.;
RA "Water deficit-responsive proteins in maritime pine";
RA Plant Mol. Biol. 14:587-596 (1998).
RN [2]
RP TISSUE:Needle;
RP MEDLINE 99274388; PubMed 10144291;
RA Costa P., Bahrman N., Figueiro J.M., Kremer A., Plomion C.;
RA Figueiro J.M., Plomion C.;
RA "Separation and characterization of needle and xylem maritime pine
RP proteins."
RP Electrophoresis 20:1398 (1999).
CC FUNCTION: ACTING AS HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNICITOUSLY EXPRESSED
CC IN ALL EUPHYTIC CELLS BY SIMILARITY.

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CM protein protein search, using sw mode:

Run on: November 5, 2003, 10:15:06 / Search path: /usr/local

without adjustment  
154,396 Matches found in 15.0 sec

Title: US-09-914-088-15

Perfect score: 112

Sequence: 1: GAGGQVQVYVCGSSSGP 20

Scoring table: BLOSUM62

Gapop: 15.0, Gapext: 0.5

Search: 81325 seqs, 258052654 residues

Total number of hits satisfying chosen parameters: 4966

Minimum DB seq length: 6

Maximum DB seq length: 20

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: SPPEMS1.231

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_humani:
- 5: sp\_invertebrate:
- 6: sp\_mammali:
- 7: sp\_rhco:
- 8: sp\_rhco:
- 9: sp\_rhco:
- 10: sp\_rhco:
- 11: sp\_rhco:
- 12: sp\_rhco:
- 13: sp\_rhco:
- 14: sp\_rhco:
- 15: sp\_rhco:
- 16: sp\_rhco:
- 17: sp\_rhco:

Pred. No. is the number of residues predicted to be in the protein.  
score greater than or equal to the score of the best hit in the database.  
and is derived by analysis of the data in the database.

# SUMMARY

Result No.	Score	Query Match	Length	ID	Protein
1	35	31.2	15	Q9TWE1	Q9TWE1 mus musculus
2	34	30.4	12	Q13865	Q13865 mus sapien
3	32	28.6	16	Q32160	Q32160 mus sapien
4	29	25.9	20	Q98414	Q98414 mus sapien
5	29	25.9	20	Q8BXG5	Q8BXG5 mus musculus
6	28	25.0	18	Q9TWE2	Q9TWE2 mus musculus
7	27	24.1	16	Q40675	Q40675 mus sapien
8	27	24.1	19	Q9TWE1	Q9TWE1 mus sapien
9	27	24.1	19	Q9TWE1	Q9TWE1 mus sapien
10	27	24.1	20	Q8TWE1	Q8TWE1 mus sapien
11	26	23.2	15	Q9TWE1	Q9TWE1 mus sapien
12	26	23.2	17	Q9TWE1	Q9TWE1 mus sapien
13	26	23.2	18	Q9TWE1	Q9TWE1 mus sapien
14	26	23.2	20	Q9TWE1	Q9TWE1 mus sapien
15	25.9	22.6	17	Q8BXG5	Q8BXG5 mus musculus
16	25.9	22.6	20	Q9TWE1	Q9TWE1 mus sapien

17	25	22.3	9	11	Q9QZ48	Q9QZ48 mus musculus
18	25	22.3	17	4	Q9TWE1	Q9TWE1 mus sapien
19	25	22.3	18	5	Q9TWE1	Q9TWE1 mus sapien
20	25	22.3	18	6	Q9TWE1	Q9TWE1 mus sapien
21	25	22.3	20	10	Q9S8C2	Q9S8C2 pinus sylve
22	24	21.4	7	11	Q55184	Q55184 rattus norv
23	24	21.4	10	4	Q9TWE1	Q9TWE1 mus sapien
24	24	21.4	13	4	Q9TWE1	Q9TWE1 mus sapien
25	24	21.4	13	6	Q9TWE1	Q9TWE1 mus sapien
26	24	21.4	13	10	Q9S8K3	Q9S8K3 glycine max
27	24	21.4	20	4	Q9TWE1	Q9TWE1 mus sapien
28	24	21.4	20	11	Q636F7	Q636F7 rattus norv
29	24	21.4	20	13	Q8BXG5	Q8BXG5 mus musculus
30	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
31	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
32	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
33	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
34	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
35	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
36	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
37	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
38	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
39	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
40	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
41	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
42	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
43	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
44	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien
45	23	20.5	22	6	Q9TWE1	Q9TWE1 mus sapien

## ALIGNMENTS

RESULT 1	Q9TWE1	PRELIMINARY	PROT	15 AA
AC	Q9TWE1			
CT	Q9TWE1			
DT	Q9TWE1			
DT	Q9TWE1			
DT	Q9TWE1			
DE	Q9TWE1			
OS	Q9TWE1			
OC	Q9TWE1			
CX	Q9TWE1			
RN	Q9TWE1			
RP	Q9TWE1			
RA	Q9TWE1			
RT	Q9TWE1			
RL	Q9TWE1			
SQ	Q9TWE1			

Query Match 31.2%, Score 35, DB 5, Length 15;  
Best Local Similarity 53.8%, Pred. No. 1.2e+02;  
Matches 7, Conservative 2, Mismatches 4, Indels 0, Gaps 0;

QY	7	WVDELCCSSSSG 19	
QB	1	WVDELCCSSSSG 19	
RESULT 2			
Q13865			
ID	Q13865		
AC	Q13865		
DT	Q13865		
DT	Q13865		
DT	Q13865		
DE	Q13865		
GN	Q13865		
OS	Q13865		

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catartini; Hominoidea; Homo.
CX NCBI_TaxID:9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE:97171116; PubMed:8945637;
RA Chetaniyevsky Y., Brown A., Jones T.A.
RT "Transfer first exon/intron characterizations and frame relocation
RT of the human light chain beta1 kinesin gene."
RL DNA Cell Biol 15:974-976; 1996.
DR EMBL: X69652; FAY4949.1;
SQ SEQUENCE 12 AA, 1274 MW, 38960.48E04.800 R 64
Query Match 20.4%; Score 64; DB 4; Length 12;
Best local similarity 27.8%; Pred No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
CY 12 LKSSSGGP 20
DB 1
2 LKSSSGGP 10
RESULT 3
ID Q2160 PRELIMINARY; PRT, 16 AA.
AC Q2160
DT 01-MAY-2003 (TRENBERG); 01, Created;
DT 01-MAY-2003 (TRENBERG); 01, Last sequence update;
DT 01-MAY-2003 (TRENBERG); 01, Last annotation update;
DE Alcohol oxidase (fragment).
OS Pichia pastoris (Yeast).
CC Eukaryota; Fungi; Ascomycota; Sacccharomycotina; Saccharomycetales;
CC Saccharomycetaceae; Pichia.
CX NCBI_TaxID:4932;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE:93349727; PubMed:7763408;
RA Kimura M.H., Seewald G.G., della Cella C.F.
RT "Conversion of starch to ethanol in a recombinant P. pastoris
RT expressing strain expressing the alpha-amylase from P.
RT putnis alcohol oxidase promoter."
RL Biotechnol Bioeng 73:114-126 1999.
DR EMBL: S6287; AA02548.1;
CX NCBI_TaxID:4932;
RN 1
RP SEQUENCE 16 AA, 1638 MW, 35600.01E04.800 A 644
Query Match 20.4%; Score 64; DB 4; Length 16;
Best local similarity 55.6%; Pred No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
CY 0 EVLVSSSS 12
DB 0
0 EVLVSSSS 16
RESULT 4
ID Q9P14 PRELIMINARY; PRT, 16 AA.
AC Q9P14
DT 01-MAY-2003 (TRENBERG); 13, Created;
DT 01-MAY-2003 (TRENBERG); 13, Last sequence update;
DT 01-MAY-2003 (TRENBERG); 13, Last annotation update;
DE BENZYL-tyrosine-linked aldehyde oxidoreductase (fragment).
OS Desulfovibrio gigas.
CC Bacteria; Proteobacteria; Delta-proteobacteria; Desulfosporosporales;
CC Desulfobacteriaceae; Desulfovibrio.
CX NCBI_TaxID:879;
RN 1
RP SEQUENCE
RX MEDLINE:9041046; PubMed:7592180;
RA Besser TE, V.L., Hayes W.R., Hansen A

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RT "Purification and characterization of a benzyl-tyrosine-linked,
RT tungsten containing aldehyde oxidoreductase from Desulfovibrio gigas."
RL J. Bacteriol. 177:6195-6200(1995);
SQ SEQUENCE 20 AA, 2128 MW, 1A9608A188:9C2BC CRC64;
Query Match 25.9%; Score 29; DB 2; Length 20;
Best local similarity 31.3%; Pred No. 1.4e+03;
Matches 5; Conservative 6; Mismatches 2; Indels 2; Gaps 1;
CY 6 LKSSSGGP 20
DB 3
3 LKSSSGGP 15
RESULT 5
ID Q8XG5 PRELIMINARY; PRT, 20 AA.
AC Q8XG5
DT 01-MAR-2003 (TRENBERG); 23, Created;
DT 01-MAR-2003 (TRENBERG); 23, Last sequence update;
DT 01-MAR-2003 (TRENBERG); 23, Last annotation update;
DE Kinesin superfamily protein 21A (fragment).
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN:CV981/62; Tissue=Cerebellum;
RX MEDLINE:22184683; PubMed:12468851;
RA The FANTOM Consortium.
RT "The FANTOM genome exploration research group phase I & II: Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK047329; BA012931.1;
CX NCBI_TaxID:10090;
RN 1
RP SEQUENCE 20 AA, 2062 MW, 51004.25E04.2075 CRC64;
Query Match 25.9%; Score 29; DB 1; Length 20;
Best local similarity 62.5%; Pred No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 2 LKSSSGGP 9
DB 0
2 LKSSSGGP 9
RESULT 6
ID Q1W62 PRELIMINARY; PRT, 18 AA.
AC Q1W62
DT 01-MAY-2003 (TRENBERG); 14, Created;
DT 01-MAY-2003 (TRENBERG); 13, Last sequence update;
DT 01-MAY-2003 (TRENBERG); 14, Last annotation update;
DE GNG-3 tyrosine peptide (fragment).
OS Pheretima vittata (Earthworm).
CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Epiplatida;
CC Loricifera; Megastomatidae; Pheretima.
CX NCBI_TaxID:46674;
RN 1
RP SEQUENCE
RX MEDLINE:9474592; PubMed:7486182;
RA Omi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Morio K.
RT "The GNG-3 tyrosine peptide tyrosine peptides isolated from the gut and
RT the whole body of the earthworms."
RL Biochem Biophys Res Commun. 216:1372-1378(1995);
SQ SEQUENCE 18 AA, 1937 MW, 581A2314B5B5F266 CRC64;
Query Match 25.9%; Score 29; DB 5; Length 18;
Best local similarity 36.7%; Pred No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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CY 13 CGSSG 18
DB 13 CGSSG 18

RESULT 7
Q0656 PRELIMINARY: PRT: 16 AA.
ID Q0656
AC Q0656
DT 01-MAY-1999 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Actin (Fragment)
GN ACT1
OS Cryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC Ehrhartoideae; Cryzeae; Cryza.
CX NCBI TaxID:4530;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B-42;
RX MEDLINE=9252956; PubMed=1753941;
RA McElroy D., Howers A.D., Jones B., Wu R.;
PT "Construction of expression vectors based on the rice actin-1 (act1)
PT 5' region for use in monocot transformation."
RL Mol. Gen. Genet. 231:150-160(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B-42;
RA Wu R.J.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: X63830; CAA45324.1;
IR Genbank: Q42656;
FT NON TER 16
SQ SEQUENCE 16 AA; 1523 MW; BF6BFA79929A2F CR764;

Query Match 24.1%; Score 27; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 14 CGSSG 19
DB 14 CGSSG 19

RESULT 8
Q0766 PRELIMINARY: PRT: 16 AA.
ID Q0766
AC Q0766
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Lactoferrin (Fragment)
OS Equus caballus (Horse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
CX NCBI TaxID:9796;
FN [1]
RP SEQUENCE FROM N.A.
RC BRAND=K.B.; Giffard J.M., Bell T.R.;
RA "Isolation of Equine Lactoferrin Gene"
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF102625; AAC77463.1;
IR HSP: Q77698; ACE2;
DE InterPro: IPRO0156; Transferrin;
DR Pfam: PF00405; Transferrin;
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 1936 MW; D8FBFA22A4A6D3 F764;

Query Match 24.1%; Score 27; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 15 CGSSG 18
DB 15 CGSSG 18

RESULT 9
Q0766 PRELIMINARY: PRT: 19 AA.
ID Q0766
AC Q0766
DT 01-MAY-2003 (TREMBlrel. 13, Created)
DT 01-MAY-2003 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 14, Last annotation update)
DE 20 kDa phosphorylation-dependent protein phosphatase-1 inhibitory
DE protein (Fragment)
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI TaxID=9823;
FN [1]
RP SEQUENCE.
RX MEDLINE=96362144; PubMed=8720121;
RA Eto M., Ohori T., Suzuki M., Futsuya K., Morita F.;
PT "A novel protein phosphatase-1 inhibitory protein: potentiated by
PT protein kinase C. Isolation from porcine aorta media and
PT characterization."
RL J. Biochem. 118:1104-1107(1995).
RN [2]
SQ SEQUENCE 19 AA; 1850 MW; 5D94CF5EF225A922 CR664;

Query Match 24.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 14 CGSSG 19
DB 14 CGSSG 16

RESULT 10
Q81213 PRELIMINARY: PRT: 20 AA.
ID Q81213
AC Q81213
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE LEF1 (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI TaxID=9606;
FN [1]
RP SEQUENCE FROM N.A.
RA Filali M., Cheng N., Abbot U., Leontiev V., Engelhardt J.F.;
RT "Wnt 3a/b-catenin Signaling Induces Transcription from the LEF-1
RT Promoter."
RL J. Biol. Chem. 276:21200(2001).
DR EMBL: AY129650; AAN56089.1;
FT NON TER 20
SQ SEQUENCE 20 AA; 1761 MW; B4F1691556FBA675 CR664;

Query Match 24.1%; Score 27; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 12 CGSSG 19
DB 4 CGSSG 11

RESULT 11
Q9TRP3

```

```

ID QTR23 PRELIMINARY; PRT; 15 AA.
AC QTR23;
CT 01-MAY-2000 (TRENBLREL.13, Created.
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update.
DE 01-OCT-2000 (TRENBLREL.15, Last annotation update.
RE LOW Mr zona pellucida binding protein (fragment).
CS Sus scrofa (pig).
CC Eukaryota; Metazoa; Chordata; Carnivora; Artiodactyla; Suidae.
CC Ximallia; Eubacteria; Cetartiodactyla; Suidae; Suidae; Suidae.
CX NCBI_TaxID=9923;
RN [1]
PF SEQUENCE.
RX MEDLINE=92378826; PubMed 15108423.
RA Parry R.V., Barker P.J., Jones R.
PT "Characterization of low Mr zona pellucida binding proteins from near
R1 spermatozoa and seminal plasma".
R2 Mol. Reprod. Dev. 33:108-115(1992).
DR HSP; P3495; ISPP.
SQ SEQUENCE 15 AA; 1656 MW; 24428AF978E1E94 DF 04.

Query Match 23.2%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY F MDVLCG15
: |||
: LDVHAGGS A
Db : LDVHAGGS A

RESULT 12
Q9P4Y9 PRELIMINARY; PRT; 17 AA
ID Q9P4Y9
AC Q9P4Y9
CT 01-MAY-2000 (TRENBLREL.13, Created.
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update.
DE 01-JUN-2000 (TRENBLREL.14, Last annotation update.
DE Aromatic amine dehydrogenase beta subunit (fragment).
CS Alcaligenes faecalis.
CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales.
CC Alcaligenaceae; Alcaligenes.
CX NCBI_TaxID=511;
RN [1]
PF SEQUENCE.
RX MEDLINE=94245619; PubMed=9189594.
RA Govindaraj S., Eisenstein E., Jones D.H., Sanders Hunt J.
RA Chistosodov A.V., Davidson V., Edwards S.L.
PT "Aromatic amine dehydrogenase, a second tryptophan catabolic enzyme".
RE Enzyme".
R2 J. Bacteriol. 176:1922-1928(1994).
DR HSP; P3495; ISPP.
SQ SEQUENCE 17 AA; 1510 MW; 68F8A9F0A0A0A0A0 DF 04.

Query Match 23.2%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GSSSSG 19
: |||
: 4 GSSSSG 9
Db : 4 GSSSSG 9

RESULT 13
Q9QV14 PRELIMINARY; PRT; 17 AA
ID Q9QV14
AC Q9QV14
CT 01-MAY-2000 (TRENBLREL.13, Created.
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update.
DE 01-JUN-2000 (TRENBLREL.14, Last annotation update.
DE Insulin-like growth factor binding protein 3 (fragment).
CS Homo sapiens (human).
CC Eukaryota; Metazoa; Chordata; Carnivora; Artiodactyla; Suidae.
CC Ximallia; Eubacteria; Cetartiodactyla; Suidae; Suidae; Suidae.
CX NCBI_TaxID=9606;
RN [1]

```

```

RP SEQUENCE
RX MEDLINE=94091816; PubMed=1726837.
RA Roghani M., Segovia B., Whitechurch C., Binoux M.
PT "Purification from human cerebrospinal fluid of insulin-like growth
R1 factor binding proteins (IGFBPs): isolation of IGFBP-2, an altered form
R2 of IGFBP-3 and a new IGFBP species".
R3 Growth Reg. 1. 1:126-130(1991).
DR HSP; P3495; ISPP.
SQ SEQUENCE 18 AA; 1689 MW; 10F551624CC6298B CRC64;

Query Match 23.2%; Score 26; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GSSSSG 19
: |||
: 1 GSSSSG 9
Db : 1 GSSSSG 9

RESULT 14
O9UR6C PRELIMINARY; PRT; 20 AA
ID O9UR6C
AC O9UR6C
CT 01-MAY-2000 (TRENBLREL.13, Created.
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update.
DE 01-JUN-2000 (TRENBLREL.14, Last annotation update.
DE 45 kDa type II keratin homolog (fragment).
CS Candida albicans (yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
CC Saccharomycetales; microsporid Saccharomycetales; Candida.
CX NCBI_TaxID=5476;
RN [1]
PF SEQUENCE.
RX MEDLINE=97064135; PubMed=8692300.
RA Colina A.R., Aurone F., Deslauriers N., Belhumeur P.
RA de Repetition 1.
PT "Evidence for degradation of gastrointestinal mucin by Candida
R1 albicans secretory aspartyl proteinase".
R2 Infect. Immun. 64:4514-4519(1996).
DR HSP; P3495; ISPP.
SQ SEQUENCE 20 AA; 1583 MW; F4389472CA6EAA05 CRC64;

Query Match 23.2%; Score 26; DB 3; Length 20;
Best Local Similarity 38.9%; Pred. No. 3.9e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

QY 3 EDGVMDCVLCGSSSGSP 20
: |||
: 1 EDGVMDCVLCGSSSGSP 19
Db : 1 EDGVMDCVLCGSSSGSP 19

RESULT 15
O85719 PRELIMINARY; PRT; 17 AA
ID O85719
AC O85719
CT 01-NOV-1996 (TRENBLREL.01, Created.
DT 01-NOV-1996 (TRENBLREL.01, Last sequence update.
DE 01-JUN-2000 (TRENBLREL.21, Last annotation update.
DE Reovirus serotype 3 S4 (fragment).
OS Reovirus (type 3 / strain Dearing).
CC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
CX NCBI_TaxID=10896;
RN [1]
PF SEQUENCE.
RX MEDLINE=94091816; PubMed=1726837.
RA McGrae M.A.
PT "Terminal structure of reovirus RNAs".
R2 J. Gen. Virol. 55:393-401(1991).
DR HSP; P3495; ISPP.
SQ SEQUENCE FROM N.A.
RX MEDLINE=63017676; PubMed=6927854.
RA Antczak J.A., Carmelo P., Pickup D.C., Joklik W.K.
PT "Sequences at both termini of the 10 genes of reovirus serotype 3
R1 (strain Dearing)".
R2 Virol. 111:107-109(1987).

```

DR EM501 002327 AAA47284.17 17  
DR InterPro: IPR000153; Reovirus\_cap.  
DR Pfam: PF00979; Reovirus\_cap. 17  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA: 1852 MW: 475458.4648; IPIFO: IPIFO44  
Query March 22.8% Score 25.00 DR 107 GenPeB 07.  
Best Local Similarity 54.5% Pred. No 1,990,000  
Matches 67 Conservative 37 Mismatches 37 Gaps 17  
CY 1 CLEDS QWMDV 10  
2b 4 CLPBGHWVSE 14

Search completed: November 5, 2003, 18:21:17  
Job time : 14 secs

GenCore version 5.1.6  
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CM protein protein search, using sw model

Run on: November 5, 2003, 18:14:41, Search time 41.8 seconds  
Without alignment  
77,428 Million cell updates/sec

Title: US-09-914 ORA 15  
Perfect score: 112  
Sequence: LGRGGQVMDVDSKGGSSGP 2

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726531 residues

Total number of hits satisfying chosen parameters: 40

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

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21 /SIDSL/cgdata/gene34/gene34p-entl-AA1949.DAT.\*  
22 /SIDSL/cgdata/gene34/gene34p-entl-AA1949.DAT.\*  
23 /SIDSL/cgdata/gene34/gene34p-entl-AA1949.DAT.\*  
24 /SIDSL/cgdata/gene34/gene34p-entl-AA1949.DAT.\*

Prod. No. is the number of results produced by the search, based on  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	112	100.0	20	21 AAB25914	Pi minotope peptid
2	112	100.0	20	22 AAB25916	Peptide P15 deriv
3	112	100.0	20	23 ABJ00316	Human IgE cyclic 1
4	105	93.8	20	23 ABJ00344	Human IgE cyclic 1
5	79	70.5	16	23 ABJ00344	Human IgE cyclic 1
6	73	65.2	13	21 AAB25917	Human IgE cyclic 1
7	73	65.2	13	22 AAB25917	Human IgE cyclic 1
8	73	65.2	13	23 ABJ00344	Human IgE cyclic 1
9	64	57.1	13	21 AAB25914	Pi minotope peptid

10	64	57.1	13	21 AAB25914	Pi minotope peptid
11	64	57.1	13	21 AAB25916	Peptide P15 deriv
12	64	57.1	13	22 AAB25917	Human IgE cyclic 1
13	64	57.1	13	22 AAB25917	Human IgE cyclic 1
14	64	57.1	13	22 AAB25917	Human IgE cyclic 1
15	64	57.1	13	23 ABJ00324	Human IgE immunog
16	64	57.1	13	23 ABJ00324	Human IgE immunog
17	60	53.6	14	23 ABJ00326	Human IgE immunog
18	60	53.6	14	23 ABJ00326	Human IgE immunog
19	60	53.6	14	23 ABJ00326	Human IgE immunog
20	60	53.6	14	23 ABJ00326	Human IgE immunog
21	57	50.9	13	21 AAB25917	Human IgE cyclic 1
22	57	50.9	13	21 AAB25917	Human IgE cyclic 1
23	57	50.9	13	21 AAB25917	Human IgE cyclic 1
24	57	50.9	13	21 AAB25917	Human IgE cyclic 1
25	47	42.0	9	21 AAB25917	Human IgE cyclic 1
26	47	42.0	9	21 AAB25917	Human IgE cyclic 1
27	47	42.0	9	21 AAB25917	Human IgE cyclic 1
28	47	42.0	9	21 AAB25917	Human IgE cyclic 1
29	47	42.0	9	21 AAB25917	Human IgE cyclic 1
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32	47	42.0	9	21 AAB25917	Human IgE cyclic 1
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39	47	42.0	9	21 AAB25917	Human IgE cyclic 1
40	47	42.0	9	21 AAB25917	Human IgE cyclic 1
41	47	42.0	9	21 AAB25917	Human IgE cyclic 1
42	47	42.0	9	21 AAB25917	Human IgE cyclic 1
43	47	42.0	9	21 AAB25917	Human IgE cyclic 1
44	47	42.0	9	21 AAB25917	Human IgE cyclic 1
45	47	42.0	9	21 AAB25917	Human IgE cyclic 1

ALIGNMENTS

RESULT 1  
AAB25922  
ID AAB25922 standard; Peptide: 20 AA.  
AC AAB25922.  
XX XX  
XX 35 AAB 2001 (1118) entry.  
XX  
XX Pi minotope peptid-3-PTC-SSG SEQ ID NO:15.  
XX  
XX Epitope, minotope, human, immunoglobulin E, IgE, C-epsilon-2 domain;  
KW allergen, esterase, immunophyllaxis, immunotherapy, antiallergic,  
KW immunosuppressive, vaccine, histamine release inhibitor, immunogen;  
KW allergy, atopy.  
XX  
XX Homo sapiens.  
XX  
XX W020050460 A1.  
XX  
XX 31 AUC 2000.  
XX  
XX 22-FEB-2000; 2000MO EPC1455.  
XX  
XX 25-FEB 1999; 99GB-0004405.  
XX 29-MAR-1999; 99GB-000715.  
XX 07-MAY 1999; 99GB-0010537.  
XX 07-MAY 1999; 99GB-0010538.  
XX 07-AUG 1999; 99GB-0018594.  
XX 07-AUG 1999; 99GB-0018602.  
XX 07-SEP-1999; 99GB-0021346.  
XX 07-SEP-1999; 99GB-0021347.  
XX 19-OCT-1999; 99GB-0025619.



PT disulfide bridge cyclized peptide and immunogenic carrier  
XX  
PE Claim 4, Page 11; 45pp; English.  
XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide immunogen derived  
CC from human immunoglobulin E (IgE), suitable for use in the invention.  
XX  
SQ Sequence 20 AA;  
Query Match 100.0%; Score 112; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CLEGGQVWVLDLGGSSGG 20  
|||||  
DB 1 CLEGGQVWVLDLGGSSGG 20  
RESULT 4  
ABJ00544  
ID ABJ00544 standard; Peptide; 20 AA.  
XX  
AC ABJ00544;  
XX  
DT 02-SEP 2002 (first entry)  
XX  
DE Human IgE cyclic immunogenic peptide SEQ ID NO: 326.  
XX  
KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic; cyclic.  
XX Homo sapiens.  
XX WO2002:6409-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG 2001; 2001WC-EP09576.  
XX PR 22-AUG 2000; 2000GB-0020717.  
XX PA (SVIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PE (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX WP: 2002-489648/52.  
XX PT Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX PS Claim 4, Page 16; 45pp; English.  
XX CC The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulphide bridge cyclised peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a cyclic peptide immunogen derived  
XX from human immunoglobulin E (IgE), suitable for use in the invention.  
XX SQ Sequence 20 AA;  
Query Match 93.8%; Score 105; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.8e-04;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CLEGGQVWVLDLGGSSGG 19  
|||||  
DB 1 CLEGGQVWVLDLGGSSGG 19

RESULT 5  
ABJ00542  
ID ABJ00542 standard; Peptide; 16 AA.  
XX  
AC ABJ00542;  
XX  
DT 02-SEP 2002 (first entry)  
XX  
DE Human IgE cyclic immunogenic peptide SEQ ID NO: 326.  
XX  
KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic; cyclic.  
XX Homo sapiens.  
XX WO2002:6409-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG 2001; 2001WC-EP09576.  
XX PR 22-AUG 2000; 2000GB-0020717.  
XX PA (SVIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PE (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX WP: 2002-489648/52.  
XX PT Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX PS Claim 4, Page 16; 45pp; English.  
XX CC The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulphide bridge cyclised peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a cyclic peptide immunogen derived  
XX from human immunoglobulin E (IgE), suitable for use in the invention.  
XX SQ Sequence 16 AA;  
Query Match 70.5%; Score 79; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CLEGGQVWVLDLGG 14  
|||||  
DB 1 CLEGGQVWVLDLGG 14  
RESULT 6  
AAB25917  
ID AAB25917 standard; Peptide; 13 AA.  
XX  
AC AAB25917;  
XX  
DT 05-JAN 2001 (first entry)  
XX  
DE P1 epitope peptide P15q SEQ ID NO:11.  
XX  
KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
XX allergic disease; immunotrophylaxis; immunotherapy; antiallergic;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.  
XX Homo sapiens.  
XX WO2000:00460 A1.  
XX PD 31-AUG 2000.

```

FF 22 FEB 2000; 2000WO-BF01455.
XX 25-FEB 1999; 99GB-0004405.
XX 29 MAR 1999; 99GB-0007151.
XX 07 MAY 1999; 99GB-0010537.
XX 07 MAY 1999; 99GB-0010538.
XX 07-AUG 1999; 99GB-0018494.
XX 07-AUG 1999; 99GB-0018602.
XX 07 SEP 1999; 99GB-0021046.
XX 07 SEP 1999; 99GB-0021047.
XX 29-OCT 1999; 99GB-0025619.
XX 24 NOV 1999; 99GB-0027698.
XX
XX (ACAY) SWITKLINE BEECHAM BIOLOGICALS.
XX (PEPT) PEPTIDE THERAPEUTICS LTD.
XX
XX Dusan M. Friede M. Greenwood J. Hewitt E. J. Jones A. Van Rhee.
XX Randall R. Turnell WG. Van Mechelen MP. Vignard G. Kass IR VP.
XX
XX WPI; 2001-521967/521.
XX
XX Peptides useful for treating, preventing and ameliorating allergic
XX diseases, comprising an isolated surface exposed group of a specific
XX domain from immunoglobulin E.
XX
XX Claim 14; Page 9; 123pp; English.
XX
XX The present invention describes a peptide (I) comprising an isolated
XX surface exposed group/epitope (E) of C-epsilon 4 domain of an
XX immunoglobulin E (IgE), or its mimotope. Also described are (II) an
XX immunogen (IIV) for treating allergy comprising (I), (IIV) and a carrier (IIV);
XX for treating allergies comprising (I); (I) a ligand (IIV) capable of
XX recognising EII; (IIV) a pharmaceutical composition (IIV) comprising (I);
XX (I) a peptide (IIV) capable of being recognised by (IIV); (I) an immunogen
XX (IIV) comprising (I); and (I) products (IIV) by method (I). (I)
XX can have anti-allergic and immunosuppressive activities, and can be used
XX as a vaccine and histamine release inhibitor. (I), (IIV) and (IIV) are
XX useful in medicine and in the manufacture of medicaments for treating
XX allergic and preventing allergies. (IIV) is useful for identifying mimotopes of (I),
XX in medicine and also in manufacturing medicaments for treating
XX allergies. (I) is useful in diagnostics and in the affinity purification
XX of circulating anti-IgE antibodies from blood. (I), (IIV) and (IIV) are
XX useful for treating a patient susceptible to or suffering from allergies.
XX (IIV) is also useful in diagnosing allergy. AAU16642 to AAU16693 represent
XX peptide sequences which are used in the exemplification of the present
XX invention.
XX
XX Sequence 13 AA.
XX
XX Query Match 65.2%; Score 73; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CUESDQWMDVLC 13
XX ||| ||| |||
XX 1 CUESDQWMDVLC 13
XX
XX RESULT 7
XX AAU16642
XX AAU16642 standard; Peptide; 13 AA.
XX
XX AAU16642.
XX
XX 07 NOV 2001 (first entry)
XX
XX Peptide- P154 derived as mimotope of C-epsilon 4 region of human IgE.
XX
XX Human; linkage technology; conjugated compound; carrier vehicle.
XX epitope; C-epsilon 2; C-epsilon 3; C-epsilon 4; immunoglobulin E.
XX IgE mediated disease; antibody response.
XX
XX Homo sapiens
XX

```

```

CS Synthetic.
XX
XX WO200145745-A2.
XX
XX 28-JUN-2001.
XX
XX 21 DEC 2000; 2000WO-BF01455.
XX
XX 21-DEC 1999; 99GB-0030213.
XX 22-FEB 2000; 2000GB-0004096.
XX 22 AUG 2000; 2000GB-0022707.
XX 22-AUG-2000; 2000GB-0022708.
XX
XX (ACAY) ACAMBI'S RES LTD.
XX (SMIK) SWITKLINE BEECHAM BIOLOGICALS.
XX
XX Flynn M. Johnson D.
XX
XX WPI; 2001-521967/521.
XX
XX A linkage comprising an immunogenic conjugate useful treatment of IgE
XX mediated diseases
XX
XX Example 4; Page 21; 45pp; English.
XX
XX The present invention relates to linkage methodology for use in the
XX conjugation of compounds (e.g. peptides) to carrier vehicles
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX biological and immunological constructs. The invention provides a
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX protein) for use in a pharmaceutical composition or a vaccine. The
XX invention describes peptides derived from or mimotopes of the
XX C-epsilon 2, C-epsilon 3 or C-epsilon 4 regions of human immunoglobulin E
XX (IgE) which are used to produce conjugated compounds. The compounds or
XX compositions of the invention are useful in the manufacture of a
XX medicament for the treatment of IgE mediated diseases. The invention
XX allows for controlled conjugation of a peptide epitope (antigen) to a
XX protein so as to form an immunogenic conjugate which may be able to
XX raise a protective antibody response in an animal or human patient.
XX AAU16632-AAU1693 represent peptides derived from or mimotopes of
XX the C-epsilon 2/C-epsilon 3/C-epsilon 4 region of human IgE.
XX
XX Sequence 13 AA.
XX
XX Query Match 65.2%; Score 73; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CUESDQWMDVLC 13
XX ||| ||| |||
XX 1 CUESDQWMDVLC 13
XX
XX RESULT 8
XX ABU00312
XX
XX 10 ARJ00312 standard; Peptide; 13 AA.
XX
XX ARJ00312.
XX
XX 02 SEP 2002 (first entry)
XX
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 96.
XX
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage.
XX
XX vacc; anti-allergic; cyclic.
XX
XX Homo sapiens.
XX
XX WO200215409-A2.
XX
XX 28-FEB 2002.
XX
XX 17-AUG 2001; 2001W-BF09576.
XX

```

XX 22 AUG 2000; 2000GB-002017.  
 XX (SMITHKLINE BEECHAM BIOLOGICALS)  
 PA (PEPTIDE THERAPEUTICS LTD)  
 XX Friede M, Mason S, Turner W, Vinals De Bassols YC,  
 XX WPI; 2002-449648/52.  
 XX Conjugate for use in vaccine for treatment of allergy, comprising  
 PT disulfide bridge cyclized peptide and immunogenic carrier;  
 XX Claim 4; Page 11; 45pp; English.  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 65.2%; Score 74; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. C.25;  
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 DQ 1 CLEDGQWMDVLC 13  
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 XX AAB25914 standard; peptide; 13 AA.  
 XX AAB25914;  
 AC AAB25914;  
 XX 01 JAN 2001 (first entry);  
 XX Antiallergy peptide mimotope sequence (E1 IgE);  
 XX Immunoglobulin E (IgE); immunogenic; immunophylaxis; immunotherapy; antiallergic;  
 KW Pioneers cancer; Haemophilus influenzae; vaccine; immunogenic disease;  
 KW salivary cystostatic; antiallergic; histamine release inhibitor; immunogen;  
 KW proteinase; Alzheimer's disease; allergy;  
 XX Homo sapiens;  
 CS Homo sapiens;  
 XX Key Location/Qualifiers  
 FT Modified site 14 /note="amidated"  
 XX WC00050077-51;  
 XX 31 AUG 2000;  
 XX 22 FEB 2000; 2000WC EPC1457;  
 XX 25 FEB 1999; 99GB-0004405;  
 XX 25 FEB 1999; 99GB-0004406;  
 XX 25 FEB 1999; 99GB-0004412;  
 XX 13-AUG 1999; 99GB-0019260;  
 XX (SMITHKLINE BEECHAM BIOLOGICALS)  
 PA Coste M, Lobet Y, Van-Mechelen ME, Vinals De Bassols YC,  
 XX WPI; 2000-572040/53;  
 XX Immunogens and vaccine comprising the tetra- and octa-peptide for preventing  
 FT and treating infectious diseases such as malaria and chronic diseases and  
 PT cancer, comprising peptide and carrier from human immunoglobulin E (IgE)

XX Claim 10; Page 15; 53pp; English.  
 XX The present invention describes an immunogen (I) comprising a peptide  
 CC (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae  
 CC or its fragment. Also described are: (i) a vaccine comprising (Ii) and  
 CC an excipient; (ii) preparation of (Ii); comprising conjugating a peptide  
 CC to protein D or its fragment; and (3) preparation of a vaccine of (Ii).  
 CC comprising formulating (i) with an excipient; (ii) has cytostatic;  
 CC antiallergic, nootropic, neuroprotective and protozoicidal activities;  
 CC (i) and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer; Alzheimer's disease of allergy in a patient;  
 CC Unlike prior art immunogens, (i) induces high levels of antipeptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC mimotope peptide sequence, which can be used in an immunogen of the  
 XX present invention.  
 XX Sequence 13 AA;  
 SQ  
 Query Match 57.1%; Score 64; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. C.25;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DQ 1 CLEDGQWMDVLC 12  
 RESULT 12  
 AAB25914  
 XX AAB25914 standard; peptide; 13 AA.  
 XX AAB25914;  
 AC AAB25914;  
 XX 05-JAN 2001 (first entry);  
 XX P1 mimotope peptide PT15 SEQ ID NO:8;  
 XX Epitope; mimotope; human; immunoglobulin E (IgE); C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy;  
 XX Homo sapiens;  
 CS Homo sapiens;  
 XX WC00050077-462 A1;  
 XX A1 AUG 2000;  
 XX 22 FEB 2000; 2000WC EPC1458;  
 XX 25-FEB 1999; 99GB-0004405;  
 XX 29-MAR 1999; 99GB-0004451;  
 XX 07-MAY 1999; 99GB-0010537;  
 XX 07-MAY 1999; 99GB-0010538;  
 XX 07-AUG 1999; 99GB-0018594;  
 XX 07-AUG 1999; 99GB-0018603;  
 XX 07-SEP 1999; 99GB-0021046;  
 XX 07-SEP 1999; 99GB-0021047;  
 XX 29-OCT-1999; 99GB-0025619;  
 XX 23-NOV-1999; 99GB-0027658;  
 XX (SMITHKLINE BEECHAM BIOLOGICALS)  
 PA (PEPTIDE THERAPEUTICS LTD)  
 XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S,  
 PI Randall P, Turner W, Vinals De Bassols YC,  
 XX WPI; 2000-572040/54;  
 XX Peptides useful for treating, preventing and ameliorating allergic





PT Flinn K, Johnson T;  
 XX WI: 2001-521967/57.  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IGE  
 XX mediated diseases.  
 XX  
 XX Example 4; Page 21; 49pp; English.  
 XX  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. The  
 XX invention describes peptides derived from or mimotopes of the  
 XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 XX (IgE) which are used to produce conjugated compounds. The compounds or  
 XX compositions of the invention are useful in the manufacture of a  
 XX medicament for the treatment of IGE mediated diseases. The invention  
 XX allows for controlled conjugation of a peptide epitope (antigen) to a  
 XX protein so as to form an immunogenic conjugate which may be able to  
 XX raise a protective antibody response in an animal or human patient.  
 XX AAU16612-AAU16913 represent peptides derived from or mimotopes of  
 XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 57.1%; Score 64; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pled No. 0.25;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEEGQVNDVLC 12  
 DQ 1 CEEGQVNDVLC 12  
 I I I I I I  
 I I I I I I  
 RESULT 13  
 AAU16641  
 ID AAU16641 standard; Peptide; 13 AA;  
 XX  
 AC AAU16641;  
 XX  
 XX 01-NOV-2001 (first entry)  
 XX  
 XX Peptide P15p derived as mimotope of Cepsilon4 region of human IgE.  
 XX  
 XX Biocage Linkage Technology; conjugated to a carrier vehicle  
 XX epitope; Cepsilon4; Cepsilon3; Cepsilon2; Cepsilon1; Cepsilon0;  
 XX IGE mediated disease; antibody to IGE  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX  
 XX WC000145945 A2;  
 XX  
 XX 25 JUN 2001;  
 XX  
 XX 21 DEC 2000; 2000WG-GR04935;  
 XX  
 XX 21 FEB 1999; 93GB 0030233  
 XX 22-FEB 2000; 2000GB-0004096  
 XX 22 AUG 2000; 2000GB 0020707  
 XX 22-AUG-2000; 2000GB-0020708;  
 XX  
 XX (ACAM) ACAM515 RES LTD;  
 XX (SMIR) SMITHKLINE BEECHAM BIOLOGICALS;  
 XX  
 XX Flinn K, Johnson T;  
 XX WI: 2001-521967/57;  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IGE

PT mediated diseases  
 XX  
 XX Example 4; Page 21; 49pp; English.  
 XX  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. The  
 XX invention describes peptides derived from or mimotopes of the  
 XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 XX (IgE) which are used to produce conjugated compounds. The compounds or  
 XX compositions of the invention are useful in the manufacture of a  
 XX medicament for the treatment of IGE mediated diseases. The invention  
 XX allows for controlled conjugation of a peptide epitope (antigen) to a  
 XX protein so as to form an immunogenic conjugate which may be able to  
 XX raise a protective antibody response in an animal or human patient.  
 XX AAU16612-AAU16913 represent peptides derived from or mimotopes of  
 XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
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 XX Sequence 13 AA;  
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 Best Local Similarity 100.0%; Pled No. 0.25;  
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 I I I I I I  
 RESULT 14  
 AAB51028  
 ID AAB51028 standard; Peptide; 13 AA;  
 XX  
 AC AAB51028;  
 XX  
 XX 21-MAR-2001 (first entry)  
 XX  
 XX IGE peptide #6.  
 XX  
 XX Vaccine; immunoglobulin E; IgE; anti allergy.  
 XX  
 XX Mammalia.  
 XX  
 XX WC000145916 A2;  
 XX  
 XX 14-JUN-2000  
 XX  
 XX 06 JUN 2000; 2000W EP01164  
 XX  
 XX 08-JUN 1999; 95GB-0013317;  
 XX  
 XX (SMIR) SMITHKLINE BEECHAM BIOLOGICALS;  
 XX  
 XX Price's 07  
 XX  
 XX WI: 2001-091150/10;  
 XX  
 XX New vaccine comprising allergy peptides linked by an inert carrier,  
 XX useful for boosting an anti-allergy immune response in an individual  
 XX susceptible to an allergic response.  
 XX  
 XX Claim 5; Page 20; 26pp; English.  
 XX  
 XX The present invention relates to a composition comprising allergy  
 XX peptides linked by an inert carrier. The allergy peptides are derived  
 XX from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 XX such peptide from IgE. The composition is useful as a vaccine or for  
 XX manufacturing a medicament for the prophylaxis or treatment of allergy.  
 XX In particular, the invention is an anti-allergy immune response in an  
 XX individual susceptible to an allergic response.

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XX
SQ Sequence 13 AA;
Query Match 57.1%; Score 64; DP 12; Begin: 12;
Best Local Similarity 100.0%; Prid. No. 0.25;
Varities 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMVDL 12
   : |||||
   : CLEGGQVMVDL 12

PE 1 CLEGGQVMVDL 12
   : |||||
   : CLEGGQVMVDL 12

REASON 15
ADJ0024
13 ADJ0024 standard; Peptide: 13 AA
XX
AC ADJ0024;
XX
CC G1-SRP 2002 (first entry)
XX
DE Human IgE immunogenic peptide SEQ ID NO: 8;
XX
KW Immunogen; human; IgE; immunoglobulin E; allergy; this entry: linkage;
KW vaccine; anti-allergic;
XX
OS Homo sapiens;
XX
PN NC200216404-A2;
XX
PC 24 FEB-2002;
XX
PF 17 AUG-2001; PDB:W0 EPC9576;
XX
PK 22-AUG-2000; E0000E-0020717;
XX
PA (SVIK) SMITHKLINE BEECHAM BIOLOGICALS
PA (PEPT) PEPTIDE THERAPEUTICS INC;
XX
PC Fildes V, Mason S, Turnell WG, Vinals Hansels Y;
XX
WP1: 2002-0406487-2;
XX
XX
XX Conjugate for use in vaccine for treatment of allergy; description
XX disulfide bridge cyclized peptide and immunogenic carrier;
XX
XX Claim 1; Page 9; 45pp; English;
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX which are conjugates comprising a multipolypeptide chain and a peptide-antigen
XX immunogenic carrier. The vaccine is for use in the treatment of
XX allergies. The present sequence is a peptide sequence derived from human
XX immunoglobulin E (IgE) suitable to be cyclized and used in the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 57.1%; Score 64; DP 12; Begin: 12;
Best Local Similarity 100.0%; Prid. No. 0.25;
Varities 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   : CLEGGQVMVDL 12

PE 1 CLEGGQVMVDL 12
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   : CLEGGQVMVDL 12

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Job time: 1.42 secs
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GenCore version 5.1.6  
Copyright (c) 1993-2003 Computer Unit

CM protein protein search, using sw model

Run on: November 5, 2003, 18:01:22 / Search time 24 seconds  
without alignment  
120 6 4 million cells at 1000/sec

Title: US-09-914-088-15

Perfect score: 112  
Sequence: 1 CLEGGQVMDVLLGGSSGDP 20

Scoring table: BLCSUM62

Gapop 10.0, Gapext 2.0

Searches: 644379 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 16120

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA\*

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- 2: /cgn2\_6/ptodata/2/futpaa/US02\_NEW\_PHE pep\*
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- 4: /cgn2\_6/ptodata/2/futpaa/US06\_PHEXMR pep\*
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- 18: /cgn2\_6/ptodata/2/futpaa/US06\_PHEXMR pep\*

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Score greater than or equal to the score of the best hit is printed.  
and is derived by analysis of the alignment of the hit to the query.

SUMMARIES

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3	47	42.0	9	12 US-10-082-014-282
4	47	42.0	9	12 US-10-082-014-282
5	45	40.2	10	12 US-10-082-014-282
6	45	40.2	14	10 US-09-909-122-1
7	42	37.5	12	9 US-09-909-122-1
8	42	37.5	14	10 US-09-909-122-1
9	42	37.5	14	14 US-10-050-688-1
10	42	37.5	14	14 US-10-050-688-1
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21	40	35.7	12	10 US-09-909-122-1
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27	40	35.7	16	10 US-09-909-122-1
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29	39	33.9	9	10 US-09-918-243-84
30	39	33.9	9	10 US-09-909-122-1
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35	37	33.0	10	14 US-10-050-688-1
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37	36	32.1	9	10 US-09-909-122-1
38	36	32.1	9	12 US-10-050-688-1
39	36	32.1	9	12 US-10-050-688-1
40	36	32.1	9	15 US-10-135-795-163
41	36	32.1	9	15 US-10-135-795-163
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ALIGNMENTS

RESULT 1  
US-10-082-014-282  
; Sequence 182, Application US/10082014  
; Publication No. US20030195858A1  
; GENERAL INFORMATION:  
; APPLICANT: Bickert, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY  
; FILE REFERENCE: US-10-0466/95124  
; CURRENT APPLICATION NUMBER: US/10082014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/910,915  
; PRICE FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent Invention 3.1  
; SEQ ID NO: 82  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: HBC seqs  
US-10-082-014-282

Query Match 43.8%, Score 49; DB 12; Length 10;  
Best Loc: Similarity 90.0%; Pred. No. 1.2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDQVMDV 11  
DB 1 MEDQVMDV 10

RESULT 2  
US-10-312-016-116  
; Sequence 136, Application US/10172076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friedl, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
 CURRENT APPLICATION NUMBER: US/10/022-21  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/086,219  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/082,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 3.2  
 SEQ ID NO 136  
 LENGTH: 12  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10-082-014-136

Query Match 43.0% Score 49; DR 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 2 EDCQWMDV 11  
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 Dp 1 EDCQWMDV 10

RESULT 4  
 US-10-082-014-273  
 Sequence 127, Application US/10/022-21  
 Publication No. US2003018586A1  
 GENERAL INFORMATION:  
 APPLICANT: Parke, Ashley J.  
 TITLE OF INVENTION: IMMUNOGENIC HBS-CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY

FILE REFERENCE: 100 130.0 4564/85124  
 CURRENT APPLICATION NUMBER: US/10/082,014  
 CURRENT FILING DATE: 2002-02-22  
 PRIOR APPLICATION NUMBER: 09/930,915  
 PRIOR FILING DATE: 2002-08-15  
 NUMBER OF SEQ ID NOS: 290  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO 273  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US 10-082-014-273

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 Dp 1 EDCQWMDV 9

RESULT 4  
 US 10-082-014-136  
 Sequence 127, Application US/10/022-21  
 Publication No. US2003018586A1  
 GENERAL INFORMATION:  
 APPLICANT: Parke, Mark  
 TITLE OF INVENTION: STABILIZED HBS-CHIMER PARTICLES AS HEPATITIS VACCINE FOR  
 TITLE OF INVENTION: CHRONIC HEPATITIS  
 FILE REFERENCE: 4564/87179  
 CURRENT APPLICATION NUMBER: US/10/082,014  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/086,219  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/082,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 3.2  
 SEQ ID NO 127  
 LENGTH: 9

TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-372-076-127

Query Match 42.0% Score 47; DR 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDCQWMDV 11  
 |||||  
 Dp 1 EDCQWMDV 9

RESULT 5  
 US-10-144-168-55  
 Sequence 55, Application US/10/144-168  
 Publication No. US20030170212A1  
 GENERAL INFORMATION:  
 APPLICANT: Cai, Zeling  
 APPLICANT: Jackson, Michael R.  
 APPLICANT: Peterson, Per A.  
 APPLICANT: Shi, Weixing  
 APPLICANT: Kong, Yan  
 APPLICANT: Degraw, Julia

TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific  
 FILE REFERENCE: 100 130.0 4564/85124  
 CURRENT APPLICATION NUMBER: US/10/144,168  
 CURRENT FILING DATE: 2002-05-13  
 PRIOR APPLICATION NUMBER: 60/291,300  
 PRIOR FILING DATE: 2001-05-15  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: Patent in version 3.2  
 SEQ ID NO 55  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

FEATURES  
 OTHER INFORMATION: Peptide antigen  
 US-10-144-168-55

Query Match 40.2% Score 45; DR 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDCQWMDV 10  
 |||||  
 Dp 3 EDCQWMDV 10

RESULT 6  
 US-09-885-441-6  
 Sequence 6, Application US/09885441  
 Patent No. US20020046470A1  
 GENERAL INFORMATION:  
 APPLICANT: Xiao, Yonghong  
 TITLE OF INVENTION: Regulation of Human Eosinophil Serine  
 TITLE OF INVENTION: Protease 1 Like Enzyme  
 FILE REFERENCE: 04974-00512  
 CURRENT APPLICATION NUMBER: US/09/885,441  
 CURRENT FILING DATE: 2001-06-21  
 PRIOR APPLICATION NUMBER: US 60/212,844  
 PRIOR FILING DATE: 2000-06-21  
 PRIOR APPLICATION NUMBER: US 60/244,171  
 PRIOR FILING DATE: 2000-10-31  
 PRIOR APPLICATION NUMBER: US 60/279,766  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/\_\_\_\_\_  
 PRIOR FILING DATE: 2001-06-20  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 14

```

1 TYPE: PPT
2 ORGANISM: Artificial Sequence
3 FEATURE:
4 OTHER INFORMATION: Peptide fragment of Thrombin
5 NAME/KEY: VARIANT
6 LOCATION: (1)...(14)
7 OTHER INFORMATION: Xaa at position six is Glu or Gln
8 OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or Val
9 US-09-914-088-15
10
11 Query Match
12 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
13 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
14
15 QY 11 DLGGSSGGP 20
16 | | | |
17 Db 3 DAXGDSGGP 12
18
19 RESULT 9
20 US-10-050-692 4
21 Sequence 4; Application US/1005692
22 Patent No. US20020162285A1
23 GENERAL INFORMATION:
24 APPLICANT: Carney, Darrell H.
25 APPLICANT: Crowther, Roger S.
26 APPLICANT: Simmons, David J.
27 APPLICANT: Yang, Clipping
28 APPLICANT: Pedin, William R.
29 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
30 TITLE OF INVENTION: PEPTIDE DERIVATIVES
31 FILE REFERENCE: 3033.1002-004
32 CURRENT APPLICATION NUMBER: US/10/050,692
33 CURRENT FILING DATE: 2002-01-16
34 PRIOR APPLICATION NUMBER: 09/909,122
35 PRIOR FILING DATE: 2001-07-19
36 PRIOR APPLICATION NUMBER: 60/219,300
37 PRIOR FILING DATE: 2000-07-19
38 NUMBER OF SEQ ID NOS: 6
39 SOFTWARE: FastSeq for Windows Version 4.0
40 SEQ ID NO: 4
41 LENGTH: 14
42
43 TYPE: PPT
44 ORGANISM: Artificial Sequence
45 FEATURE:
46 OTHER INFORMATION: Fragment of human prothrombin
47 NAME/KEY: VARIANT
48 LOCATION: (1)...(13)
49 OTHER INFORMATION: Xaa = Glu or Gln
50 NAME/KEY: VARIANT
51 LOCATION: (13)...(13)
52 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
53 US-10-050-692-4
54
55 Query Match
56 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
57 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
58
59 QY 11 DLGGSSGGP 20
60 | | | |
61 Db 3 DAXGDSGGP 12
62
63 RESULT 10
64 US-10-050-692 4
65 Sequence 4; Application US/1005692
66 Patent No. US20020162285A1
67 GENERAL INFORMATION:
68 APPLICANT: Carney, Darrell H.
69 APPLICANT: Crowther, Roger S.
70 APPLICANT: Simmons, David J.
71 APPLICANT: Yang, Clipping
72 APPLICANT: Pedin, William R.
73 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
74 TITLE OF INVENTION: PEPTIDE DERIVATIVES
75 FILE REFERENCE: 3033.1002-001
76 CURRENT APPLICATION NUMBER: US/09/909,122
77 CURRENT FILING DATE: 2001-07-19
78 PRIOR APPLICATION NUMBER: US/09/909,122
79 PRIOR FILING DATE: 2000-07-19
80 NUMBER OF SEQ ID NOS: 5
81 SOFTWARE: FastSeq for Windows Version 4.0
82 SEQ ID NO: 4
83 LENGTH: 14

```

```

1 APPLICANT: Bergmann, John
2 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
3 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
4 TITLE OF INVENTION: RECEPTOR
5 FILE REFERENCE: 1331, 1203-024
6 CURRENT APPLICATION NUMBER: US/10/294,025
7 CURRENT FILING DATE: 2002-07-12
8 PRIOR APPLICATION NUMBER: 09/909,148
9 PRIOR FILING DATE: 2001-07-19
10 PRIOR APPLICATION NUMBER: 60/219,800
11 PRIOR FILING DATE: 2000-07-20
12 NUMBER OF SEQ ID NOS: 6
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 4
15 LENGTH: 14
16 TYPE: PPT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: peptide fragment of thrombin
20 NAME/KEY: VARIANT
21 LOCATION: (6)...(16)
22 OTHER INFORMATION: Xaa = Gly or Gln
23 NAME/KEY: VARIANT
24 LOCATION: (11)...(11)
25 OTHER INFORMATION: Xaa = Phe, Met, I, Leu, His or Val
26 US 10-294,025-4
27
28 Query Match: 37.5% Score 42; DB 14; Length 14;
29 Best Local Similarity: 70.0%; Pref. No. 18;
30 Matches: 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
31
32 QY 11 DCCGSSSTP 20
33 | | | | |
34 1 DCCGSSSTP 12
35
36 RESULT 11
37 US 10-294,025-4
38 Sequence 1032: Application US/10/294,025
39 Publication No. US2003018430A1
40 GENERAL INFORMATION:
41 APPLICANT: Xu, Jianzhun
42 APPLICANT: Milham, Jennifer D.
43 APPLICANT: Barakker, Susan J.
44 APPLICANT: Akana, Yvonne
45 APPLICANT: Bergman, Robert A.
46 APPLICANT: Kalos, Michael F.
47 APPLICANT: Parker, Gary R.
48 APPLICANT: Retter, Marc W.
49 APPLICANT: Stolk, John A.
50 APPLICANT: Guy, Craig H.
51 APPLICANT: Verlick, Thomas S.
52 APPLICANT: Carter, Patrick
53 APPLICANT: Wada, Akiun
54 APPLICANT: Kawa, Akiun
55 APPLICANT: Skeiky, Yasir A. W.
56 APPLICANT: Apple, William C.
57 APPLICANT: Hurai, John
58 APPLICANT: Xenellis, Patricia D.
59 APPLICANT: Houghton, Raymond L.
60 APPLICANT: Vinals y de Bassols, Carolina
61 APPLICANT: Eoy, Teresa M.
62 APPLICANT: Katsube, Yoshinori
63 APPLICANT: Peng, Ya
64 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
65 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
66 FILE REFERENCE: 21611, 427C29
67 CURRENT APPLICATION NUMBER: US/10/294,025
68 CURRENT FILING DATE: 2002-11-12
69 NUMBER OF SEQ ID NOS: 1038
70 SOFTWARE: FastSeq for Windows Version 3.0
71 SEQ ID NO 1032
72 LENGTH: 15
73 TYPE: PPT
74 ORGANISM: Homo sapiens
75 US 10-294,025-1032

```

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1 SOFTWARE: FastSeq for Windows Version 3.0
2 SEQ ID NO 1042
3 LENGTH: 15
4 TYPE: PPT
5 ORGANISM: Homo sapiens
6 US-10-144-078A-1032
7
8 Query Match: 37.5% Score 42; DB 12; Length 15;
9 Best Local Similarity: 70.0%; Pref. No. 18;
10 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
11
12 QY 11 DCCGSSSTP 20
13 | | | | |
14 1 DCCGSSSTP 11
15
16 RESULT 12
17 US-10-294-078-1032
18 Sequence 1032: Application US/10/294,025
19 Publication No. US2003018430A1
20 GENERAL INFORMATION:
21 APPLICANT: Xu, Jianzhun
22 APPLICANT: Kalos, Michael F.
23 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
24 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
25 FILE REFERENCE: 21611, 427C29
26 CURRENT APPLICATION NUMBER: US/10/294,025
27 CURRENT FILING DATE: 2002-11-12
28 NUMBER OF SEQ ID NOS: 1038
29 SOFTWARE: FastSeq for Windows Version 3.0
30 SEQ ID NO 1032
31 LENGTH: 15
32 TYPE: PPT
33 ORGANISM: Homo sapiens
34 US 10-294,025-1032
35
36 Query Match: 37.5% Score 42; DB 12; Length 15;
37 Best Local Similarity: 70.0%; Pref. No. 18;
38 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
39
40 QY 11 DCCGSSSTP 20
41 | | | | |
42 1 DCCGSSSTP 11
43
44 RESULT 13
45 US-09-904-090-1
46 Sequence 904: Application US/09/904,090
47 Patent No. US6,600,000A1
48 GENERAL INFORMATION:
49 APPLICANT: Guiney, Daniel
50 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
51 TITLE OF INVENTION: PEPTIDES
52 FILE REFERENCE: 3031, 1200-021
53 CURRENT APPLICATION NUMBER: US/09/904,090
54 CURRENT FILING DATE: 2001-07-12
55 PRIOR APPLICATION NUMBER: US 6,721,758
56 PRIOR FILING DATE: 2000-07-12
57 NUMBER OF SEQ ID NOS: 4
58 SOFTWARE: FastSeq for Windows Version 4.0
59 SEQ ID NO 2
60 LENGTH: 12
61 TYPE: PPT
62 ORGANISM: Artificial Sequence
63 FEATURE:
64 OTHER INFORMATION: Polypeptide, fragment of thrombin
65 US-09-904-090-2
66
67 Query Match: 36.4% Score 41; DB 9; Length 12;
68 Best Local Similarity: 70.0%; Pref. No. 19;
69 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: November 5, 2003, 18:26:31  
Job time : 29 secs

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CY      11  DCCGSSGSP 20
DB      1  DCCGSSGSP 10

RESULT 14
US 09-804-156-34
? Sequence 34, Application US/0904156
? Patent No. US2000/005912CA1
? GENERAL INFORMATION:
? APPLICANT: SERO, S.A.
? TITLE OF INVENTION: Serine protease polynucleotides, polypeptides, and antibodies
? FILE REFERENCE: PTO05F4
? CURRENT APPLICATION NUMBER: US/09/04156
? CURRENT FILING DATE: 2001-03-13
? PRIOR APPLICATION NUMBER: 60/189,025
? PRIOR FILING DATE: 2000-03-14
? NUMBER OF SEQ ID NOS: 39
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 34
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-804-156 34

Query Match      36.6%  Score 417  DB 3, Length 12,
Best local Similarity 70.0%  Pred. No. 197
Matches      7:  Conservative      0:  Mismatches      3:  Gaps      0:

CY      11  DCCGSSGSP 20
DB      1  DCCGSSGSP 10

RESULT 15
US 09-946-643-19
? Sequence 19, Application US/09046633
? Patent No. US2002/0119925A1
? GENERAL INFORMATION:
? APPLICANT: NI, et al.
? TITLE OF INVENTION: PTO05P1
? FILE REFERENCE: Serine proteases
? CURRENT APPLICATION NUMBER: US/09/04156
? CURRENT FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 03/597,899
? PRIOR FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: 60/333,439
? PRIOR FILING DATE: 1999-05-17
? PRIOR APPLICATION NUMBER: 02/115,114
? PRIOR FILING DATE: 1999-05-20
? PRIOR APPLICATION NUMBER: 02/147,006
? PRIOR FILING DATE: 1999-08-03
? PRIOR APPLICATION NUMBER: 60/152,915
? PRIOR FILING DATE: 1999-09-09
? PRIOR APPLICATION NUMBER: 60/162,979
? PRIOR FILING DATE: 1999-11-01
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 19
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Homo sapiens
US 09-946 643-19

Query Match      36.6%  Score 417  DB 3, Length 12,
Best local Similarity 70.0%  Pred. No. 197
Matches      7:  Conservative      0:  Mismatches      3:  Gaps      0:

CY      11  DCCGSSGSP 20
DB      1  DCCGSSGSP 10

```







US-09-102-608C-34

Query Match 35.7% Score 40; DB 4; Length 13;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 11 DSCGQVYVLCGSGSG 20

DB 2 DSCGQVYVLCGSGSG 11

RESULT 6

US-09-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,302

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE DOCKET NUMBER: 106818

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-495-302-53

Query Match 34.8% Score 39; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVYVLCGSGSG 19

DB 1 LSCGQVYVLCGSGSG 18

RESULT 9

US-08-495-302-53

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

```

1 FILING DATE: 07-JUN-1995
2 CLASSIFICATION: 514
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Stevens, Lauren L.
5 REGISTRATION NUMBER: 46,691
6 REFERENCE/DOCKET NUMBER: 1088 1A
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 415-496-2300
9 TELEFAX: 415-424-0912
10 INFORMATION FOR SEQ ID NO: 58:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 20 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: peptide
17 US-08 475 169-58
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19 Query Match: 34.8% Score 19: DB 1: Smith 20:
20 Best Local Similarity 44.4% Pred No. 39:
21 Matches 8: Conservative 3: Mismatches 7: Indels 0: Gaps 0:
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APPLICANT: Stemmer, Willem P.C.  
APPLICANT: Gates, Christian M.  
TITLE OF INVENTION: Peptide Library and Screening Method  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Street Tower Suite 100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PC/US96/09469  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,544  
FILING DATE: 26-OCT-1995  
APPLICATION NUMBER: US 08/230,641  
FILING DATE: 15-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,121  
FILING DATE: 15-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 32,223  
REFERENCE/DOCKET NUMBER: 1652A PC1240US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2422  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PRT-US96 09469-91

Query Match 34.8%; Score 38; DB 5; Length 20;  
Best Local Similarity 44.4%; Pred. No. 91;  
Matches 8; Conservative 3; Mismatches 1; Gaps 0

CY 2 LENSQVVELQSSGSG 19  
DB 1 LENSQVVELQSSGSG 19

RESULT 12  
US-08-502-600-84  
Sequence 84, Application US/59502600A  
Patent No. 6294344  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
FILE REFERENCE: 06223CIP-C  
CURRENT FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US/09/502,600A  
PRIOR FILING DATE: 03-14-1998  
NUMBER OF SEQ ID NOS: 136  
SEQ ID NO 84  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Residues 201-210 of the above protein  
US 09-502 600-84

Query Match 33.9%; Score 38; DB 3; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2,5e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0

CY 13 CGGSSGGP 10  
DB 4 CGGSSGGP 8

RESULT 13  
US-08-472-228A 19  
Sequence 19, Application US/08472228A  
Patent No. 5807978  
GENERAL INFORMATION:  
APPLICANT: Kokolus, William J.  
APPLICANT: Fritzsche, Herbert A.  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,228A  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 17,642  
REFERENCE/DOCKET NUMBER: UTSC:188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 419-1000  
TELEFAX: (512) 474 7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-228A 19

Query Match 33.9%; Score 38; DB 1; Length 20;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0

CY 13 CGGSSGGP 20  
DB 4 CGGSSGGP 11

RESULT 14  
US-09-146-831-19  
Sequence 19, Application US/09146831  
Patent No. 6326471  
GENERAL INFORMATION:  
APPLICANT: Kokolus, William J.  
APPLICANT: Fritzsche, Herbert A.  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,831A  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 17,642  
REFERENCE/DOCKET NUMBER: UTSC:188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 419-1000  
TELEFAX: (512) 474 7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-146-831-19

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1  NUMBER OF SEQUENCES: 22
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Arnold, White & Durkin
4  STREET: P.O. Box 4433
5  CITY: Houston
6  STATE: Texas
7  COUNTRY: United States of America
8  ZIP: 77210
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC DOS/MS DOS
13 SOFTWARE: Patent In Release #17, Version #1.0
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/14- 411
16 FILING DATE:
17 CLASSIFICATION:
18 PRIORITY APPLICATION DATA:
19 APPLICATION NUMBER: US 08/472,116
20 FILING DATE: 07-JUN-1995
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Highlander, Steven L
23 REGISTRATION NUMBER: 37,642
24 REFERENCE/DOCKET NUMBER: JTS000000
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (512) 418-3000
27 TELEFAX: (512) 474-7577
28 CITE: 79-0924
29 INFORMATION FOR SEQ ID NO: 19:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 20 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36
37 15 29 146-831 19
38
39 Query Match: 33.9%; Score 38; DB 5; Length 20;
40 Best Local Similarity: 75.0%; Pred. No. 53;
41 Matches: 6; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;
42
43 QY 13 CQSSSGSP 20
44 1 |||
45 4 CQSSSGSP 11
46
47 Search Completed: November 5, 2003, 16:22:24
48 Job time: 22 secs
49
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GenCore Version 3.0.1  
Copyright (c) 1995-1999 Copyright LLC

CM protein - protein search, using sw method

Run on: November 5, 2003, 14:16:57, Search time: 21.59 sec

Title: Perfect score: 116  
Sequence: 1 CLESDQWQVDPFPEAAEQHK 21  
Gapop 10.0, Gapext 0.5

Scoring table: BLOSUM62

Searched: 25308 seqs, 9618692 residues

Total number of hits satisfying chosen parameters: 458

Minimum DB seq length: 2

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 761\*

1: p141\*

2: p141\*

3: p141\*

4: p141\*

Pred. No. is the number of results predicted by the program to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match Length	DP	ID	Description
1	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
2	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
3	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
4	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
5	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
6	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
7	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
8	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
9	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
10	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
11	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
12	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
13	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
14	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
15	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
16	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
17	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
18	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
19	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
20	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
21	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
22	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
23	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
24	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
25	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
26	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
27	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
28	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)
29	24	20	2	S32502	Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)

30 22 19.0 15 2 PH1631  
31 22 19.0 16 2 B484C6  
32 22 19.0 16 2 B484C6  
33 22 19.0 19 2 A49725  
34 22 19.0 20 2 A46454  
35 22 19.0 20 2 S28434  
36 22 19.0 21 2 PX0079  
37 22 19.0 21 2 PX0079  
38 22 19.0 21 2 143659  
39 22 19.0 21 2 143657  
40 22 19.0 21 2 143657  
41 22 19.0 21 2 143657  
42 22 19.0 21 2 143657  
43 22 19.0 21 2 143657  
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45 22 19.0 21 2 143657

ALIGNMENTS

RESULT 1

S32502

Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)

Accession: S32502

Species: Sus scrofa domestica (domestic pig)

Date: 02 Dec 1993 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999

Accession: S32502

Author: N. Crawford, C.

FEBS Lett. 322, 65-69, 1993

Article: Structural modifications associated with the change in Cal(2+)-sensitivity on ac

Accession: S32502

Accession: S32502

Accession: S32502

Accession: S32502

Accession: S32502

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Accession: S32502

Accession: S32502





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RESULT 3
SI0499
Title: Mycobacterium tuberculosis (fragment)
Species: Mycobacterium tuberculosis
Date: 11 Jan 1995 #sequence_revision: 11 Jan 1995 #text_revision: 11 Jan 1995
Accession: S16899
Author: R. Chard, N. Kimura, M. Higashii, Y. Yamada, T.
ERS Lett. 331, 3-14, 1993
Abstract: Initiation and amino acid sequence of the 5S rRNA subunit from Mycobac
Reference number: S16897; MIMD:940400001; PMID:1426414
Accession: S16899
Status: preliminary
Molecule type: protein
Antisides: 1-12 cDNA
Keywords: protein biosynthesis; ribosome

Query March 20.7% Score 24; DE 21; Length 127
Best Local Similarity 50.0%; Pred E: 2.8e-17
Matches 4; Conservative 2; Mismatches 2; Gaps 0;

CY 6 QUMDQDF 13
EB 6 EIMVDAF 12
      |||
PESIDE 10
PH0765
T-cell receptor beta chain (H1) - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 13 Jul 1992 #sequence_revision: 13 Jul 1992 #text_revision: 13 May 1994
Accession: PH0765
Author: Kasarova, J. L., Romero, P., Widmann, R., Kozlitsky, E., Korynski, J. L.
J. Exp. Med. 174, 1371-1383, 1991
Abstract: T cell receptor genes in a series of class I and II heteroreceptibility complex
allelic excision and antigen specific repertoire
Reference number: PH0766; MIMD:9204446; PMID:1836615
Accession: PH0765
Molecule type: mRNA
Residues: 1-14 <AS>
Cross-references: EMBL:X60859, NID:R11179; FIMD:940400001; MIMD:951140
Experimental source: T lymphocyte
Keywords: T cell receptor

Query March 20.7% Score 24; DE 21; Length 127
Best Local Similarity 44.4%; Pred E: 2.8e-17
Matches 4; Conservative 1; Mismatches 2; Gaps 0;

CY 12 CEFKAEEL 20
EB 1 CASSARQ 9
      |||
RESULT 11
A49177
Title: Crithidia fasciculata (fragment)
Species: Crithidia fasciculata
Date: 19 May 1994 #sequence_revision: 19 May 1994 #text_revision: 19 May 1994
Accession: A49177; PH:526
Author: Tittawalla, T.
Exp. Cell Res. 206, 143-151, 1993
Title: Identification of DNA-binding proteins in the 100 kDa fraction from Crithidia fas
Reference number: A49177; MIMD:9324912; PMID:846436
Accession: A49177
Molecule type: protein
Residues: 1-15 <TIT>
Note: sequence extracted from NCBI database. Nucleotide se
Comment: This protein binds with mitochondrial DNA.
Keywords: DNA binding; mitochondrion

Query March 20.7% Score 24; DE 21; Length 127
Best Local Similarity 45.6%; Pred E: 2.8e-17

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C:Function:
A:Description: EC 3.4.19.1 [validated, MID:9388716]
S:Superfamily: acylaminoacyl-peptidase
C:Keywords: hydrolase; omega peptidase

Query Match:      20.7%  Score 24,  DB 21,  Length 21,
Best Local Similarity 44.4%  Pred. No. 3.9e+04,
Matches  4,  Conservative  3,  Mismatches  2,  Indels  0,  Gaps  0

CY      13  PRDAAGGCK 21
DB      2  PDALKCC 10
      11 111

RESULT 15
S47207
T:Cell receptor C-alpha wvlll: Human (fragment)
C:Species: Homo Sapiens (man)
P:Date: 06 Feb 1995 #sequence_revision 06 Feb 1995 #text_revision 05-Nov-1999
C:Accession: S47207
R:Plaza, A.; Kono, J.H.; Theofilopoulos, A.N
Submitted to the EMBL Data Library, February 1993
A:Reference number: S47207
A:Accession: S47207
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-21 <PIA>
A:Cross references: EMBL:U71032, NID:9516610, GENBANK:U71032, F039510318
C:Keywords: T-cell receptor

Query Match:      20.7%  Score 24,  DB 21,  Length 21,
Best Local Similarity 57.1%  Pred. No. 3.9e+04,
Matches  4,  Conservative  1,  Mismatches  2,  Indels  0,  Gaps  0

CY      9  VMNVCCP 13
DB      12  VPERCCP 18
      11 111

Search completed: November 5, 2003, 14:27 hr
Run time: 0.01 secs

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GenCore version 3.1.1.6  
Copyright (c) 1993-2003 Comogen Inc.

CM protein protein search, using sw model

Run on: November 5, 2003, 18:22:23 Search time: 11.89 hours  
100-hour alignment  
49,708 Multiple Cell updates/sec

Title: US-09-914-088-16

Perfect score: 118

Sequence: 1 CLEGGVMDVCPRLAESEK .1

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searches: 129861 sets, 4702675 residues

Total number of hits satisfying chosen parameters: 1,76

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.4

Pred. No. is the number of results predicted by database to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY

Result No.	Score	Query Match	Length	DB ID
1	25	21.6	21	TRYP PR AT
2	24	20.7	17	ITHE HIRME
3	24	20.7	20	ACPH BRVIN
4	24	20.7	21	ATPH BRVIN
5	23	19.8	11	PQCG EREPT
6	23	19.8	14	RS11 T1 EP
7	23	19.8	14	PS11 EREPT
8	23	19.8	14	PS11 EREPT
9	22	19.0	16	YERF VALER
10	22	19.0	9	CCG1 EREPT
11	22	19.0	9	DNF1 EREPT
12	22	19.0	9	OXVT CVIVA
13	22	19.0	12	RS11 EREPT
14	22	19.0	16	FIBA CER31
15	21	18.1	11	RRFL CHAV
16	21	18.1	15	CXJA GNGU
17	21	18.1	21	GYRA STRSH
18	20	17.2	10	GACU HIRAN
19	20	17.2	19	FIBA HIRSE
20	20	17.2	19	PHS1 EREPT
21	20	17.2	20	SC19 VERMA
22	20	17.2	20	VR9C EREPT
23	20	17.2	21	GRX BURIN
24	20	17.2	21	OMP4 PASHA
25	20	17.2	21	REV HZD2
26	19.5	16.8	19	HMD METW3
27	19	16.4	9	COMC GARGE
28	19	16.4	14	SCN3 EREPT
29	19	16.4	16	FIBA APEVA
30	19	16.4	16	KTRC APEVA
31	19	16.4	17	TR22 EREPT
32	19	16.4	20	TS44 EREPT
33	19	16.4	21	OMP1 ACTE1

34	13	16.4	21	SP13 SOLTU
35	18.5	15.9	20	RL10 PROMU
36	18.5	15.9	21	PER PYRWO
37	13	15.5	9	OXVT RAJCL
38	13	15.5	12	PPK4 PERAX
39	13	15.5	12	PPK4 PERFU
40	13	15.5	12	V23K WSSV
41	13	15.5	13	FIBA CAVPO
42	13	15.5	13	LPAA PCRG1
43	13	15.5	14	GR75 CANFA
44	13	15.5	15	KLOM LUNTE
45	13	15.5	15	RKGG CAROR

## ALIGNMENTS

RESULT 1  
TRYP PROAT STANDARD: PRT: 21 AA.  
AC P35051:  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Trypsin precursor (EC 3.4.21.4) (Fragment)  
CS Proteolysis aethiops (Marbled lungfish)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Dipnoi; Lepidosireniiformes; Protopterygia; Protopterus.  
OX NCBI\_TaxID=9886;  
RN 11;  
RP SEQUENCE:  
RC 1-SSUE-Paraceras:  
RA Herndonson V.A., Tyb P.W., Rebeck G.R., Neuzath H., Walsh K.A.  
RT Comparison of the amino terminal sequences of bovine, dogfish, and  
RL lungfish trypsinogen.  
RL FEBS Lett. 4:222-224 (1971).  
CC 1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.  
CC 1- SUBCELLULAR LOCATION: Extracellular.  
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR PIR: A27719; A27719.  
DR MEROPS: S01.151;  
DR InterPro: IPR001254; Ser protease Try.  
DR PROSITE: PS02040; TRYPSIN\_DOM; PARTIAL.  
DR PROSITE: PS02040; TRYPSIN\_HIS; PARTIAL.  
DR PROSITE: PS02040; TRYPSIN\_SER; PARTIAL.  
KW Hydrolase; Serine protease; Zymogen.  
FT PROPEP 1-7 ACTIVATION PEPTIDE.  
FT CHAIN 8-21 TRYPSIN.  
FT NAME: 1 21  
SQ SEQUENCE 11 AA: 444 KW: R82FBIID130729F CRG64;

Query Match: 21.6% Score 25; DB 1; Length 21;  
Best Local Similarity 41.7% Pred. No. 1-2e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 3 EDGGMVDCVPR 14  
DB 5 EDKIVGSGYCPK 16

RESULT 2  
ITHE HIRME STANDARD: PRT: 17 AA.  
AC P28502:  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DE Hirudin 1A (Fragment)  
OS Hirudo medicinalis (Medicinal leech)  
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
CC Arynobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=421;  
RN 11;





```

genome analysis program.
Theor. Appl. Genet. 93:997-1005(1994).
FUNCTION CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP.
CATALYTIC ACTIVITY: ATP + L-methionine + H2O = S-adenosyl-L-methionine +
diphosphate + S-adenosyl-L-methionine.
COFACTOR: Binds 2 divalent ions, such as magnesium, zinc, and
1 potassium ion per subunit. Pentameric.
PATHWAY: Activated methyl cycle.
MISCELLANEOUS: ON THE 2D-GEL THE HETEROMERIC FORM OF THIS PROTEIN
PROTEIN IS: 5.9, ITS MW IS: 43.3 kDa.
SIMILARITY: BELONGS TO THE ADENET SYNTHETASE FAMILY
Name: ADPASE; P06616; COLICOLPTE
Mol. mass: 123338;
Interact: IPSC0133; S-AdoMet synth.
Pfam: PF02772; S-AdoMet synthase.
PROSITE: PS00776; ADENET SYNTHETASE 1; PARTIAL.
PROSITE: PS00777; ADENET SYNTHETASE 2; PARTIAL.
Transferrase; One-carbon metabolism; Multiple catalytic site binding.
Manganese; Potassium; Metal-binding.
NON_TER 1 15
NUNTER 1 15
SEQUENCE 15 AA; 180 MW; 2436 EDAS; 128612 R 64.

Query Match: 19.0%, Score 23; DB 1; Length 9;
Best Local Similarity 15.0%, Pred. No. 1,30+05;
Matches 3; Conservative 1; Mismatches 2; Gaps 0;

QY 12 PERADAR 2;
DB 2 PERADAR 10;

RESULT 4
CONV CONVE STANDARD; PRT: 9 AA;
AC P06487;
DT 01-NOV-1994 (Rel. 09, Created);
DT 01-NOV-1994 (Rel. 09, Last sequence update);
DT 24-FEB-2003 (Rel. 41, Last annotation update);
DE Amino-oxidase.
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
OCX NCB: TaxID=117992;
RN 1;
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
TISSUE: Ventricle.
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schmitta W.E., Asenari P., Pollicelli F.;
RT "Coniophan-Va: a novel peptide from the venom of the Mediterranean
small conus ventricosus";
RC Biochem. Biophys. Res. Commun. 288:908-913(2001);
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- TISSUE SPECIFICITY: Expressed by the ventricle.
CC 1- MASS SPECTROMETRY: MW=1089.6; METHOD=MALDI.
CC 1- SIMILARITY: BELONGS TO THE CONIOPHAN FAMILY.
KW Toxin; Amino-oxidation; L-lysine acid.
FT DISULFID 3 2
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 109 MW; 20186763236768A CRC64;

Query Match: 19.0%, Score 23; DB 1; Length 9;
Best Local Similarity 15.0%, Pred. No. 1,30+05;
Matches 3; Conservative 1; Mismatches 2; Gaps 0;

QY 12 PERADAR 2;
DB 2 PERADAR 10;

RESULT 10
CONV CONVE STANDARD; PRT: 9 AA;
AC P06487;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Coniophan-Va.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
OCX NCB: TaxID=117992;
RN 1;
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
TISSUE: Ventricle.
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schmitta W.E., Asenari P., Pollicelli F.;
RT "Coniophan-Va: a novel peptide from the venom of the Mediterranean
small conus ventricosus";
RC Biochem. Biophys. Res. Commun. 288:908-913(2001);
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- TISSUE SPECIFICITY: Expressed by the ventricle.
CC 1- MASS SPECTROMETRY: MW=1089.6; METHOD=MALDI.
CC 1- SIMILARITY: BELONGS TO THE CONIOPHAN FAMILY.
KW Toxin; Amino-oxidation; L-lysine acid.
FT DISULFID 3 2
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 109 MW; 20186763236768A CRC64;

Query Match: 19.0%, Score 23; DB 1; Length 9;
Best Local Similarity 15.0%, Pred. No. 1,30+05;
Matches 3; Conservative 1; Mismatches 2; Gaps 0;

QY 12 PERADAR 2;
DB 2 PERADAR 10;

RESULT 10
CONV CONVE STANDARD; PRT: 9 AA;
AC P06487;
DT 01-AUG-1996 (Rel. 15, Created);
DT 01-AUG-1996 (Rel. 15, Last sequence update);
DT 15-DEC-1998 (Rel. 37, Last annotation update);
DE Locusta migratoria migratorioides F1/F2;
OS Locusta migratoria migratorioides F1/F2;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoconcha;
OC Acridoidea; Acrididae; Caelidipodidae; Locusta.
OCX NCB: TaxID=7004;
RN 1;
SEQUENCE.
TISSUE: Subesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=8817077; PubMed=3689410;
RA Froux J., Valleron J.A., L.J.P., Carney R.D., Girardie A.;
RT "Isolation of an arginine vasopressin-like diuretic hormone from
Locusta migratoria";
RC Biochem. Biophys. Res. Commun. 149:160-166(1987);
RN 1;
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
TISSUE: Subesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=8817077; PubMed=3689410;
RA Froux J., Valleron J.A., L.J.P., Carney R.D., Girardie A.;
RT "Isolation of an arginine vasopressin-like diuretic hormone from
Locusta migratoria";
RC Biochem. Biophys. Res. Commun. 149:160-166(1987);
RN 1;
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
TISSUE: Subesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=8817077; PubMed=3689410;
RA Froux J., Valleron J.A., L.J.P., Carney R.D., Girardie A.;
RT "Isolation of an arginine vasopressin-like diuretic hormone from
Locusta migratoria";
RC Biochem. Biophys. Res. Commun. 149:160-166(1987);
RN 1;
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

```

CC -1 SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY  
 DR PIR: A29477; A29477;  
 DR Interferon; IPRO00981; Neutryp\_horm.  
 DA PFam: PF002220; hormone4; 1;  
 DA PROSITE: PS00264; NEURGHYPOPHYS\_H\_4; 1;  
 KW Hormone; Neuropeptide; Activation  
 FT DISULFID 1 6 IN F1  
 FT DISULFID 1 1 INTER-BRAIN WITH C-TER IN F2  
 FT DISULFID 3 6 INTER-BRAIN WITH C-TER IN F2  
 FT NOD RES 5 9 AMILATION  
 SQ SEQUENCE 9 AA: 976 MW; 56EB376B845A612 (5624)  
 Query Match 19.0%; Score 20; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1; 25;  
 Matches 3; Conservative 1; Mismatches 0; Gaps 0;  
 QY 11 DCRP 14  
 DB 5 NCRP 9  
 RESULT 12  
 QXVT\_CVICA STANDARD; PRT; 9 AA  
 AC P3895; 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DB Vasocerin  
 OS Cyprinus carpio (Common carp), and  
 CS Petryzox ratinus (Sea lamprey)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariichthyes; Cyprinodontes;  
 CC Cyprinidae; Cyprinus  
 OX NCBI\_TaxID:7962, 7157;  
 RN 1;  
 RP SEQUENCE  
 AC SPECIES: Cyprinus; TISSUE: pituitary;  
 RA Acher R., Chauvet J., Chauvet M., Crepy B.  
 RT "Characterization of neurohypophysial hormones from a fresh water bony  
 fish, the carp, *Cyprinus carpio*. Comparison with hormones from sea  
 water bony fishes".  
 RI Comp. Biochem. Physiol. 14:245-247 (1981)  
 RV 12;  
 RP SEQUENCE  
 AC SPECIES: ratinus; TISSUE: pituitary;  
 RA WHELINE, 882:56944; PubMed:1371646;  
 RA Lane T.P., Sweet S.A., Kawachi H.  
 RT "Arginine vasopressin from the pituitary gland of the lamprey  
 (*Petoryzox ratinus*): isolation and characterization".  
 PL Gen. Comp. Endocrinol. 70:152-157 (1981)  
 CC -1 SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY  
 DR PIR: B61364; B61364;  
 DR PIR: S63375; S63375;  
 DR Interferon; IPRO00981; Neutryp\_horm  
 DA PFam: PF002220; hormone4; 1;  
 DA PROSITE: PS00264; NEURGHYPOPHYS\_H\_4; 1;  
 KW Hormone; Activation  
 FT DISULFID 1 6  
 FT NOD RES 5 9  
 SQ SEQUENCE 9 AA: 1053 MW; 17EB376B845A612 (5624)

Query Match 19.0%; Score 20; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1; 25;  
 Matches 3; Conservative 1; Mismatches 0; Gaps 0;

QY 11 DCRP 14  
 DB 5 NCRP 9

RESULT 13

RS19\_ELYEP STANDARD; PRT; 12 AA;  
 ID RS19\_ELYEP  
 AC Q47881;  
 DT 30-MAY-2000 (Rel. 13, Created)  
 DT 30-MAY-2000 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S19 (fragment)  
 DE RPSS OR RPS19  
 OS Elr yeilows phycotasma  
 CC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 CC Acholeplasmataceae; Phycoplasma  
 CC NCBI\_TaxID:35774;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:94352802; PubMed:8071198;  
 RA Gundersen D.E., Lee T.M., Palmer S.A., Davis R.E., Kingsbury D.T.  
 RT "Phylogeny of mycoplasma-like organisms (phycoplasmas): a basis for  
 their classification"  
 RL J. Bacteriol. 176:5244-5254 (1994)  
 CC -1 FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S11 THAT BINDS STRONGLY  
 TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -1 SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL, curators of  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: L27022; AAA93942.1;  
 DR HAMAP: MP\_005311;  
 DR InterPro: IPR002422; Ribosomal\_S19  
 DR PROSITE: PS00323; RIBOSOMAL\_S19; PARTIAL  
 KW Ribosomal protein; rRNA-binding  
 FT NON TER 1  
 SQ SEQUENCE 12 AA: 1283 MW; 2CC47B9D58333AA8 CPC64;  
 Query Match 19.0%; Score 22; DB 1; Length 12;  
 Best Local Similarity 40.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 3; Gaps 0;  
 QY 12 AB30K 2;  
 DB 3 AR30K 3  
 RESULT 14  
 FIBA\_CERS STANDARD; PRT; 16 AA;  
 ID FIBA\_CERS  
 AC P14535;  
 DT 01-JAN-1993 (Rel. 13, Created)  
 DT 01-JAN-1993 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (fragment)  
 GN FGA  
 OS Ceratotherium simum (White rhinoceros) [Square-lipped rhinoceros]  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium  
 CC NCBI\_TaxID:9927;  
 RN 1;  
 RP SEQUENCE  
 RA O'Neill P.B., Doolittle R.F.  
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences."  
 RL Syst. Zool. 22:590-595 (1973)  
 CC -1 FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLASLET  
 AGGREGATION  
 CC -1 SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC -1 CHAINS: ALPHA, BETA AND GAMMA, LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1 VISCELLAR CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 THROMBIN, AND IT CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA 5 BETA 1

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CC CHAINS, AND THUS EXPOSES THE TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT AGG.
KW BLOOD COAGULATION, Plasma.
FT PEPTIDE 12 16 FIBRINOGENPTIDE A.
FT KNTTER 16 16
SQ SEQUENCE 16 AA: 1639 MW: 035803662924201 19743
Query Match 19 (1) Score 20.000 E-value 0.0
Best Local Similarity 66.0%, Prod No. 21000000
Matches 4: Conservative 0; Mismatches 4; Indels 0; Gaps 0
QY 15 RAARD 20
DB 2 ESTED 7

RESULT 15
RRC_CHAV
1D RRC_CHAV STANDARD: PRI. 11 AA.
AC P13179
DT 01 JAN 1990 (Rel. 13, Created)
DT 01 JAN 1990 (Rel. 13, Last sequence update)
DT 28 FEB 2003 (Rel. 41, Last annotation update)
DE RRA polymerase beta subunit (EC 2.7.7.44) [large structural protein]
DE C. protein (fragment).
GN C.
OS Chandipura virus (strain 16535.4).
OC Viruses; ssRNA negative-strand viruses, Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
CX NBR: TXID:11272;
RN 111
PF SEQUENCE FROM N.A.
RX MEDLINE: 89299473; PubMed: 2741947.
RA Masters P.S., Bello R.S., Butcher M., Fodor B., Rucklberg
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus." J. Virol. 63:1285-1290(1989).
RL Virgosity 111285-1290(1989).
CC 1: FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC COMPLEX OF POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY A SYNTHESIS.
CC 2: CATALYTIC ACTIVITY: Nucleoside triphosphatase, N-substrate +
CC (PPA)(H2O) -> SUBSTRATE THOUGHT TO FORM A TRANSFERRED COMPLEX WITH THE
CC NUCLEOSIDIC END PROTEIN.
CC 3: SIMILARITY WITH THE C-PROTEIN OF OTHER RABDOPUS VIRUSES AND
CC PARAMYXOVIRUSES.
CC This SWISS PROTEIN entry is copyrighted by the Swiss Institute for
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CC reproduced or transmitted in any form or by any means electronic or
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CC modified and this statement is not removed. The use of this database
CC entries requires a license agreement. See http://www.ebi.ac.uk/infocentre/
CC or send an email to license@ebi.ac.uk.
CC ENBL: 034350; AAA2912.1
CC Transfrase; RNA-directed RNA polymerase
FT SEQ 11 11
SQ SEQUENCE 11 AA: 1189 MW: 0231063140.034 19743
Query Match 18 (1) Score 20.000 E-value 0.0
Best Local Similarity 45.6%, Prod No. 21000000
Matches 5: Conservative 3; Mismatches 2; Indels 0; Gaps 0
QY 8 YUVCSPRAAE 18
DB 1 MELNPDVCAAE 11

```



GenCore version 5.1.1  
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QM protein protein search, using sw b. tel

Run on: November 5, 2003, 18:15:22 : Search time 13 sec  
without alignment  
164,215 Matrix Cell updates/sec

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CLEUCQVMDVDFREAMECK 21

Scoring table: BLOSUM62

Gapop 12.0, Gapext 2.5

Searched: 81055 seqs, 259052654 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0

Maximum DB seq length: 21

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

```
SPTRMBL 23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_rhiz:
8: sp_organeller:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_invertebrate:
14: sp_invertebrate:
15: sp_unclassified:
16: sp_bacteriophage:
17: sp_bacteriophage:
18: sp_archaea:
```

Pred. No. is the number of results predicted by the search engine. A score greater than or equal to the score of the best hit is printed, and is derived by analysis of the total score list.

# SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	34	24.3	18	Q9TRX7	Q9TRX7 Bos taurus
2	34	23.3	21	Q9TRX5	Q9TRX5 Bos taurus
3	30	25.9	21	Q9N0P6	Q9N0P6 Canis familiaris
4	29	25.0	20	Q8BXH3	Q8BXH3 Mus musculus
5	27	23.3	15	Q9TX24	Q9TX24 Locusta migratoria
6	27	23.3	18	Q9T6E8	Q9T6E8 Equus caballus
7	27	23.3	20	Q9T6E5	Q9T6E5 Methanococcus
8	27	23.3	20	Q9T6E4	Q9T6E4 Methanococcus
9	26	22.4	16	Q774V1	Q774V1 Mytilus edulis
10	26	22.4	20	Q9S5T4	Q9S5T4 Proteus mirabilis
11	25.5	22.0	17	Q8S5T4	Q8S5T4 Proteus mirabilis
12	25	21.6	19	Q9Q2A4	Q9Q2A4 Mus musculus
13	25	21.6	16	Q9R4V4	Q9R4V4 Proteus mirabilis
14	25	21.6	16	Q9T6E3	Q9T6E3 Bos taurus
15	25	21.6	19	Q8M1N3	Q8M1N3 Homo sapiens
16	25	21.6	20	Q9RVE	Q9RVE Proteus mirabilis

17	24	20.7	15	5	Q9TMU4	Q9TMU4 Crithidia fasciculata
18	24	20.7	20	11	Q63667	Q63667 Rattus norvegicus
19	24	20.7	21	6	Q9TR63	Q9TR63 Bos taurus
20	24	20.7	21	12	Q93C47	Q93C47 Maize stria
21	24	20.7	21	12	Q93C44	Q93C44 Maize stria
22	24	20.7	21	12	Q93C46	Q93C46 Maize stria
23	24	20.7	21	12	Q931B1	Q931B1 Porcine circovirus
24	24	20.7	19	13	Q8AV17	Q8AV17 Gallus gallus
25	23	19.8	16	6	Q8S5T4	Q8S5T4 Proteus mirabilis
26	23	19.8	16	13	Q9R2Z4	Q9R2Z4 Bothrops jarrovi
27	23	19.8	17	3	Q8H5Q2	Q8H5Q2 Acanthamoeba castellanii
28	23	19.8	17	3	Q9H5Q3	Q9H5Q3 Acanthamoeba castellanii
29	23	19.8	17	3	Q9H5Q1	Q9H5Q1 Acanthamoeba castellanii
30	23	19.8	17	10	Q9S5M7	Q9S5M7 Lycopodium obscurum
31	23	19.8	20	6	Q9N1B8	Q9N1B8 Equus caballus
32	23	19.8	21	2	Q9R4E7	Q9R4E7 Streptomyces
33	23	19.8	21	2	Q930S0	Q930S0 Maize stria
34	22	19.0	11	3	Q9F5Z2	Q9F5Z2 Xenopus laevis
35	22	19.0	13	2	Q9F5B5	Q9F5B5 Duck hepatitis virus
36	22	19.0	15	2	Q9F5Z5	Q9F5Z5 Streptococcus
37	22	19.0	15	10	Q9F5Y6	Q9F5Y6 Gossypium hirsutum
38	22	19.0	16	3	P79314	P79314 Emeticella
39	22	19.0	17	4	Q9G9G6	Q9G9G6 Homo sapiens
40	22	19.0	17	11	Q9QVC6	Q9QVC6 Rattus norvegicus
41	22	19.0	18	4	Q8NED1	Q8NED1 Homo sapiens
42	22	19.0	19	2	Q9R576	Q9R576 Streptococcus
43	22	19.0	19	2	Q9S6B1	Q9S6B1 Streptomyces
44	22	19.0	19	6	P81948	P81948 Bos taurus
45	22	19.0	19	13	Q8UVE0	Q8UVE0 Gallus gallus

## ALIGNMENTS

### RESULT 1

Q9TRX7 EMBL:U00000.1, 18 AA.  
ID Q9TRX7 EMBL:U00000.1, 18 AA.  
AC Q9TRX7 EMBL:U00000.1, 18 AA.  
DT 01-MAY-2000 (TrEMBL) 13, Created:  
DT 01-MAY-2000 (TrEMBL) 13, Last sequence update:  
DT 01-JUN-2002 (TrEMBL) 21, Last annotation update:  
DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumetazoa; Chordata; Chordata; Bovidae; Bovinae; Bos.  
OC Bovidae; Bovinae; Bos.  
OX MCH; TaxID:9913;  
RN 1;  
RP SEQUENCE.  
RX YEDLIN:9133094; subMed:1854724;  
RA Ozturk D.H., Coman R.F.;  
RT Identification of cysteine-219 as the target amino acid of 8-(14-bromo-2,3-dioxoketylthio)adenosine 5'-triphosphate in bovine liver:  
RT glutamate dehydrogenase.  
RL Biochemistry 30:7126-7134(1991).  
DR HSSP; 500166; IMX; 1934 MW; E86930DF714BD260 CRC64;  
SQ SEQUENCE 18 AA: 1934 MW; E86930DF714BD260 CRC64;

Query Match: 29.3% Score 14; DB 6; Length 18;  
Best Local Similarity 44.4%; Pred. No. 2.3e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

### RESULT 2

Q9TRX5 EMBL:U00000.1, 21 AA.  
ID Q9TRX5 EMBL:U00000.1, 21 AA.  
AC Q9TRX5 EMBL:U00000.1, 21 AA.  
DT 01-MAY-2000 (TrEMBL) 13, Created:  
DT 01-MAY-2000 (TrEMBL) 13, Last sequence update:  
DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumetazoa; Chordata; Chordata; Bovidae; Bovinae; Bos.  
OC Bovidae; Bovinae; Bos.  
OX MCH; TaxID:9913;  
RN 1;  
RP SEQUENCE.  
RX YEDLIN:9133094; subMed:1854724;  
RA Ozturk D.H., Coman R.F.;  
RT Identification of cysteine-219 as the target amino acid of 8-(14-bromo-2,3-dioxoketylthio)adenosine 5'-triphosphate in bovine liver:  
RT glutamate dehydrogenase.  
RL Biochemistry 30:7126-7134(1991).  
DR HSSP; 500166; IMX; 1934 MW; E86930DF714BD260 CRC64;  
SQ SEQUENCE 21 AA: 1934 MW; E86930DF714BD260 CRC64;

Query Match: 29.3% Score 14; DB 6; Length 18;  
Best Local Similarity 44.4%; Pred. No. 2.3e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

### RESULT 3

Q9TRX5 EMBL:U00000.1, 21 AA.  
ID Q9TRX5 EMBL:U00000.1, 21 AA.  
AC Q9TRX5 EMBL:U00000.1, 21 AA.  
DT 01-MAY-2000 (TrEMBL) 13, Created:  
DT 01-MAY-2000 (TrEMBL) 13, Last sequence update:  
DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumetazoa; Chordata; Chordata; Bovidae; Bovinae; Bos.  
OC Bovidae; Bovinae; Bos.  
OX MCH; TaxID:9913;  
RN 1;  
RP SEQUENCE.  
RX YEDLIN:9133094; subMed:1854724;  
RA Ozturk D.H., Coman R.F.;  
RT Identification of cysteine-219 as the target amino acid of 8-(14-bromo-2,3-dioxoketylthio)adenosine 5'-triphosphate in bovine liver:  
RT glutamate dehydrogenase.  
RL Biochemistry 30:7126-7134(1991).  
DR HSSP; 500166; IMX; 1934 MW; E86930DF714BD260 CRC64;  
SQ SEQUENCE 21 AA: 1934 MW; E86930DF714BD260 CRC64;

Query Match: 29.3% Score 14; DB 6; Length 18;  
Best Local Similarity 44.4%; Pred. No. 2.3e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DT 01 JUN 2002 (TREMSELrel. 21, Last annotation update)  
 CC Glutamate dehydrogenase (EC 1.4.1.3) (Fragment)  
 OS Bos taurus (Bovidae)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovinae; Bovidae; Bovinae; Bos.  
 CX NCBI: TaxID:9013;  
 RN 1;  
 RP SEQUENCE  
 RX MEDLINE 9118094, Pubmed 1864724;  
 SA Orlitz D.H., Corbin R.F.;  
 PT Identification of cysteine 119 as the target of the 119-114  
 PT bis-(2,3-dichloroethyl)phosphoradenosine 5'-triphosphate inhibitor  
 RC Glutamate dehydrogenase.  
 Z1 Biochemistry 10:1126-7114(1991)  
 RP RSDP: F00366; 18WX;  
 SQ SEQUENCE 21 AA; 2279 MW; 6003FAH696CF 1 09764,  
 Query Match 29.3%; Score 47; DB 11; Length 21;  
 Best Local Similarity 44.4%; Pred. No. 127403;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 DGGQWQVD 12  
 DB 11111111  
 1 EUSTEFVN 1;  
 RESULT 1  
 Q97649 PRELIMINARY; PRT; 21 AA;  
 AC Q97649  
 DT 01 OCT 2002 (TREMSELrel. 19, Created)  
 DT 01 OCT 2002 (TREMSELrel. 17, Last sequence update)  
 DT 01 OCT 2002 (TREMSELrel. 22, Last annotation update)  
 DE Class III beta-tubulin (Fragment)  
 OS Canis familiaris (Dog)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Carnivora; Farnipedia; Canidae; Canis.  
 CX NCBI: TaxID:9615;  
 RN 1;  
 RP SEQUENCE FR M N A  
 SA Adair R.J.;  
 PT Crystallization of isotype specific region of the C-terminal of  
 PT canine beta-tubulin and their kinase binding site  
 Z1 Submitted (JAN 1999) to the EMBL database  
 Z1 EMBL: A01010, EAA0411.2;  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 21 AA; 2401 MW; 1547...  
 Query Match 25.9%; Score 27; DB 57; Length 21;  
 Best Local Similarity 31.6%; Pred. No. 127403;  
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EFGXVETDESEACQPK 21  
 DB 11111111  
 1 EFGXVETDESEACQPK 21  
 RESULT 4  
 Q97649 PRELIMINARY; PRT; 21 AA;  
 AC Q97649  
 DT 01 MAR 2003 (TREMSELrel. 21, Created)  
 DT 01 MAR 2003 (TREMSELrel. 21, Last sequence update)  
 DT 01 MAR 2003 (TREMSELrel. 23, Last annotation update)  
 DE Kinetic superfamily protein 21A (Fragment)  
 OS Mus musculus (Mouse)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurimorphia; Muridae; Mus.  
 CX NCBI: TaxID:10097;  
 RN 1;  
 RP SEQUENCE FR M N A

RC STRAIN-05/BL767; ISSUES=Cerebellum;  
 RX MEDLINE 12354633, Pubmed 12466851;  
 RA The PANTOM Consortium;  
 RA The PIREN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK047208; SAGE:2492.1;  
 FT NON TER  
 SQ SEQUENCE 23 AA; 1062 MW; E1D049E6D4A2075 CRC64;  
 Query Match 25.0%; Score 29; DB 11; Length 20;  
 Best Local Similarity 32.5%; Pred. No. 15603;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LEDGQVDC 9  
 DB 11111111  
 2 LEDGQVDC 9  
 RESULT 5  
 Q97649 PRELIMINARY; PRT; 15 AA;  
 AC Q97649  
 DT 01 MAY 2000 (TREMSELrel. 13, Created)  
 DT 01 MAY 2000 (TREMSELrel. 13, Last sequence update)  
 DT 01 JUN 2002 (TREMSELrel. 21, Last annotation update)  
 DE PROPHENGLAXIDASE inhibitor N terminus (Fragment)  
 OS Locusta migratoria (Insecta; Hemiptera; Coreidae)  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psocoptera;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Cedicodinae; Locusta.  
 CX NCBI: TaxID:7904;  
 RN 1;  
 RP SEQUENCE FR M N A  
 RX MEDLINE 9139003; Pubmed 1510340;  
 RA Brockell M., Bielegrain R.A., Dill G., Coletti-Previero M.A.;  
 RT Purification of a protease inhibitor which controls prophormotaxidase  
 RT activation in hemolymph of Locusta migratoria (Insecta; Hemiptera; Coreidae; Locusta migratoria).  
 RL Biochem. Biophys. Res. Commun. 199,841-846(1991).  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 15 AA; 1267 MW; C690EAE811166C7 CRC64;  
 Query Match 23.3%; Score 27; DB 57; Length 15;  
 Best Local Similarity 32.5%; Pred. No. 127403;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EFGXVETDESEACQPK 21  
 DB 11111111  
 1 EFGXVETDESEACQPK 21  
 RESULT 6  
 Q97649 PRELIMINARY; PRT; 18 AA;  
 AC Q97649  
 DT 01 MAY 1999 (TREMSELrel. 10, Created)  
 DT 01 MAY 1999 (TREMSELrel. 10, Last sequence update)  
 DT 01 JUN 2001 (TREMSELrel. 17, Last annotation update)  
 DE Laccase (Fragment)  
 OS Equus caballus (Horse)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CX NCBI: TaxID:9796;  
 RN 1;  
 RP SEQUENCE FR M N A  
 SA Stracke S.P., Sittard J.M., Bell T.K.;  
 RT Purification of Equine Lacciferin (Enzyme)  
 RL Submitted (JAN 1999) to the EMBL database  
 Z1 EMBL: A01010, EAA0411.2;  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 18 AA; 1967 MW; 1547...

```

OR  P107, PFC6400, transfection; 1;
FT  NON_TER 1
DE  18
SQ  SEQUENCE 18 AA; 1936 MW; D8PFAA26AA67039 C37044.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CQDQ 5
DB 1 CQDQ 5

RESULT 7
CQDQ15 PRELIMINARY; PRT: 20 AA.
AC CQDQ15
DT 01-MAY-2000 (TRENBLREL 13, Created;
DT 01-MAY-2000 (TRENBLREL 13, Last sequence update;
DT 01-JUN-2000 (TRENBLREL 14, Last annotation update;
DE Membrane-associated ATPase alpha subunit (fragment);
OS Methanococcus voltae;
OC Archaea; Euryarchaeota; Methanococci; Methanococcaceae;
OC Methanococcaceae; Methanococcus;
CX NCBI_TaxID=2198;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 1965 MW; 8251D17B344FAC C37044.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQDQVDCVCFPAAGDQ 21
DB 3 CQDQVDCVCFPAAGDQ 19

RESULT 8
CQDQ1 PRELIMINARY; PRT: 20 AA.
AC CQDQ1
DT 01-MAY-2000 (TRENBLREL 13, Created;
DT 01-MAY-2000 (TRENBLREL 13, Last sequence update;
DT 01-OCT-2002 (TRENBLREL 22, Last annotation update;
DE APYLAKINILAVINE N acetyltransferase (fragment);
OS Drosophila melanogaster (fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Insecta; Diptera;
OC Neoptera; Endopterygota; Diptera; Phlebotomina; Muscidae;
OC Ephydriidae; Ephydriidae; Ephydriidae;
CX NCBI_TaxID=7227;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2215 MW; 2CF5E1D41B344FAC C37044.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQDQVDCVCFPAAGDQ 21
DB 3 CQDQVDCVCFPAAGDQ 19

```

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DB 1 VQDQCP 6

RESULT 9
C77491 PRELIMINARY; PRT: 16 AA.
AC C77491
DT 01-NOV-1998 (TRENBLREL 38, Created;
DT 01-NOV-1998 (TRENBLREL 38, Last sequence update;
DT 01-DEC-2001 (TRENBLREL 19, Last annotation update;
DE D4 dopamine receptor (D4DR) (fragment);
OS Nicticebus concolor (Slow loris);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nicticebus;
CX NCBI_TaxID=9470;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1621 MW; 1864522CFC84FEE7 CRC64;

Query Match 22.4%; Score 26; DB 6; Length 16;
Best Local Similarity 80.0%; Pred. No. 3; 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 VQDQCP 13
DB 11 VQDQCP 15

RESULT 10
Q8R574 PRELIMINARY; PRT: 20 AA.
AC Q8R574
DT 01-MAY-2000 (TRENBLREL 13, Created;
DT 01-MAY-2000 (TRENBLREL 13, Last sequence update;
DT 01-JUN-2002 (TRENBLREL 21, Last annotation update;
DE NPFA MENNASE-RESISTANCE/PROTEUSLIKE (MR/P) fimbrial subunit (fragment);
OS Proteus mirabilis;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CX NCBI_TaxID=5184;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 1923 MW; 6B3AD0B464F4CD11 CRC64;

Query Match 22.4%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4; 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 CQDQVDCVCFPAAGDQ 21
DB 11 CQDQVDCVCFPAAGDQ 19

```



```

KW 11
RP SEQUENCE FROM N.A.
EC TISSUE-SKIN
WA Strausberg P.
RG Submitted (CGI 2003) to the EMBL/GenBank/DBI databases
ORF ENCL: BC019387; AAH19387.1
KW Hypothetical protein
FI NON-TER
SQ SEQUENCE 19 AA, 2067 MW, 2062246554.601 (P 2.4)

Query Match 21.63; Score 25; DB 4; Length 199
Best Local Similarity 44.44; Pctid 50.5;
Matches 4; Conservative 1; Mismatches 4; Gap 0

CY 11 DCPREAAE 19
EC 10 DCASSVAJ 18

Search completed: November 5, 2003, 16:44:14
Job time : 35 secs

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GenCore version 5.1.5  
Copyright (c) 1993-2003 Copyright Ltd

SW protein - protein search, using sw model

Run on: November 5, 2003, 16:21:57, Search time: 40 Seconds  
without alignment  
83,332 Million cell of database

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CAGCGQWMDVDFEAAEGDK 31

Scoring table: PRC52M62

Gapop 10.0, Gapext 0.5

Sequences: 167860 seqs, 15872653 residues

Total number of hits satisfying chosen parameters: 49674

Minimum EE seq length: 2

Maximum PR seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq 19Jun03.\*  
1 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT  
2 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT  
3 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT  
4 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT  
5 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT  
6 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT  
7 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT  
8 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT  
9 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT  
10 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
11 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
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14 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
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19 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
20 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
21 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
22 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
23 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT  
24 /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT

Pred. No is the number of results predicted by query to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Query	Score	Match	Length	DB	ID	Description
1	116	100.0	21	21	AAB25942	PR	P1 mimotope peptid
2	116	100.0	21	22	AAU16647	PR	Peptide P1078 der
3	116	100.0	21	23	ARJ05917	PR	Human IgE cycli
4	111	95.7	20	21	AAB25942	PR	P1 mimotope peptid
5	111	95.7	20	22	AAU16646	PR	Peptide P1078HC
6	111	95.7	20	23	ABJ00217	PR	Human IgE cycli
7	100.5	86.6	21	21	AAB25942	PR	P1 mimotope peptid
8	100.5	86.6	21	22	AAU16647	PR	Peptide P1078HC
9	100.5	86.6	21	23	ABJ00217	PR	Human IgE cycli

10	69	59.5	14	23	ABJ00540	Human IgE cycli
11	60	51.7	13	21	AAB20872	Anti-allergy peptid
12	60	51.7	13	21	AAB25914	P1 mimotope peptid
13	60	51.7	13	21	AAB25917	P1 mimotope peptid
14	60	51.7	13	22	AAU16639	Peptide P15 deriv
15	60	51.7	13	22	AAU16642	Peptide P15 deriv
16	60	51.7	13	22	ABJ00228	IgE peptide #6, M
17	60	51.7	13	23	ARJ00312	Human IgE immunoge
18	60	51.7	13	23	ARJ00312	Human IgE cycli
19	60	51.7	15	23	ABJ00542	Human IgE cycli
20	60	51.7	20	21	AAB25942	P1 mimotope peptid
21	60	51.7	20	22	AAU16646	Peptide P1078GS d
22	60	51.7	20	23	ABJ00316	Human IgE cycli
23	60	51.7	20	23	ARJ00544	Human IgE cycli
24	59.5	51.3	21	22	AAU16637	Peptide C67/8-2 de
25	51	44.0	10	21	AAB25929	P1 mimotope peptid
26	51	44.0	10	22	AAU16654	Peptide P15 deriv
27	51	44.0	10	23	ABJ00228	Human IgE immunoge
28	51	44.0	13	21	AAB25916	Peptide P15p deriv
29	51	44.0	13	22	AAU16641	Human IgE immunoge
30	51	44.0	13	23	ABJ00226	Human IgE cycli
31	51	44.0	20	21	AAB23440	Human IgE cycli
32	50	43.1	13	23	ABJ00541	Human IgE cycli
33	47	40.5	9	21	AAB20857	Immunoglobulin E
34	47	40.5	9	22	AAU16632	IgE C-epsilon-2 do
35	47	40.5	9	22	AAU16632	Peptide P1 deriv
36	47	40.5	9	22	AAU16632	IgE peptide #1, M
37	47	40.5	9	23	ABJ00217	Human IgE immunoge
38	45	38.8	10	24	AAE35057	Immunoglobulin E
39	43.5	37.5	19	21	AAB25968	P1 mimotope (P1mAb
40	43.5	37.5	19	22	AAU16639	Peptide #34 deriv
41	43.5	37.5	19	23	ABJ00335	Human IgE cycli
42	42.5	36.6	19	21	AAB25970	P1 mimotope (P1mAb
43	42.5	36.6	19	22	AAU16695	Peptide #36 deriv
44	42.5	36.6	19	23	ABJ00357	Human IgE cycli
45	38.5	33.2	19	21	AAB25967	P1 mimotope (P1mAb

ALIGNMENTS

RESULT 1  
AAB25922  
ID AAB25942 standard; Peptide: 21 AA  
AC AAB25942  
XX  
XX  
DT 05-JAN-2001 (first entry)  
XX  
DE P1 mimotope peptide P1078 SEQ ID NO:16  
XX  
KW Epitope; mimotope, human; immunoglobulin E; IgE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; anti-allergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.  
XX  
OS Homo sapiens.  
XX  
PN WC28003460 A1  
XX  
PC 31-AUG-2000  
XX  
PF 22-FEB-2000, 2000WB-EF01455  
XX  
PR 25-FEB-1999, 99GB-0004405  
PR 29-MAR-1999, 99GB-0007151  
PR 07-MAY-1999, 99GB-0010537  
PR 07-MAY-1999, 99GB-0210538  
PR 07-AUG-1999, 99GB-0018594  
PR 07-AUG-1999, 99GB-0018603  
PR 07-SEP-1999, 99GB-0021046  
PR 07-SEP-1999, 99GB-0021047  
PR 29-OCT-1999, 99GB-0025619

15 21-NOV-1999: 593B-0227658.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Dwyer M., Friebe M., Greenwood C., Hewitt F., Larned A., Martin S.,  
PI Randall R., Turnell W.G., Van Machelen W.F., Vinals De Bassols Y.C.  
XX  
XX WPI: 2001-521967/51.  
XX  
XX Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed part of a specific  
PT domain from immunoglobulin E.  
XX  
XX Claim 14: Page 32; 129pp; English.  
XX  
XX The present invention describes a peptide (I), comprising an isolated  
XX surface exposed group/epitope (E1) of C epsilon 2 domain B of  
XX immunoglobulin E (IgE), or its mimotope. Also described are: (II) an  
XX immunogen (II) for treating allergy comprising (I); (III) a vaccine (III)  
XX for treating allergies comprising (I); (IV) a blend (IV) capable of  
XX recognising (I); (V) a pharmaceutical composition (V) comprising (I);  
XX (VI) a peptide (VI) capable of being recognised by (I); (VII) an immunogen  
XX (VII) comprising (I); and (VIII) producing (I) by producing (I). (I)  
XX can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (IV) is useful for identifying analogues of (I),  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (V) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (I), (II) and (III) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (IV) is also useful in diagnosing allergy. AA025490.1, AA025490.2 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 21 AA:  
SQ  
Query Match 100.0%; Score 116; DR 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2, 9e-10;  
Matches 21; Conservative 0; Mismatches 0; Gaps 0;  
QY 1 CLEDSQVMDVCFREAAAEKDK 21  
DB 1 CLEDSQVMDVCFREAAAEKDK 21  
RESULT 3  
AB-00317  
ID AAGC 110 Standard, Peptide: 21 AA.  
XX  
XX ASJ03417,  
XX  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 101.  
XX  
XX Immunogen: human IgE; immunoglobulin E; allergy; thio ether linkage;  
XX vaccine; antihistetic; cyclic.  
XX  
XX HOMO sapiens.  
XX  
XX W020216409 A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001W-EP09576  
XX  
XX 22-AUG-2000; 2000P-020717  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friebe M., Martin S., Turnell W.G., Vinals Passols Y.C.  
XX  
XX WPI: 2001-521967/51.  
XX  
XX (PEPT) Peptide Therapeutics Ltd.  
XX  
XX (PEPT) Peptide Therapeutics Ltd. comprises





invention describes peptides derived from or mimetics of the C-epitope, C-epitope regions of human immunoglobulin E (IgE) which are used to produce conjugated compositions. The compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope to a protein so as to form an immunogenic molecule which may be used to raise a protective antibody response in an animal or human patient.

AA1663: AA1663 represents peptide derived from or mimetics of the C-epitope/C-epitope/C-epitope region of human IgE

Sequence: 20 AA:  
Certy Maltin 95.74, Score: 111, Pos: 22, Length: 20  
Best local similarity: 100.0%, Pctd: 100.0, Pos: 22, Length: 20  
Matches: 20, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CV: 1 CIEGQWVWVDCPREAREGD 20  
||||| ||||| |||  
14: 1 CIEGQWVWVDCPREAREGD 20  
||||| ||||| |||

RESULT 7  
AA25972  
ID: AA25972 standard: Peptide; 21 AA  
XX  
AC: AA25972  
XX  
DT: C5-JAN-2001 (first entry)  
XX  
DE: P1 mimotope peptide PT-0799HC SEQ ID NO:66  
XX  
KW: Epitope; mimotope; human; immunoglobulin E; IgE; C-epitope; 2 domain; allergic disease; immunoglobulin; immunotherapy; anti-allergic;  
KW: immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW: allergy; atopy.  
XX  
OS: Homo sapiens.  
XX  
PN: WO200050440-A1  
XX  
PD: 31-AUG-2000  
XX  
PF: 22-SEP-2000; 20-MAR-EP01455  
XX  
PR: 25-FEB-1999; 99GB-0034405  
PR: 29-MAR-1999; 99GB-0007161  
PR: 07-MAY-1999; 99GB-0010537  
PR: 07-MAY-1999; 99GB-0010538  
PR: 07-AUG-1999; 99GB-0018594  
PR: 07-AUG-1999; 99GB-0018603  
PR: 07-SEP-1999; 99GB-0021046  
PR: 07-SEP-1999; 99GB-0021047  
PR: 29-OCT-1999; 99GB-0035619  
PR: 24-NOV-1999; 99GB-0027698  
XX  
PA: (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
PA: (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
PI: Dymov M, Friede V, Greenwood J, Hewitt R, Lamont A, Mason S, Randall P, Turner M, Van Mechelen W, Vinals De Bassols Y  
XX  
PI: (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
XX  
PI: (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
PS: Example 1, Page 41, 1, pp. English  
XX  
PT: Peptides useful for treating, preventing and ameliorating allergic diseases, comprising an isolated surface exposed group of a specific domain from immunoglobulin E  
XX  
CC: The present invention describes a peptide (I) comprising an isolated surface exposed group/epitope (II) of C-epitope-2 domain (D) of immunoglobulin E (IgE), or its mimotope. Also described are: (i) an immunogen (II) for treating allergy comprising (i); (2) a vaccine (III) for treating allergy comprising (i); (3) a ligand (IV) capable of recognising (i); (4) a pharmaceutical composition (PC) comprising (IV); (5) a peptide (I) capable of being recognised by (IV); (6) an immunogen (I) comprising (I) and (II) producing (III) by producing (III); (i) can have anti-allergic and immunosuppressive activities, and can be used as a vaccine and histamine release inhibitor. (i), (ii) and (iii) are useful in medicine and in the manufacture of medicaments for treating and preventing allergies. (iv) is useful for identifying microscopes of PL in medicine and also in manufacturing medicaments for treating allergies. (v) is useful in diagnostics and in the affinity purification of (i) using anti (i) antibodies from blood. (i), (ii) and (iii) are useful for treating a patient susceptible to or suffering from allergies. (iv) is also useful in diagnosing atopy. AA25972 to AA26099 represent peptide sequences which are used in the exemplification of the present invention.

invention describes peptides derived from or mimetics of the C-epitope, C-epitope regions of human immunoglobulin E (IgE) which are used to produce conjugated compositions. The compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope to a protein so as to form an immunogenic molecule which may be used to raise a protective antibody response in an animal or human patient.

AA1663: AA1663 represents peptide derived from or mimetics of the C-epitope/C-epitope/C-epitope region of human IgE

Sequence: 20 AA:  
Certy Maltin 95.74, Score: 111, Pos: 22, Length: 20  
Best local similarity: 100.0%, Pctd: 100.0, Pos: 22, Length: 20  
Matches: 20, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CV: 1 CIEGQWVWVDCPREAREGD 20  
||||| ||||| |||  
14: 1 CIEGQWVWVDCPREAREGD 20  
||||| ||||| |||

RESULT 7  
AA25972  
ID: AA25972 standard: Peptide; 21 AA  
XX  
AC: AA25972  
XX  
DT: C5-JAN-2001 (first entry)  
XX  
DE: P1 mimotope peptide PT-0799HC SEQ ID NO:66  
XX  
KW: Epitope; mimotope; human; immunoglobulin E; IgE; C-epitope; 2 domain; allergic disease; immunoglobulin; immunotherapy; anti-allergic;  
KW: immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW: allergy; atopy.  
XX  
OS: Homo sapiens.  
XX  
PN: WO200050440-A1  
XX  
PD: 31-AUG-2000  
XX  
PF: 22-SEP-2000; 20-MAR-EP01455  
XX  
PR: 25-FEB-1999; 99GB-0034405  
PR: 29-MAR-1999; 99GB-0007161  
PR: 07-MAY-1999; 99GB-0010537  
PR: 07-MAY-1999; 99GB-0010538  
PR: 07-AUG-1999; 99GB-0018594  
PR: 07-AUG-1999; 99GB-0018603  
PR: 07-SEP-1999; 99GB-0021046  
PR: 07-SEP-1999; 99GB-0021047  
PR: 29-OCT-1999; 99GB-0035619  
PR: 24-NOV-1999; 99GB-0027698  
XX  
PA: (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
PA: (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
PI: Dymov M, Friede V, Greenwood J, Hewitt R, Lamont A, Mason S, Randall P, Turner M, Van Mechelen W, Vinals De Bassols Y  
XX  
PI: (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
XX  
PI: (PEPT) PEPTIDE THERAPEUTICS LTD.  
XX  
PS: Example 1, Page 41, 1, pp. English  
XX  
PT: Peptides useful for treating, preventing and ameliorating allergic diseases, comprising an isolated surface exposed group of a specific domain from immunoglobulin E  
XX  
CC: The present invention describes a peptide (I) comprising an isolated surface exposed group/epitope (II) of C-epitope-2 domain (D) of immunoglobulin E (IgE), or its mimotope. Also described are: (i) an immunogen (II) for treating allergy comprising (i); (2) a vaccine (III) for treating allergy comprising (i); (3) a ligand (IV) capable of recognising (i); (4) a pharmaceutical composition (PC) comprising (IV); (5) a peptide (I) capable of being recognised by (IV); (6) an immunogen (I) comprising (I) and (II) producing (III) by producing (III); (i) can have anti-allergic and immunosuppressive activities, and can be used as a vaccine and histamine release inhibitor. (i), (ii) and (iii) are useful in medicine and in the manufacture of medicaments for treating and preventing allergies. (iv) is useful for identifying microscopes of PL in medicine and also in manufacturing medicaments for treating allergies. (v) is useful in diagnostics and in the affinity purification of (i) using anti (i) antibodies from blood. (i), (ii) and (iii) are useful for treating a patient susceptible to or suffering from allergies. (iv) is also useful in diagnosing atopy. AA25972 to AA26099 represent peptide sequences which are used in the exemplification of the present invention.



PF 17-AUG-2003; 2003WO-EP09576.  
 XX  
 PF 22-AUG-2003; 2003EP-0020717.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 PF Friede M, Mason S, Turnell WJ, Virals Bassols YC.  
 XX WPI: 2002-459648/52.  
 XX  
 PF Conjugate for use in vaccine for treatment of allergic conditions  
 PF disulfide bridge cyclized peptide and immunogen carrier  
 XX  
 PS Claim 4; Page 16; 45pp; English.  
 XX  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 CC  
 SQ Sequence 14 AA;  
 Query Match 59.5%; Score 69; DR 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.6319;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CY 1 CLEDGQWMDVC 12  
 DB 1 CLEDGQWMDVC 14  
 RESULT 11  
 AAB25914  
 ID AAB25914 standard; peptide; 13 AA.  
 XX  
 AC AAB25914.  
 XX  
 DT 35-CAN-2001 (first entry)  
 XX  
 DE Antiallergy peptide minitope sequence SEQ ID NO:11.  
 XX  
 KW Immunoglobulin E (IgE) immunogen; immunogen; protein; protein;  
 KW protein; cancer; Haemophilus influenzae; vaccine; vaccine; disease;  
 KW malaria; cytostatic; anti-allergic; anti-allergic; anti-allergic;  
 KW protein; cancer; Alzheimer's disease; allergy  
 XX  
 OS Homo sapiens.  
 XX  
 PF Key location/Qualifiers  
 PF Modified site 11  
 PF Note= "amidated"  
 XX  
 PF 31-AUG-2003; 2003WO-EP01457.  
 XX  
 PF 25-FEB-1999; 93GB-0004405.  
 XX  
 PF 25-FEB-1999; 93GB-0004408.  
 PF 25-FEB-1999; 93GB-0004412.  
 PF 13-AUG-1999; 93GB-0019260.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PF Coste M, Lobet Y, Van Vechelen WJ, Verhaert J.  
 XX  
 PF WPI: 2000-572040/53.  
 XX  
 PF Immunogens and vaccine comprising the group per se used in the treatment  
 PF and treating infectious diseases of malaria and other diseases and

PF cancer, comprises peptide and carrier from protein D of influenzae  
 XX  
 PS Claim 10; Page 38; 33pp; English.  
 XX  
 CC The present invention describes an immunogen (I) comprising a peptide  
 CC (Ia) and a carrier (II) derived from protein D of Haemophilus influenzae  
 CC or its fragment. Also described are: (1) a vaccine comprising (I), and  
 CC an excipient; (2) preparation of (I), comprising conjugating a peptide  
 CC to protein D or its fragment; and (3) preparation of a vaccine of (I),  
 CC comprising formulating (I) with an excipient. (I) has cytostatic,  
 CC antiallergic, neurotropic, neuroprotective and protozoicidal activities.  
 CC (I) and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (I) induces high levels of anti-peptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC minitope peptide sequence, which can be used in an immunogen of the  
 CC present invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 51.7%; Score 60; DR 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CY 1 CLEDGQWMDVC 11  
 DB 1 CLEDGQWMDVC 11  
 RESULT 12  
 AAB25914  
 ID AAB25914 standard; Peptide; 13 AA.  
 XX  
 AC AAB25914.  
 XX  
 DT 35-CAN-2001 (first entry)  
 XX  
 DE Pl minitope peptide PT15 SEQ ID NO:8.  
 XX  
 KW Epitope; minitope; human; immunoglobulin E; IgE; C-peptide-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; anti-allergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.  
 XX  
 PF W0200505460-A1.  
 XX  
 PF 31-AUG-2003.  
 XX  
 PF 22-FEB-2003; 2003WO-EP01455.  
 XX  
 PF 25-FEB-1999; 93GB-0004405.  
 PF 25-MAR-1999; 93GB-0001151.  
 PF 07-MAY-1999; 93GB-0010537.  
 PF 07-MAY-1999; 93GB-0010538.  
 PF 07-AUG-1999; 93GB-0018594.  
 PF 07-AUG-1999; 93GB-0018603.  
 PF 07-SEP-1999; 93GB-0021046.  
 PF 29-SEP-1999; 93GB-0021047.  
 PF 29-OCT-1999; 93GB-0025619.  
 PF 23-NOV-1999; 93GB-0027698.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PF Dyson M, Friede M, Greenwood J, Hewitt E, Lament A, Mason S,  
 PF Sandall R, Turnell WJ, Van Vechelen WJ, Virals De Bassols YC.  
 XX  
 PF WPI: 2001-072071/54.  
 XX







```

1 FILE REFERENCE: 4564/9179
2 CURRENT APPLICATION NUMBER: US/10/102,076
3 CURRENT FILING DATE: 2003-02-21
4 PRIOR APPLICATION NUMBER: 10780,249
5 PRIOR FILING DATE: 2002-02-21
6 PRIOR APPLICATION NUMBER: 10782,019
7 PRIOR FILING DATE: 2002-02-22
8 NUMBER OF SEQ ID NOS: 128
9 SOFTWARE: Patent in version 3.2
10 SEQ ID NO: 136
11 LENGTH: 12
12 TYPE: EST
13 ORGANISM: Homo sapiens
14 US 10 372 076 136

Query Match
Best Local Similarity: 42.8% Score 43 DB 149 Length 127
Matches: 9 Conservative 12 Mismatches 6 Gaps 0

QY 2 LEDGQWMLV 11
DB 1 MEDGQWMLV 10

RESULT 1
US 10 082 014 271
Sequence 271 Application US/10/82014
Publication No. US2003/018-858A1
GENERAL INFORMATION
APPLICANT: BUCKLE, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HRC TUMOR PATTERNS CHARACTERIZED WITH AN N TERMINAL CY
FILE REFERENCE: 100 130 0 4564/95124
CURRENT APPLICATION NUMBER: US/10/24,114
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/2930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 296
SOFTWARE: Patent in version 3.2
SEQ ID NO: 271
LENGTH: 12
TYPE: EST
ORGANISM: Homo sapiens
US 10 082 014 271

Query Match
Best Local Similarity: 40.8% Score 42 DB 149 Length 127
Matches: 9 Conservative 12 Mismatches 6 Gaps 0

QY 4 LEDGQWMLV 11
DB 1 MEDGQWMLV 10

RESULT 4
US 10 372 076 136
Sequence 136 Application US/10/372076
Publication No. US2003/108456A1
GENERAL INFORMATION
APPLICANT: Lipp, Mark
TITLE OF INVENTION: STABILIZED HRC TUMOR CARCINOGENIC HEPATOC
FILE REFERENCE: 1564/9179
CURRENT APPLICATION NUMBER: US/10/372076
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10780,249
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10782,019
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patent in version 3.2
SEQ ID NO: 136
LENGTH: 12
TYPE: EST
ORGANISM: Homo sapiens
US 10 372 076 136

Query Match
Best Local Similarity: 48.4% Score 45 DB 127 Length 107
Matches: 9 Conservative 12 Mismatches 6 Gaps 0

QY 4 LEDGQWMLV 11
DB 1 MEDGQWMLV 10

RESULT 6
US 10 225 567A 1497
Sequence 1497 Application US/10/225567A
Publication No. US2003/11399A1
GENERAL INFORMATION
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Palmer, Emma C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 1901 4 4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 1998-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patent in version 3.1
SEQ ID NO: 1497
LENGTH: 17
TYPE: EST
ORGANISM: Homo sapiens
US 10 225 567A 1497

```

Query Match 31.0% Score 16; DB 16; Length 16;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 CPKALSGD 20  
 DB 1 CPKALSGD 9

RESULT 7

US-06-927-919-62  
 ; Sequence 62, Application US/289233;  
 ; Publication No. US600306642A;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: GIALGER, David J.  
 ; TITLE OF INVENTION: Compounds and methods to inhibit or  
 ; TITLE OF INVENTION: augment an inflammatory response.  
 ; FILE REFERENCE: 295.022051;  
 ; CURRENT APPLICATION NUMBER: US/08/927-919  
 ; CURRENT FILING DATE: 1997-09-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: FASTSEQ for Windows Version 1.0  
 ; SEQ ID NO 62  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-06-927-919-62

Query Match 29.3% Score 14; DB 14; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 QVMDVCPREA 16  
 DB 5 RINQCPREA 15

RESULT 8

US-10-105-232-368  
 ; Sequence 368, Application US/10105212  
 ; Publication No. US20030180328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
 ; FILE REFERENCE: 09425-46904  
 ; CURRENT APPLICATION NUMBER: US/10/105-232  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/363,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/146,755  
 ; PRIOR FILING DATE: 1998-09-04  
 ; PRIOR APPLICATION NUMBER: 09/817,144  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 08/198,139  
 ; PRIOR FILING DATE: 1994-02-17  
 ; NUMBER OF SEQ ID NOS: 535  
 ; SOFTWARE: Patent 2.1  
 ; SEQ ID NO 368  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-232-368

Query Match 28.9% Score 13.5; DB 12; Length 16;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 1;

QY 3 EDGQVMDVCPREAAEGDK 21

DB 1 KDS- -DKNCTIECAQGGK 16

RESULT 9

US-10-105-437-375  
 ; Sequence 375, Application US/10189437  
 ; Publication No. US20030194414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE  
 ; FILE REFERENCE: 09425-46905  
 ; CURRENT APPLICATION NUMBER: US/10/189-437  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 10/105,232  
 ; PRIOR FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 09/984,057  
 ; PRIOR FILING DATE: 2001-10-26  
 ; PRIOR APPLICATION NUMBER: 60/303,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 729  
 ; SOFTWARE: Patent 2.1  
 ; SEQ ID NO 375  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-437-375

Query Match 28.9% Score 33.5; DB 12; Length 16;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 3 EDGQVMDVCPREAAEGDK 21  
 DB 1 KDS- -DKNCTIECAQGGK 16

RESULT 10

US-10-105-232-367  
 ; Sequence 367, Application US/10105212  
 ; Publication No. US20030180328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
 ; FILE REFERENCE: 09425-46904  
 ; CURRENT APPLICATION NUMBER: US/10/105-232  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/363,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/146,755  
 ; PRIOR FILING DATE: 1998-09-04  
 ; PRIOR APPLICATION NUMBER: 09/817,144  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 08/198,139  
 ; PRIOR FILING DATE: 1994-02-17  
 ; NUMBER OF SEQ ID NOS: 535  
 ; SOFTWARE: Patent 2.1  
 ; SEQ ID NO 367  
 ; LENGTH: 21  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-232-367

Query Match 28.9% Score 33.5; DB 12; Length 21;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 3; Gaps 1;



```

QY      3  EGGQNDVCCPREAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-4
RESULT 11
? Sequence 4, Application US/101894/7
? Publication No. US20030194414A
? GENERAL INFORMATION:
? APPLICANT: BOOCH, SAMUEL
? TITLE OF INVENTION: REP/TKIN PEPTIDES AND ANTIBODIES IN VACCINATION AGAINST
? FILE REFERENCE: 09425/4609
? CURRENT APPLICATION NUMBER: US/101894/7
? PRIOR FILING DATE: 2002-07-08
? PRIOR APPLICATION NUMBER: 10105,212
? PRIOR FILING DATE: 2002-03-26
? PRIOR APPLICATION NUMBER: 097984,067
? PRIOR FILING DATE: 2001-10-26
? PRIOR APPLICATION NUMBER: 602304,396
? PRIOR FILING DATE: 2001-07-09
? PRIOR APPLICATION NUMBER: 602278,763
? PRIOR FILING DATE: 2001-03-27
? NUMBER OF SEQ ID NOS: 729
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 374
? LENGTH: 21
? TYPE: PRT
? ORGANISM: Plasmodium falciparum
US-10-236-091-4
Query Match      28.4% Score 13; DB 12; Length 15;
Best Local Similarity 42.1%; Pred. No. 1.6e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 1;

QY      3  EGGQNDVCCPREAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-4
RESULT 12
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-4
Query Match      28.4% Score 13; DB 12; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-4
RESULT 13
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 4
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-4
Query Match      28.4% Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-4
RESULT 14
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 2
? LENGTH: 16
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-2
Query Match      28.4% Score 13; DB 12; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-2
RESULT 15
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-3
Query Match      28.4% Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-3
RESULT 16
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-3
Query Match      28.4% Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : KGG  DTXTLECAQGGK 16

US-10-236-091-3
RESULT 17
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, MARC
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HEV-K18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195,506
? CURRENT APPLICATION NUMBER: US/10236091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-3
Query Match      28.4% Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e-02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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1 Sequence 2 : Application US/09526290
2 Patent No. US20020164658A1
3 GENERAL INFORMATION:
4 APPLICANT: Duhem, L. Kathryn
5 APPLICANT: Friedman, David L.
6 APPLICANT: Herath, Herath Mudiyatunga Arundha (Sri Lanka)
7 APPLICANT: Kimbel, Linda H.
8 APPLICANT: Parakh, Rakesh Bhikhu
9 APPLICANT: Pottier, David M.
10 APPLICANT: Rehiff, Christian
11 APPLICANT: Silber, R. Michael
12 APPLICANT: Stager, Thomas R.
13 APPLICANT: Sunderland, P. Trey
14 APPLICANT: Townsend, Robert Reid
15 APPLICANT: White, Frost
16 APPLICANT: Williams, Stephen A.
17 TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
18 Title of Invention: Uses Thereof, Including Diagnosis and Treatment of
19 Title of Invention: Alzheimer's Disease
20 FILE REFERENCE: 2572-1-C01 N2
21 CURRENT APPLICATION NUMBER: US/99/824,133
22 CURRENT FILING DATE: 2001-04-30
23 PRIOR APPLICATION NUMBER: US 60/194,104
24 PRIOR FILING DATE: 2000-04-03
25 PRIOR APPLICATION NUMBER: US 60/253,043
26 PRIOR FILING DATE: 2000-11-28
27 NUMBER OF SEQ ID NOS: 492
28 SOFTWARE: FastSeq for Windows Version 4.0
29 SEQ ID NO 25
30 LKNTSL 12
31 TYPE: PRT
32 ORGANISM: homo sapien
33 NC_008062.13.25
34
35 Query Watch 28.03 Score 100.00 100.00 100.00
36 Best Local Similarity 66.7% Pred. NO 1.500000
37 Matches 81 Conservative 17 Mismatches 51 Indels 10 Gaps 17
38
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Search completed: November 5, 2003, 06:44:15  
 Job time: 1:10 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw-mat-1

Run on: November 5, 2003, 18:27:28 / Search time (h:m:s): 0:00:00  
without alignment  
19,223 William cell lines/sec

Title: US-09-914-088-16

Patent score: 116

Sequence: 1 CLEDIQVMDVDCPRAAEKXK 21

Scoring table: PLOSUM2

Gapop 15.0, Gapext 0.5

Seatched: 428757 seqs, 30991878 residues

Total number of hits satisfying chosen parameters: 944,000

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database: Pending Patents, AA-Mat \*
- 1: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 2: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 3: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 4: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 5: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 6: /cgn2\_6/prodata/1/paa/US076 US Pat \*
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  - 8: /cgn2\_6/prodata/1/paa/US076 US Pat \*
  - 9: /cgn2\_6/prodata/1/paa/US076 US Pat \*
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  - 12: /cgn2\_6/prodata/1/paa/US076 US Pat \*
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  - 28: /cgn2\_6/prodata/1/paa/US076 US Pat \*
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  - 32: /cgn2\_6/prodata/1/paa/US076 US Pat \*

Freq. No. is the number of results previously obtained with a score greater than or equal to the score of the current entry, and is derived by analysis of the whole database.

Summary:

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2	116	100.0	21	29 US-10-362-527-101
3	111	95.7	20	24 US-09-914-088-65
4	111	95.7	20	29 US-10-362-527-142
5	102.5	86.6	21	24 US-09-914-088-66
6	102.5	86.6	21	29 US-10-362-527-143
7	69	59.5	14	29 US-10-362-527-324
8	60	51.7	13	24 US-09-914-088-10
9	60	51.7	13	24 US-09-914-088-8
10	60	51.7	13	24 US-09-914-088-11
11	60	51.7	13	29 US-10-362-527-8
12	60	51.7	13	29 US-10-362-527-96
13	60	51.7	13	29 US-10-362-527-326
14	60	51.7	20	29 US-09-914-088-15
15	60	51.7	20	29 US-10-362-527-100
16	60	51.7	20	29 US-10-362-527-328
17	51	44.0	10	24 US-09-914-088-23
18	51	44.0	10	29 US-10-362-527-12
19	51	44.0	13	24 US-09-914-088-10
20	51	44.0	13	29 US-10-362-527-10
21	50	43.1	13	29 US-10-362-527-325
22	49	42.2	10	26 US-10-082-014-282
23	49	42.2	10	29 US-10-372-076-136
24	47	40.5	9	24 US-09-914-088-5
25	47	40.5	9	24 US-09-914-088-1
26	47	40.5	9	24 US-10-082-014-273
27	47	40.5	9	29 US-10-362-527-1
28	47	40.5	9	29 US-10-372-076-127
29	45	38.9	10	27 US-10-144-188-55
30	43.5	37.5	19	24 US-09-914-088-62
31	43.5	37.5	13	29 US-10-362-527-139
32	42.5	36.6	19	24 US-09-914-088-64
33	42.5	36.6	19	29 US-10-362-527-141
34	38.5	33.2	19	24 US-09-914-088-61
35	38.5	33.2	19	29 US-10-362-527-138
36	37.5	32.3	19	24 US-09-914-088-55
37	37.5	32.3	19	29 US-10-362-527-132
38	37	31.9	17	12 US-08-821-827-8
39	37	31.9	17	12 US-08-821-827-8
40	36.5	31.5	19	24 US-09-914-088-56
41	36.5	31.5	19	24 US-09-914-088-60
42	36.5	31.5	19	29 US-10-362-527-133
43	36.5	31.5	19	29 US-10-362-527-137
44	36	31.5	16	29 US-10-325-567A-127
45	36	31.5	16	29 US-10-325-567A-127

REFERENCES

- RESULT 1
- US-09-914-088-16
- 1 Sequence 16, Application US/09914088
  - 1 GENERAL INFORMATION:
  - 1 APPLICANT: DYSON, Michael
  - 1 APPLICANT: Fiedler, Martin
  - 1 APPLICANT: Greenwood, Judith
  - 1 APPLICANT: Hewitt, Ellen
  - 1 APPLICANT: Lamont, Sean
  - 1 APPLICANT: Mason, Sean
  - 1 APPLICANT: Randall, Roger
  - 1 APPLICANT: Turner, William Gordon
  - 1 APPLICANT: Van Nochemen, Marcelle Paulette
  - 1 APPLICANT: Vinals y de Bassols, Carola
  - 1 TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
  - 1 TITLE OF INVENTION: C-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their
  - 1 TITLE OF INVENTION: Therapeutic Uses
  - 1 FILE REFERENCE: BASF 12
  - 1 CURRENT APPLICATION NUMBER: US/09/914,088
  - 1 CURRENT FILING DATE: 2001-08-02
  - 1 PRIOR APPLICATION NUMBER: US/0044048-9
  - 1 PRIOR FILING DATE: 1997-02-25
  - 1 PRIOR APPLICATION NUMBER: US/98-04-011-6
  - 1 PRIOR FILING DATE: 1997-13-29

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1 PRIOR APPLICATION NUMBER: GB 9910537.1
2 PRIOR FILING DATE: 1999-05-07
3 PRIOR APPLICATION NUMBER: GB 9910538.9
4 PRIOR FILING DATE: 1999-05-07
5 PRIOR APPLICATION NUMBER: GB 9918594.4
6 PRIOR FILING DATE: 1999-08-07
7 PRIOR APPLICATION NUMBER: GB 9918603.3
8 PRIOR FILING DATE: 1999-08-07
9 NUMBER OF SEQ ID NOS: 193
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 16
12 TYPE: PRT
13 LENGTH: 20
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Chimeric
17
18 us-09-914-088-16
19
20 Query Match 100.0% Score 116; DB 24; Length 20;
21 Best Local Similarity 100.0%; Pred. No. 3.9e-11;
22 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23
24 QY 1 CLEGGQWVDCPFEAAEGD 21
25 ||| ||||| |||||
26 1 CLEGGQWVDCPFEAAEGD 21
27
28 RESULT 2
29 US-10-162-527-142
30 Sequence 142; Application US/10162527
31 GENERAL INFORMATION:
32 APPLICANT: Friede, Martin
33 APPLICANT: Tarnelli, William Gordon
34 APPLICANT: Vinals Y De Bassols, Carlota
35 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
36 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
37 FILE REFERENCE: B45236
38 CURRENT APPLICATION NUMBER: US/10162527
39 PRIOR FILING DATE: 2003-02-21
40 PRIOR APPLICATION NUMBER: PCT/EP01/69576
41 PRIOR FILING DATE: 2001-06-17
42 PRIOR APPLICATION NUMBER: GB 0020717.5
43 PRIOR FILING DATE: 2000-08-22
44 NUMBER OF SEQ ID NOS: 128
45 SOFTWARE: FastSeq for Windows Version 4.0
46 SEQ ID NO: 101
47 LENGTH: 21
48 TYPE: PRT
49 ORGANISM: Artificial Sequence
50 FEATURE:
51 OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
52 US-10-162-527-142
53
54 Query Match 100.0% Score 116; DB 24; Length 21;
55 Best Local Similarity 100.0%; Pred. No. 3.9e-11;
56 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
57
58 QY 1 CLEGGQWVDCPFEAAEGD 21
59 ||| ||||| |||||
60 1 CLEGGQWVDCPFEAAEGD 21
61
62 RESULT 3
63 US-09-914-088-16
64 Sequence 65; Application US/09914088
65 GENERAL INFORMATION:
66 APPLICANT: Dyson, Michael
67 APPLICANT: Friede, Martin
68 APPLICANT: Greenwood, Cudity
69 APPLICANT: Rawlitt, Ellen
70 APPLICANT: Lamont, Alan
71 APPLICANT: Vinals, Sean
72
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1 APPLICANT: Randall, Roger
2 APPLICANT: Tarnelli, William Gordon
3 APPLICANT: Vinals Y De Bassols, Carlota
4 TITLE OF INVENTION: Epitopes of Mimotopes Derived from the
5 TITLE OF INVENTION: C-Epsilon-2 Domain of IgE, Antagonists Thereof, and their
6 FILE REFERENCE: B45132
7 CURRENT APPLICATION NUMBER: US/09/914,088
8 CURRENT FILING DATE: 2001-08-22
9 PRIOR APPLICATION NUMBER: GB 9904485.9
10 PRIOR FILING DATE: 1999-02-25
11 PRIOR APPLICATION NUMBER: GB 9907151.6
12 PRIOR FILING DATE: 1999-03-29
13 PRIOR APPLICATION NUMBER: GB 9910537.1
14 PRIOR FILING DATE: 1999-05-07
15 PRIOR APPLICATION NUMBER: GB 9910538.9
16 PRIOR FILING DATE: 1999-05-07
17 PRIOR APPLICATION NUMBER: GB 9918594.4
18 PRIOR FILING DATE: 1999-08-07
19 PRIOR APPLICATION NUMBER: GB 9918603.3
20 PRIOR FILING DATE: 1999-08-07
21 NUMBER OF SEQ ID NOS: 193
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO: 65
24 LENGTH: 20
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Chimeric
29
30 us-09-914-088-16
31
32 Query Match 95.7% Score 111; DB 24; Length 20;
33 Best Local Similarity 100.0%; Pred. No. 3.9e-10;
34 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
35
36 QY 1 CLEGGQWVDCPFEAAEGD 20
37 ||| ||||| |||||
38 1 CLEGGQWVDCPFEAAEGD 20
39
40 RESULT 4
41 US-10-162-527-142
42 Sequence 142; Application US/10162527
43 GENERAL INFORMATION:
44 APPLICANT: Friede, Martin
45 APPLICANT: Masch, Sean
46 APPLICANT: Tarnelli, William Gordon
47 APPLICANT: Vinals Y De Bassols, Carlota
48 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
49 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
50 FILE REFERENCE: B45236
51 CURRENT APPLICATION NUMBER: US/10162527
52 CURRENT FILING DATE: 2003-02-21
53 PRIOR APPLICATION NUMBER: PCT/EP01/69576
54 PRIOR FILING DATE: 2001-06-17
55 PRIOR APPLICATION NUMBER: GB 0020717.5
56 PRIOR FILING DATE: 2000-08-22
57 NUMBER OF SEQ ID NOS: 128
58 SOFTWARE: FastSeq for Windows Version 4.0
59 SEQ ID NO: 142
60 LENGTH: 20
61 TYPE: PRT
62 ORGANISM: Artificial Sequence
63 FEATURE:
64 OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
65 US-10-162-527-142
66
67 Query Match 95.7% Score 111; DB 29; Length 20;
68 Best Local Similarity 100.0%; Pred. No. 3.9e-10;
69 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
70
71 QY 1 CLEGGQWVDCPFEAAEGD 20
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
US-10-362-527-143

Query Match      86.6%; Score 100.5; DB 29; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.0012;
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

CY 1 CLEGGQWMDVLCPREAEGD 20
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DB 1 CLEGGQWMDVLCPREAEGD 21

RESULT 7
US-10-362-527-324
; Sequence 324, Application US/10362527
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mascon, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
US-10-362-527-324

Query Match      89.5%; Score 69; DB 29; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CLEGGQWMDVLC 12
   |||||  |||||
DB 3 CLEGGQWMDVLC 14

RESULT 8
US-09-914-080-10
; Sequence 10, Application US/09914080
; GENERAL INFORMATION:
; APPLICANT: Coste, Michel
; APPLICANT: Lobet, Yves
; APPLICANT: Van Wecheler, Marcelle Paulette
; APPLICANT: Verriest, Christophe
; TITLE OF INVENTION: Immunogens Comprising a Peptide and a
; TITLE OF INVENTION: Carrier Derived from H. Influenzae Protein D
; FILE REFERENCE: B45171
; CURRENT APPLICATION NUMBER: US/09/914,080
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 9904412.5
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9904408.3
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
US-10-362-527-143

Query Match      86.6%; Score 100.5; DB 29; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.0012;
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

CY 1 CLEGGQWMDVLCPREAEGD 20
   |||||  |||||  |||||
DB 1 CLEGGQWMDVLCPREAEGD 21

RESULT 6
US-10-362-527-143
; Sequence 143, Application US/10362527
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mascon, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-09-914-089-66

Query Match      86.6%; Score 100.5; DB 29; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.0012;
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

CY 1 CLEGGQWMDVLCPREAEGD 20
   |||||  |||||  |||||
DB 1 CLEGGQWMDVLCPREAEGD 21

RESULT 5
US-09-914-088-66
; Sequence 66, Application US/09914088
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judith
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mascon, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Wecheler, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of Ige Antigenic Therof, and Their
; TITLE OF INVENTION: Therapeutic Uses
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/09/914,088
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910533.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910438.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918494.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918604.4
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-09-914-089-66
```

? PRIOR APPLICATION NUMBER: GB 9919260.1  
 ? PRIOR FILING DATE: 1999-08-13  
 ? PRIOR APPLICATION NUMBER: 09/719,179  
 ? PRIOR FILING DATE: 1999-05-28  
 ? PRIOR APPLICATION NUMBER: PCT/US99/11980  
 ? PRIOR FILING DATE: 1999-05-28  
 ? PRIOR APPLICATION NUMBER: GB 9812613.3  
 ? PRIOR FILING DATE: 1998-06-11  
 ? NUMBER OF SEQ ID NOS: 19  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO: 10  
 ? LENGTH: 13  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Chimeric  
 US 09-914-088 10

Query Match 51.7%; Score 60; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pct. Id. 100%;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDV 11  
 DB 1 CLEGGQVMDV 11

RESULT 9

US-09-914-088-8

Sequence 4, Application US/09914088

GENERAL INFORMATION:

? APPLICANT: Dyson, Michael  
 ? APPLICANT: Friede, Martin  
 ? APPLICANT: Greenwood, Judith  
 ? APPLICANT: Hewitt, Ellen  
 ? APPLICANT: Lamont, Alan  
 ? APPLICANT: Mason, Sean  
 ? APPLICANT: Randall, Roger  
 ? APPLICANT: Turneil, William Gordon  
 ? APPLICANT: Van Mechelen, Marcelle Paulette  
 ? APPLICANT: Vinals y de Bassols, Carlota  
 ? TITLE OF INVENTION: Epitopes or Mimotopes Derived from the  
 ? TITLE OF INVENTION: 2-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their  
 ? FILE REFERENCE: B4-112  
 ? CURRENT APPLICATION NUMBER: US/09/914,088  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR APPLICATION NUMBER: GB 9904405.9  
 ? PRIOR FILING DATE: 1999-02-25  
 ? PRIOR APPLICATION NUMBER: GB 9907151.6  
 ? PRIOR FILING DATE: 1999-03-29  
 ? PRIOR APPLICATION NUMBER: GB 9910538.9  
 ? PRIOR FILING DATE: 1999-05-07  
 ? PRIOR APPLICATION NUMBER: GB 9918594.4  
 ? PRIOR FILING DATE: 1999-08-07  
 ? PRIOR APPLICATION NUMBER: GB 9918603.3  
 ? NUMBER OF SEQ ID NOS: 193  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO: 11  
 ? LENGTH: 11  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Chimeric  
 US 09-914-088-11

Query Match 51.7%; Score 60; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pct. Id. 100%;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDV 11  
 DB 1 CLEGGQVMDV 11

RESULT 11

US-10-362-527-8

Sequence 8, Application US/10362527

GENERAL INFORMATION:

? APPLICANT: Friede, Martin  
 ? APPLICANT: Mason, Sean  
 ? APPLICANT: Turneil, William Gordon  
 ? APPLICANT: Vinals y de Bassols, Carlota  
 ? TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptid  
 ? TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
 ? FILE REFERENCE: B4-112  
 ? CURRENT APPLICATION NUMBER: US/10/362,527  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR APPLICATION NUMBER: PCT/EP01/09596  
 ? PRIOR FILING DATE: 2001-08-17  
 ? PRIOR APPLICATION NUMBER: GB 982819.5  
 ? PRIOR FILING DATE: 1998-06-11

```

: NUMBER OF SEQ ID NOS: 328
: SOFTWARE: FASTSEQ for Windows Version: 4.0
: SEQ ID NO: 6
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Homo sapiens
: 1-10-162 527-9

```

Query Match	51.78	Score 10	DB 24	Length 10
Best local Similarity	100.00	Cpred. No. 5.000		
Matches 10	Conservative 0	Mismatches 0	Indels 0	Misses 0

cy  
; CUEGGQVNDV I:  
||  
; CUEEGVAVMDV I:  
|||

```

RESULT 12
US/10-162-507-96
Sequence 96, Application US/1036527
GENERAL INFORMATION:
APPLICANT: Filide, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnelly, William Gordon
APPLICANT: Vinals, Jeaneels, Carlotta
TITLE OF INVENTION: Vaccine Immunogens of
TITLE OF INVENTION: and Use Thereof in
FILE REFERENCE: 845136
CURRENT APPLICATION NUMBER: US/10362796
PRIORITY FILING DATE: 2003-02-21
PRIORITY APPLICATION NUMBER: PCT/EP01/01576
PRIORITY FILING DATE: 2001-08-27
PRIORITY APPLICATION NUMBER: GB 0002713
PRIORITY FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 96
LENGTH: 13
TYPE: PNT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial variant of
US/10-162-507-96

```

Geary March	51.0%	Scarcely different	51.0%
Best local Similarity	100.0%	Full	100.0%
Matches 11; Conservative	0	Matched	0

Q: C T E D J O W N M E D 1 1  
Q: C T E D J O W N M E D 1 1

```

1 RESULT 13
2 US 10-362 67-326
3 1 Sequence 126, Application US/10362527
4 2 GENERAL INFORMATION:
5 3 APPLICANT: Friede, Martin
6 4 APPLICANT: Mason, Sean
7 5 APPLICANT: Turner, William Gordon
8 6 APPLICANT: Vinals, De Bassols, Carola
9 7 TITLE OF INVENTION: Vaccine Immunogenes
10 8 TITLE OF INVENTION: and Use Thereof in a
11 9 FILE REFERENCE: B45216
12 10 CURRENT APPLICATION NUMBER: US/10362527
13 11 CURRENT FILING DATE: 2003-03-21
14 12 PRIORITY APPLICATION NUMBER: FC78EP01/2003-07
15 13 PRIORITY FILING DATE: 2001-08-17
16 14 PRIORITY APPLICATION NUMBER: GR 02071716
17 15 PRIORITY FILING DATE: 2000-08-22
18 16 NUMBER OF SEQ. IN NOS: 128
19 17 SOFTWARE PASSED FOR WINDOWS VERSION: 1.0
20 18 SEQ. ID NO: 136

```

```

: LENGTH: 16
:
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
:
: OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide
US-10-362-527-324

```

```
Query Match      51.74; Score 60; DB 29; Length 16;
Best Local Similarity 100.00; P-Val. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy : CLEDGOMVEU 11  
: 111111  
Qb : CLEDGOMVEU 11

```

1 RESULT: 14
2 US-09-914-088-15
3 Sequence 15, Application US-09914088
4 GENERAL INFORMATION:
5 APPLICANT: Dyson, Michael
6 APPLICANT: Friede, Martin
7 APPLICANT: Greenwood, Judith
8 APPLICANT: Hewitt, Ellen
9 APPLICANT: Lambert, Alan
10 APPLICANT: Mason, Sean
11 APPLICANT: Raddall, Roger
12 APPLICANT: Turcotte, William Gordon
13 APPLICANT: Van Nethelen, Marcelle Fialette
14 APPLICANT: Vinals y de Bassols, Carlotia
15 TITLE OF INVENTION: Epitopes or Microtopes Derived from the
16 TITLE OF INVENTION: C-Esillon 2 Domain of TgE, Antagonists Thereof, and Their
17 TITLE OF INVENTION: Therapeutic Uses
18 FILE REFERENCE: B45172
19 CURRENT APPLICATION NUMBER: US09/914,088
20 CURRENT FILING DATE: 2001-08-22
21 PRIOR APPLICATION NUMBER: GB 9804400-9
22 PRIOR FILING DATE: 1999-02-25
23 PRIOR APPLICATION NUMBER: GB 980751-6
24 PRIOR FILING DATE: 1999-03-29
25 PRIOR APPLICATION NUMBER: GB 9910597-1
26 PRIOR FILING DATE: 1999-05-07
27 PRIOR APPLICATION NUMBER: GB 9910598-9
28 PRIOR FILING DATE: 1999-05-07
29 PRIOR APPLICATION NUMBER: GB 9918994-4
30 PRIOR FILING DATE: 1999-08-09
31 PRIOR APPLICATION NUMBER: GB 9918993-3
32 PRIOR FILING DATE: 1999-08-07
33 NUMBER OF SEQ ID NOS: 193
34 SOFTWARE: FastSeq for Windows Version 4.0
35 SEQ ID NO 15
36 LENGTH: 20
37 TYPE: PRT
38 ORGANISM: Artificial Sequence
39 FEATURE:
40 OTHER INFORMATION: Chimeric
41 US-09-914-088-15

```

Query Match:	51.7%	Score: 60	DB: 24	Length: 20
Best Local Similarity:	100.0%	Pred. No.: 0.05		
Matches: 11	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0

Qy 1 CLEGGQVMDVE 11  
|||  
Qc 1 CLEGGQVMDVE 11

```

RESULT 15
US 10-362-127 100
; Sequence 100, Application US/10-362-127
; GENERAL INFORMATION
; APPLICANT: Friede, Mathis
; APPLICANT: Mason, Alan

```

```
1 APPLICANT: Tunnell, William Gordon
2 APPLICANT: Viana's Y De Bassols, Carlota
3 TITLE OF INVENTION: Vaccine Immunogens Comprising Disubstituted Peptides Cyclised Peptide
4 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
5 FILE REFERENCE: H45236
6 CURRENT APPLICATION NUMBER: US/10/362,527
7 PRIOR FILING DATE: 2003-02-21
8 PRIOR APPLICATION NUMBER: ECT/EP01/034506
9 PRIOR FILING DATE: 2001-08-17
10 PRIOR APPLICATION NUMBER: GB 0020771.5
11 PRIOR FILING DATE: 2000-08-22
12 NUMBER OF SEQ ID NOS: 328
13 SOFTWARE: FASTSEQ for Windows Version 4.0
14 SEQ ID NO: 100
15 LENGTH: 20
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Artificial variant of Hom. Superoxide Dismutase
20 US 10 362 527.100
21
22 Query Match: 51.7%; Score 63; DB: B, Length: 20
23 Best Local Similarity: 100.0%; Pred No. Gaps: 0
24 Mismatches: 11; Conservative: 0; Mismatches: 11; Indels: 0; Gaps: 0
25
26 07 1 CLEDSQVQVVD 11
27 1111111111
28 1 CLEDSQVQVVD 11
29
30 MATCH COMPUTED: November 5, 2003, 18:41:36
31 Elapsed Time: 0.065 sec
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GenCore version: 9.1.6  
Copyright (c) 1993 - 2001 CompuLink Ltd.

OX protein - protein search, using sw model

Run on: November 5, 2003, 18:16:39, search time: 21 seconds  
without alignment  
42,311 Million cell updates/sec

Title: US-09-914-088-16

Perfect score: 116  
Sequence: 1 CLEOQVMDVRCPRAEAGGX 21

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 421,0958 residues

Total number of hits satisfying chosen parameters: 1,593

Minimum DB seq length: 0  
Maximum DB seq length: 21

Post-processing: Minimum Match 0  
Maximum Match 100%  
Listing first 45 summaries

Database: Issue Patents AA\*  
1: /cgn2/6/prodata/1/aa/AA COMP Exp\*  
2: /cgn2/6/prodata/1/aa/AA COMP Exp\*  
3: /cgn2/6/prodata/1/aa/AA COMP Exp\*  
4: /cgn2/6/prodata/1/aa/AA COMP Exp\*  
5: /cgn2/6/prodata/1/aa/AA COMP Exp\*  
6: /cgn2/6/prodata/1/aa/AA COMP Exp\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Rank	Score	Query Match	Length	DB ID	Score	Length	DB ID
1	1	116	100%	21	US-09-914-088-16	116	21	US-09-914-088-16
2	2	115	100%	21	US-09-914-088-16	115	21	US-09-914-088-16
3	3	114	100%	21	US-09-914-088-16	114	21	US-09-914-088-16
4	4	113	100%	21	US-09-914-088-16	113	21	US-09-914-088-16
5	5	112	100%	21	US-09-914-088-16	112	21	US-09-914-088-16
6	6	111	100%	21	US-09-914-088-16	111	21	US-09-914-088-16
7	7	110	100%	21	US-09-914-088-16	110	21	US-09-914-088-16
8	8	109	100%	21	US-09-914-088-16	109	21	US-09-914-088-16
9	9	108	100%	21	US-09-914-088-16	108	21	US-09-914-088-16
10	10	107	100%	21	US-09-914-088-16	107	21	US-09-914-088-16
11	11	106	100%	21	US-09-914-088-16	106	21	US-09-914-088-16
12	12	105	100%	21	US-09-914-088-16	105	21	US-09-914-088-16
13	13	104	100%	21	US-09-914-088-16	104	21	US-09-914-088-16
14	14	103	100%	21	US-09-914-088-16	103	21	US-09-914-088-16
15	15	102	100%	21	US-09-914-088-16	102	21	US-09-914-088-16
16	16	101	100%	21	US-09-914-088-16	101	21	US-09-914-088-16
17	17	100	100%	21	US-09-914-088-16	100	21	US-09-914-088-16
18	18	99	100%	21	US-09-914-088-16	99	21	US-09-914-088-16
19	19	98	100%	21	US-09-914-088-16	98	21	US-09-914-088-16
20	20	97	100%	21	US-09-914-088-16	97	21	US-09-914-088-16
21	21	96	100%	21	US-09-914-088-16	96	21	US-09-914-088-16
22	22	95	100%	21	US-09-914-088-16	95	21	US-09-914-088-16
23	23	94	100%	21	US-09-914-088-16	94	21	US-09-914-088-16
24	24	93	100%	21	US-09-914-088-16	93	21	US-09-914-088-16
25	25	92	100%	21	US-09-914-088-16	92	21	US-09-914-088-16
26	26	91	100%	21	US-09-914-088-16	91	21	US-09-914-088-16
27	27	90	100%	21	US-09-914-088-16	90	21	US-09-914-088-16

ALIGNMENTS

RESULT 1  
US-08-821-827C-8  
Sequence 8, Application US/08821827C  
Patent No. 6297425  
GENERAL INFORMATION:  
APPLICANT: Scelorge, Christopher J.  
APPLICANT: Bidney, Dennis L.  
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM  
FILE REFERENCE: 0561A  
CURRENT APPLICATION NUMBER: US/08/821-827C  
CURRENT FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 8  
LENGTH: 17  
TYPE: PPT  
ORGANISM: Aspergillus phoenices  
US 08-821-827C-8

Query Match: 32.94, Score 17, DB 3, Length 17,  
Best Local Similarity: 42.64, Pred. No. 237  
Matches: 6, Conservative 5, Mismatches 4, Indels 0, Gaps 0

QY 2 LDEGQVMDVRCPRAEAGGX 16  
DB 2 LDEGQVMDVRCPRAEAGGX 16

RESULT 2  
US-09-290-202B-8  
Sequence 8, Application US/09290202B  
Patent No. 6133846  
GENERAL INFORMATION:  
APPLICANT: Scelorge, Christopher J.  
APPLICANT: Bidney, Dennis L.  
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM  
FILE REFERENCE: 0561C  
CURRENT APPLICATION NUMBER: US/09/290-202B  
CURRENT FILING DATE: 1999-04-12  
PRIOR APPLICATION NUMBER: 08/821-827  
PRIOR FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 17  
TYPE: PPT  
ORGANISM: Aspergillus phoenices  
US 09-290-202B-8

Patent No. 5202551  
Sequence 107, App  
Sequence 142, App  
Sequence 25, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 17, App  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 6, Appl  
Sequence 25, Appl  
Sequence 314, App  
Sequence 75, App  
Sequence 15, Appl  
Sequence 1, Appl



TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-052 P37.11

Query Match 26.7%; Score 31; DB 4; Length 12;  
Best Local Similarity 63.6%; Pred. No. 1.26+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 CLEDOGVNEDV 11

DB 1 CLEDTCKHEDV 11

RESULT 2

US-09-329-820-110  
Sequence 115, Application US/08329820  
Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: RIPPWANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: VERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /product= "Res-Lys-Roc"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 2

OTHER INFORMATION: /product= "Thr-Roc"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product= "Asp-Roc"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5  
OTHER INFORMATION: /product= "Cys-Tyr"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: /product= "Arg-Gly-Tyr"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /product= "Asn-Tyr"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "His-Tyr"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "Lys-Ile-Glu"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /product= "Gly-Orn"  
US-09-329-820-110

Query Match 26.7%; Score 31; DB 1; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1.26+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 11 CDPREAREG 19

DB 4 DCFNPHKG 12

RESULT 7

US-08-329-820-115

Sequence 115, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIPPWANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: VERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 115:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US:08 329-820-186

Query Match 26.7% Score 17 DB 17 Length 12  
Best Local Similarity 55.6% Pref No. 130-02  
Matches 5 Conservative 1 Mismatches 7 Gaps 0

QY 11 DFFEAAG 19  
DB 4 DFFPKHKS 12

RESULT 8

US:08 329-820-173

Sequence 173, Application US/08129812

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIEMANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.0 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1635

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDNESS

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROPHOBIC: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product= "Cys-Trip"

FEATURE:

NAME KEY: Modified-site

LOCATION: 12

OTHER INFORMATION: /product= "Cys-Trip"

US:08 329-820-186

Query Match 26.7% Score 17 DB 17 Length 12  
Best Local Similarity 55.6% Pref No. 130-02  
Matches 5 Conservative 1 Mismatches 7 Gaps 0

QY 11 DFFEAAG 19

DB 4 DFFPKHKS 12

RESULT 1

US:08 329-820-186

Sequence 186, Application US/0813820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIEMANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.0 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1635

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDNESS

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROPHOBIC: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product= "Cys-Trip"

FEATURE:

NAME KEY: Modified-site

LOCATION: 12

OTHER INFORMATION: /product= "Cys-Trip"

1 APPLICATION NUMBER: DE 4336758.5  
2 FILING DATE: 28-OCT-1993  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Hamlet-King, Diana  
5 REGISTRATION NUMBER: 33,302  
6 REFERENCE/DOCKET NUMBER: MERCK 1635  
7 TELEPHONE: 703-243-6333  
8 TELEFAX: 703-243-6410  
9 INFORMATION FOR SEQ ID NO: 187:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 12 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS:  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 HYPOTHETICAL: YES  
17 ANTI-SENSE: NO  
18 FRAGMENT TYPE: N-terminal  
19 FEATURE:  
20 NAME/KEY: Modified-site  
21 LOCATION: 5  
22 OTHER INFORMATION: /product= "CysMe"  
23 US-09-914-088-16

Query Match: 26.7% Score 31; DB 1; Length 12;  
Best Local Similarity 55.6% Pref No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19  
DB 4 DCFRNPHG 12

RESULT 11  
US-09-914-088-16  
1 Sequence 188, Application US/0932982  
2 Patent No. 5747457  
3 GENERAL INFORMATION:  
4 APPLICANT: JONCZYK, ALFRED  
5 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
6 APPLICANT: DIESENBRACH, BEATE  
7 APPLICANT: RIPPWANN, FRIEDRICH  
8 TITLE OF INVENTION: Linear Adhesion Inhibitors  
9 NUMBER OF SEQUENCES: 228  
10 COMPUTER READABLE FORM:  
11 MEDIA TYPE: floppy disk  
12 COMPUTER: IBM PC compatible  
13 OPERATING SYSTEM: PC-DOS/MS-DOS  
14 SOFTWARE: Patent In Release #1.0, Version #1.0  
15 CURRENT APPLICATION DATA:  
16 FILING DATE: 28-OCT-1993  
17 ATTORNEY/AGENT INFORMATION:  
18 NAME: Hamlet-King, Diana  
19 REGISTRATION NUMBER: 33,302  
20 REFERENCE/DOCKET NUMBER: MERCK 1635  
21 TELEPHONE: 703-243-6333  
22 TELEFAX: 703-243-6410  
23 INFORMATION FOR SEQ ID NO: 187:  
24 SEQUENCE CHARACTERISTICS:  
25 LENGTH: 12 amino acids  
26 TYPE: amino acid  
27 STRANDEDNESS:  
28 TOPOLOGY: linear  
29 MOLECULE TYPE: peptide  
30 HYPOTHETICAL: YES  
31 ANTI-SENSE: NO

1 FRAGMENT TYPE: N-terminal  
2 FEATURE:  
3 NAME/KEY: Modified-site  
4 LOCATION: 5  
5 OTHER INFORMATION: /product= "CysMe"  
6 US-09-914-088-16  
Query Match: 26.7% Score 31; DB 1; Length 12;  
Best Local Similarity 55.6% Pref No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19  
DB 4 DCFRNPHG 12

RESULT 12  
US-09-914-088-16  
1 Sequence 188, Application US/0932982  
2 Patent No. 5747457  
3 GENERAL INFORMATION:  
4 APPLICANT: JONCZYK, ALFRED  
5 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
6 APPLICANT: DIESENBRACH, BEATE  
7 APPLICANT: RIPPWANN, FRIEDRICH  
8 TITLE OF INVENTION: Linear Adhesion Inhibitors  
9 NUMBER OF SEQUENCES: 228  
10 COMPUTER READABLE FORM:  
11 MEDIA TYPE: floppy disk  
12 COMPUTER: IBM PC compatible  
13 OPERATING SYSTEM: PC-DOS/MS-DOS  
14 SOFTWARE: Patent In Release #1.0, Version #1.0 (EPC)  
15 CURRENT APPLICATION DATA:  
16 FILING DATE: 28-OCT-1993  
17 ATTORNEY/AGENT INFORMATION:  
18 NAME: Hamlet-King, Diana  
19 REGISTRATION NUMBER: 33,302  
20 REFERENCE/DOCKET NUMBER: MERCK 1635  
21 TELEPHONE: 703-243-6333  
22 TELEFAX: 703-243-6410  
23 INFORMATION FOR SEQ ID NO: 188:  
24 SEQUENCE CHARACTERISTICS:  
25 LENGTH: 12 amino acids  
26 TYPE: amino acid  
27 STRANDEDNESS:  
28 TOPOLOGY: linear  
29 MOLECULE TYPE: peptide  
30 HYPOTHETICAL: YES  
31 ANTI-SENSE: NO  
32 FRAGMENT TYPE: N-terminal  
33 FEATURE:  
34 NAME/KEY: Modified-site  
35 LOCATION: 5  
36 OTHER INFORMATION: /product= "CysMe"  
37 US-09-914-088-16

Query Match: 26.7% Score 31; DB 1; Length 12;  
Best Local Similarity 55.6% Pref No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19  
DB 4 DCFRNPHG 12

RESULT 13  
US-09-914-088-16

Sequence 189, Application US/08329820  
 Patent No. 5747457  
 GENERAL INFORMATION:  
 APPLICANT: JONCZYK, ALFRED  
 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
 APPLICANT: DIEFENBACH, BEATE  
 APPLICANT: RIPPWACH, FRIEDRICH  
 TITLE OF INVENTION: Linear Adhesion Inhibitors  
 NUMBER OF SEQUENCES: 228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129,820  
 FILING DATE: 27-OCT-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 436759.5  
 FILING DATE: 28 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamlet-Kieser, Diana  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1635  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 189:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5  
 OTHER INFORMATION: /product="Syn-BL1"  
 Query Match: 26.7% Score 317 DB 17 Length 12  
 Best Local Similarity: 55.6% Pred. No. 1.2e+02  
 Matches: 5, Conservative: 1, Mismatches: 1, Indels: 0,  
 Cys: 11 DECREASED 19  
 DB: 4 DECREASED 12  
 RESULT 15  
 US-08-329 820-191  
 Sequence 191, Application US/0819870  
 Patent No. 5747457  
 GENERAL INFORMATION:  
 APPLICANT: JONCZYK, ALFRED  
 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
 APPLICANT: DIEFENBACH, BEATE  
 APPLICANT: RIPPWACH, FRIEDRICH  
 TITLE OF INVENTION: Linear Adhesion Inhibitors  
 NUMBER OF SEQUENCES: 228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129,820  
 FILING DATE: 27 OCT-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 436759.5  
 FILING DATE: 28 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamlet-Kieser, Diana  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1635  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 191:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5  
 OTHER INFORMATION: /product="Syn-BL1"  
 Query Match: 26.7% Score 317 DB 17 Length 12  
 Best Local Similarity: 55.6% Pred. No. 1.2e+02  
 Matches: 5, Conservative: 1, Mismatches: 1, Indels: 0,  
 Cys: 11 DECREASED 19  
 DB: 4 DECREASED 12

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 436759.5  
 FILING DATE: 28 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamlet-Kieser, Diana  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1635  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 190:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5  
 OTHER INFORMATION: /product="Cyst-BL1"  
 US-08-329 820-190  
 Query Match: 26.7% Score 317 DB 17 Length 12  
 Best Local Similarity: 55.6% Pred. No. 1.2e+02  
 Matches: 5, Conservative: 1, Mismatches: 1, Indels: 0,  
 Cys: 11 DECREASED 19  
 DB: 4 DECREASED 12  
 RESULT 15  
 US-08-329 820-191  
 Sequence 191, Application US/0819870  
 Patent No. 5747457  
 GENERAL INFORMATION:  
 APPLICANT: JONCZYK, ALFRED  
 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
 APPLICANT: DIEFENBACH, BEATE  
 APPLICANT: RIPPWACH, FRIEDRICH  
 TITLE OF INVENTION: Linear Adhesion Inhibitors  
 NUMBER OF SEQUENCES: 228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.0.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129,820  
 FILING DATE: 27 OCT-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 436759.5  
 FILING DATE: 28 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamlet-Kieser, Diana  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1635  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 191:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5  
 OTHER INFORMATION: /product="Cyst-BL1"  
 US-08-329 820-190

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1  ANTI-SENSE: NC
2  FRAGMENT TYPE: N-terminal
3  FEATURE:
4  NAME/KEY: Modified-site
5  LOCATION: 5
6  OTHER INFORMATION: /product= "Cys10p21"
US-09-329 890-191

Query Match      26.7% Score 41 DB 12 Length 120
Best Local Similarity 55.6% Pred. No. 120-32
Matches 5: Conservative 1: Mismatches 4: Gaps 0:

QY 11 DCPREARR 19
   |||
LE 4 DCPREARR 12

Search completed: November 5, 2003, 18:25:41
Job time : 22 secs

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GenCore version 5.0.1  
Copyright (c) 1993-2003 Copyright Ltd

CM protein protein search, using sw -b-l

Run on: November 5, 2003, 17:03:45 Search time 11 seconds  
(without alignment)  
87,424 Million cell updates/sec

Title: US-09-914-088-24  
Perfect score: 52  
Sequences: 1 CSTRQBELA 10

Scoring table: ELOSUM62  
Gapop 10.0, Gapext 0.5

Seatched: 283308 seqs, 9616982 residues

Total number of hits satisfying chosen parameters: 1106

Minimum DB seq length: 5  
Maximum DB seq length: 10

Post processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 56.0  
1: p1r1  
2: p1r2  
3: p1r3  
4: p1r4

Pred. No. is the number of results predicted by the search, where a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	34.5	9	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
2	19	34.5	9	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
3	18	34.5	9	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
4	18	34.5	9	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
5	17	32.7	10	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
6	17	32.7	10	2 PH0910	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
7	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
8	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
9	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
10	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
11	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
12	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
13	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
14	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
15	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
16	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
17	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
18	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
19	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
20	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
21	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
22	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
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24	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
25	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
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28	16	30.9	8	2 XGH01	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
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30	14	26.9	10	2 S65728	hemoglobin, extrac
31	14	26.9	10	2 S65728	T-cell receptor alpha chain V-D-J region (clone 8) - rat (fragment)
32	14	26.9	10	2 S65728	collagen alpha 1(V
33	14	26.9	10	2 PH0926	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
34	13	25.0	9	2 J70522	Ig kappa chain V1
35	13	25.0	9	2 S29861	Na+/K+-exchanging
36	13	25.0	9	2 S29861	glycoprotein compo
37	13	25.0	9	2 S29861	T-cell receptor be
38	13	25.0	9	2 S29861	major fat globule
39	13	25.0	9	2 S29861	NADH2 dehydrogenas
40	13	25.0	9	2 S29861	hypothetical pesti
41	13	25.0	9	2 S29861	peptidyl dipeptida
42	13	25.0	9	2 S29861	metallothionein is
43	13	25.0	9	2 S29861	T-cell receptor be
44	13	25.0	9	2 S29861	neural cell adhesi
45	13	25.0	9	2 S29861	calsequestrin, car

## ALIGNMENTS

### RESULT 1

PH0910  
T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0910  
R:Gold, D.E.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.E.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0910; XUID:92078857; PMID:836012  
A:Accession: PH0910  
A:Reference number: PH0910  
A:Molecule type: mRNA  
A:Residues: 1-9 <GO>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor

Query Match: 38.5% Score 20; DB 2; Length 9;  
Best Local Similarity: 33.3% Pred. No. 2.8e+05;  
Matches: 2; Conservative: 4; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 CSTRQ 6  
DB 1 CSTRQ 6

### RESULT 2

PH0910  
T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0910  
R:Gold, D.E.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.E.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0910; XUID:92078857; PMID:836012  
A:Accession: PH0910  
A:Reference number: PH0910  
A:Molecule type: mRNA  
A:Residues: 1-9 <GO>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor

Query Match: 36.5% Score 19; DB 2; Length 9;  
Best Local Similarity: 28.8% Pred. No. 2.8e+05;  
Matches: 2; Conservative: 4; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 CSTRQ 6  
DB 1 CSTRQ 6

### RESULT 3

PH0910



T-cell receptor beta chain V-D-J region (Hybridoma 8B349) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 30 May 1997  
 C:Accession: PH0902  
 R:Gold, D.P., Offner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A., Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:9207857; PMID:183612  
 A:Accession: PH0902  
 A:Molecule type: mRNA  
 A:Residues: 1-9 <GG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T cell receptor

Query Match 34.6% Score 18; DB 2; Length 9;  
 Best Local Similarity 22.2% Pred. No. 2 Re+CS;  
 Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSTTQGEEL 9  
 DB 1 CASSTSGNV 9

RESULT 4  
 PH0902  
 T-cell receptor beta chain V-D-J region (clone 15) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 30 May 1997  
 C:Accession: PH0900  
 R:Gold, D.P., Offner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A., Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:9207857; PMID:183612  
 A:Accession: PH0900  
 A:Molecule type: mRNA  
 A:Residues: 1-9 <GG>  
 A:Experimental source: myelin basic protein immunized T-cell  
 C:Keywords: T cell receptor

Query Match 34.6% Score 18; DB 2; Length 9;  
 Best Local Similarity 22.2% Pred. No. 2 Re+CS;  
 Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSTTQGEEL 9  
 DB 1 CASSTSGNV 9

RESULT 5  
 PH0904  
 Protein (Xenopus) - Anaxipopsis thaliana (frog)  
 C:Species: Anaxipopsis thaliana (Xenopus laevis)  
 C:Date: 07 Feb 1996 #sequence revision 10 Apr 1996 #text change 30 May 1997  
 C:Accession: PH0904  
 R:Kawaguchi, A., Karm, M., Kawakami, M., Seki, Y.  
 Submitted to JIPED, December 1995  
 A:Description: Two dimensional electrophoresis of protein from whole and standardization of  
 A:Reference number: PH0903  
 A:Accession: PH0904  
 A:Molecule type: protein  
 A:Residues: 1-10 <TS>  
 A:Experimental source: leaf

Query Match 32.7% Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0% Pred. No. 4 Re+CS;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTAED 7  
 DB 1 PTAED 7

RESULT 6  
 PH0905  
 T-cell receptor beta chain V-D-J region (Hybridoma 8B349) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 30 May 1997  
 C:Accession: PH0905  
 R:Gold, D.P., Offner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A., Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:9207857; PMID:183612  
 A:Accession: PH0905  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T cell receptor

Query Match 32.7% Score 17; DB 2; Length 10;  
 Best Local Similarity 25.0% Pred. No. 4 Re+CS;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSTTQGEEL 9  
 DB 1 CASSTSGNV 9

PH0895  
 T-cell receptor beta chain V-D-J region (rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 30 May 1997  
 C:Accession: PH0895  
 R:Gold, D.P., Offner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A., Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:9207857; PMID:183612  
 A:Accession: PH0895  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T cell receptor

Query Match 32.7% Score 17; DB 2; Length 10;  
 Best Local Similarity 25.0% Pred. No. 4 Re+CS;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSTTQGEEL 9  
 DB 1 CASSTSGNV 9

RESULT 7  
 A20186  
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
 C:Species: Cryptolagus cuniculus (domestic rabbit)  
 C:Date: 05 Jun 1997 #sequence revision 05 Jun 1997 #text change 05 May 2000  
 C:Accession: A20186  
 R:McCarthy, A.D., Atkeson, A., Hardie, G., Santikarn, S., Williams, D.H.  
 FEBS Lett. 160, 294-300, 1983  
 A:Title: Amino acid sequence around the active serine in the acyl: transference domain of  
 A:Reference number: A20186; MIMD:8428768; PMID:6554204  
 A:Accession: A20186  
 A:Molecule type: protein  
 A:Residues: 1-6 <MG>  
 C:Keywords: acyl:transference; coenzyme A

Query Match 30.8% Score 16; DB 2; Length 6;  
 Best Local Similarity 75.0% Pred. No. 2 Re+CS;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GEA 10  
 DB 3 GEA 4

RESULT 8  
 XGH05U  
 Urine glycopeptide human  
 C:Species: Homo sapiens (man)  
 C:Date: 20 Jun 2000 #sequence revision 20 Jun 2000 #text change 20 Jun 2000  
 C:Accession: XGH05U  
 R:Lote, C., Weiss, J.E.  
 Biochem. J. 123, 257, 1971  
 A:Title: Identification in urine of a low-molecular weight polar glycopeptide containing  
 A:Reference number: XGH05U; MIMD:7262338; PMID:5126985  
 A:Accession: XGH05U  
 A:Molecule type: protein  
 A:Residues: 1-8 <CG>  
 C:Comment: The identity of the glycoprotein from which this peptide is derived is unknown  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: glycoprotein  
 C:Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 20.8% Score 16; DB 2; Length 8;  
 Best Local Similarity 49.6% Pred. No. 2 Re+CS;  
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GEA 10  
 DB 3 GEA 4

Db : CERSHDS 7

## RESULT 9

P28854  
 fibrinopeptide B - olive baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RES 8

Db 2 RES 4

## RESULT 10

P28854  
 fibrinopeptide B - olive baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RES 8

Db 2 RES 4

## RESULT 11

P28854  
 fibrinopeptide B - hamadryas baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RES 8

Db 2 RES 4

Db : CERSHDS 4

## RESULT 12

P28854  
 fibrinopeptide B - gelada baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RES 7

Db 2 RES 4

## RESULT 13

P28854  
 fibrinopeptide B - gelada baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RES 7

Db 2 RES 4

## RESULT 14

P28854  
 fibrinopeptide B - gelada baboon  
 C:Species: *Thrypacosoma brucei*  
 C:Date: 28-Oct-1994 #sequence\_revision 08-Oct-1994 #text\_change 17-May-1999  
 C:Accession: D61512  
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycopeptides from varicell surface glycoproteins of *Thrypacosoma brucei*. C-term  
 A:Reference number: A61512; MUIB:84162836; PMID:6423621  
 A:Accession: D61512

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NA>  
 C:Keywords: glycoprotein

Query Match 30.8%; Score 16; DP 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RES 7

Db 2 RES 4

```

RESULT 15
PH0943
T-cell receptor beta chain V-D-J region (clone 14) [at 100000]
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 09 May 1997
C:Accession: PH0943
R:Gold, D. P., Offner, H., Sun, D., Wiley, S., Vandenbark, A. A., Wilson, D. B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0943; M01D:9207853; M01D:1156212
A:Accession: PH0943
A:Molecule type: mRNA
A:Residues: 13 aaGL
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the coding GAC for residue 4 as GAA
C:Keywords: T-cell receptor

Query Match          32.8%  Score 167  DP 27  Length 63
Best Local Similarity 50.3%  Pred No. 2 Ref-25
Matches  2; Conservative  2; Mismatches  1; Indels  0; Gaps  0;

Cq      1 CSIT 4
DB      1 CSIT 4

Search completed: November  5, 2003, 10:15:12
Job time 1:12 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw Model

Run on: November 5, 2003, 17:23:40 : Search time: 2.3333 seconds  
(without alignment)  
64.127 Million cell updates/sec

Title: US-09 914-088-24  
Perfect score: 52  
Sequence: 1 CSTTQSGELA 10

Scoring table: HLOSUM62  
Gapop 10.0 , Gapext 0.5

Sequences: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:ES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	34.6	10	1 SPI_HAIRO	Q1997 Halocynthia
2	16	30.6	7	1 UF01_MOUSE	P38641 mus musculus
3	16	30.8	8	1 CLP_THUOB	P4188 thicbacille
4	16	30.8	8	1 GLUR_HUMAN	P60229 homo sapien
5	16	30.4	9	1 FIBR_PAPAE	P30744 papio arabic
6	16	20.9	9	1 FIBR_PAPAE	P30744 papio arabic
7	16	30.4	9	1 FIBR_THRGE	P30742 thaladipther
8	16	30.8	10	1 AMPN_HUMAN	P41111 homo sapien
9	16	30.8	10	1 URAL_HUMAN	P38141 homo sapien
10	15	28.8	9	1 TAL1_PICJA	P42391 picchia jadi
11	14	28.8	7	1 E105_LITPU	P42391 picchia jadi
12	14	28.9	9	1 TAL1_PICJA	P42391 picchia jadi
13	13	25.0	7	1 MNP1_LEPDE	P42384 lepridorsis
14	13	25.0	7	1 UH11_RAT	P54576 rattus norv
15	13	25.0	8	1 LMT2_LGCM	P27196 locusta mig
16	13	25.0	9	1 FARD_CALVO	P41969 calliphora
17	13	25.0	9	1 OXYM_ESFCO	P42388 ctenia toe
18	13	25.0	10	1 COXC_RAT	P50412 rattus norv
19	13	25.0	10	1 PPCK_FASHE	P50425 fasciola he
20	12	23.1	5	1 BIOA_CITFR	P13771 citrobacter
21	12	23.1	7	1 PPH2_LYCES	P61379 lycopersico
22	12	23.1	8	1 RSL_EKACH	P37265 erwinia chr
23	12	23.1	9	1 ALC_CHRE	P42678 chlamydomon
24	12	23.1	9	1 SAP_STOVA	P42647 stomopnetie
25	11	21.2	8	1 UPAT_HUMAN	P42687 homo sapien
26	11	21.2	8	1 WPI_PBRAT	P31395 pekinsus a
27	11	21.2	9	1 ALI1_CARMA	P41924 carcinus ma
28	11	21.2	9	1 DI_NEPNC	P24436 neprops no
29	11	21.2	9	1 DNFI_LGCM	P16139 locusta mig
30	11	21.2	9	1 DSIF_RABIT	P41158 cryptotagus
31	11	21.2	9	1 FARI_CALVO	P41856 calliphora
32	11	21.2	9	1 FARI_CALVO	P41856 calliphora
33	11	21.2	9	1 UF02_MOUSE	P38640 mus musculus

34	11	21.2	9	1 ULAH_HUMAN	P31934 homo sapien
35	11	21.2	10	1 COXA_ONCVY	P80128 oncorhynch
36	11	21.2	10	1 COXA_THUOB	P80982 thunnus oce
37	11	21.2	10	1 GLEM_HUMAN	P32728 homo sapien
38	11	21.2	10	1 PNEU_HUMAN	P22103 homo sapien
39	11	21.2	10	1 PNEU_RAT	P21996 rattus norv
40	11	21.2	10	1 URAT_HUMAN	P34990 homo sapien
41	11	19.2	5	1 PSK_DAUCA	P58261 daucus car
42	10	19.2	7	1 UC24_MAIZE	P80630 zea mays lm
43	10	19.2	7	1 UN06_PINES	P81675 pinus pinas
44	10	19.2	8	1 ORNY_GRELI	P82455 onocretes
45	10	19.2	8	1 TH09_RAT	P56575 rattus norv

# ALIGNMENTS

RESULT: 1

SPI\_HAIRO STANDARD: PRT: 10 AA.

AC Q1C997:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Serine proteinase inhibitor (Fragment)

OS Halocynthia roretzi (Sea squirt)

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;

OC Stolidobranchia; Fysulidae; Halocynthia

OC NCBI\_TaxID=7729;

PN 11

RP SEQUENCE

RC Tissue: Hemolymph;

RA MEDLINE=96321313; PubMed=9759295;

RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.

RT "Purification and characterization of a 58,000-Da proteinase

inhibitor from the hemolymph of a solitary ascidian, Halocynthia

roretzi";

RL Comp. Biochem. Physiol. 114B:1-9(1996);

CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.

CC -2- SUBUNIT: Monomer.

CC -3- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR InterPro: IPR000215: Serpin.

DR PROSITE: PS00284; SERPIN; PARTIAL.

KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.

FT NON TER 10 10

SQ SEQUENCE 10 AA, 100% YW, 4225AT3B181RTAA3 CRC64;

Query Match: 34.4% Score 18; DB 1; Length 10;

Best local similarity: 50.0%; Pred. No. 9.2e+02;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TIOEGE 8

DB 1 TKRGE 6

RESULT: 2

UF01\_MOUSE

ID UF01\_MOUSE STANDARD: PRT: 7 AA.

AC P38641;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OC NCBI\_TaxID=10090;

PN 31

RP SEQUENCE

RC Tissue=Embryoblast;

RA MEDLINE=95029907; PubMed=7523108;

RA Verrick B.A., Patterson R.M., Michler L.L., He C., Seikirk C.K.;

RT "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis";  
 PL Electrophoresis 15:735-745(1994).  
 CC - MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 IS THIS UNKNOWN  
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa  
 FT NON TER  
 SQ SEQUENCE 7 AA: 6AA72B10B5B151 CRC64;

Query Match 30.8% Score 16; DB 1; Length 7;  
 Best Local Similarity 60.0% Pred. No. 1.3e-05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 9  
 DB 2 EFAEL 6

RESULT 1  
 ID CLP HICU STANDARD; PRT; 8 AA.  
 AC P2488;  
 DT 01-OCT-1994 (Rel. 14, Created;  
 DT 01-OCT-1994 (Rel. 14, Last sequence update;  
 DT 01-OCT-1994 (Rel. 14, Last annotation update;  
 DE Chemokine receptor specific protein (Fragment)  
 OS Thelazia callipalpus  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Gram-negative; Thiomonas.  
 CX NCBI TaxID 16962;  
 RN 1;  
 RP SEQUENCE  
 SC STEIN DM 5494;  
 RA Martin J, Acuto A.X., Jerez C.A., Amis P., Alad A, et  
 PL Submitted SEP-1995 to the SWISS PROT data bank.  
 CC - MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC IN SEMI-CONTINUOUSLY.  
 FT NON TER  
 SQ SEQUENCE 8 AA: 485 MW: 9148TH0602046 CRC64.

Query Match 30.8% Score 16; DB 1; Length 8;  
 Best Local Similarity 100.0% Pred. No. 1.4e-06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 7  
 DB 6 QCG 3

RESULT 4  
 ID CLP HUMAN STANDARD; PRT; 8 AA.  
 AC P2729;  
 DT 01-JUL-1988 (Rel. 21, Created;  
 DT 01-JUL-1988 (Rel. 21, Last sequence update;  
 DT 26-OCT-2001 (Rel. 42, Last annotation update;  
 DE Urine glycoprotein  
 OS Homo sapiens; Hominidae;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Anthropia; Primates; Catarrhini; Hominoidea; Hominidae;  
 CC NCBI TaxID 9606;  
 RN 1;  
 RP SEQUENCE  
 SC MEDLINE#262345, PubMed#5126885,  
 RA Kato C.J., Weiss J.B.;  
 RT Identification in urine of a low-molecular-weight urinary protein  
 PL Biochem. J. 123:25P-25P(1971).  
 CC - FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE  
 CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
 CC ASSIGNED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A  
 CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.

FT A3386, XGHEJ.  
 SQ SEQUENCE 76; Extracellular; NAG.

KW Glycoprotein.  
 FT CARBHYD 1  
 SQ SEQUENCE 8 AA: 855 MW: 02D87A1F59EB1E CRC64;

Query Match 30.8% Score 16; DB 1; Length 8;  
 Best Local Similarity 29.6% Pred. No. 1.3e-05;  
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSTQCG 7  
 DB 1 CFSHCG 7

RESULT 5  
 ID FIBB JAPAN STANDARD; PRT; 9 AA.  
 AC P19344;  
 DT 01-NOV-1990 (Rel. 16, Created;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update;  
 DT 26-FEB-2003 (Rel. 41, Last annotation update;  
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 OS Papio anubis (Olive baboon).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecinae; Papio.  
 CX NCBI TaxID=9555;  
 RN 1;  
 RP SEQUENCE  
 SC MEDLINE#4161822; PubMed#6423521;  
 RA Nakamura S., Takekura G., Takahashi K.;  
 RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,  
 RT and Theropithecus gelada): their amino acid sequences and  
 RT evolutionary rates and a molecular phylogeny for the baboons.";  
 RL J. Biochem. 94:1973-1978(1983).  
 CC - FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATSEI  
 CC AGGREGATION.

CC - SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC - MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THIS EXPOSES THEN TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT GEL.

FT 12954; DBTER4.  
 DR INTERPRO:PRO0111; Fibrinogen  
 DR PROSITE, PS00514; FIBRIN AGGREGATION; PARTIAL  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
 FT NON TER 9 3  
 SQ SEQUENCE 9 AA: 1076 MW: DCFE6499C7287H06 CRC64;

Query Match 30.8% Score 16; DB 1; Length 9;  
 Best Local Similarity 100.0% Pred. No. 1.3e-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 7  
 DB 2 QCG 4

RESULT 6  
 ID FIBB JAPHA STANDARD; PRT; 9 AA.  
 AC P19344;  
 DT 01-NOV-1990 (Rel. 16, Created;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update;  
 DT 26-FEB-2003 (Rel. 41, Last annotation update;  
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 OS Papio hamadryas (Hamadryas baboon).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

CC Cercarial dermatitis; Papio.  
OX NCBI TaxID 9557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinopeptides A and B of baboon (Papio anubis, Papio anubis),  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:1973-1978 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL "HEAD"  
CC "TAIL" (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F38854; E38854;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE ; 9 FIBRINOPEPTIDE B.  
FT PEPTIDE ; 9  
FT NCN TER ; 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QES 7  
DB 1  
2 QES 4  
  
RESULT 7  
FIBRIN-THREE  
ID FIBRIN-THREE STANDARD; PRT: 9 AA.  
AC P19142;  
DT 01-NOV-1990 (Rel. 16, Created);  
DT 01-NOV-1990 (Rel. 16, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);  
OS Theropithecus gelada (Gelada baboon);  
OC Eukaryota; Chordata; Mammalia; Primates; Catarrhini; Hominoidea;  
OC Cercopithecoidea; Theropithecus.  
OX NCBI TaxID=9557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio anubis),  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:1973-1978 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL "HEAD"  
CC "TAIL" (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F38854; E38854;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE ; 9 FIBRIN PEPTIDE B.  
FT PEPTIDE ; 9  
FT NCN TER ; 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;

CC Cercarial dermatitis; Papio.  
OX NCBI TaxID 9557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinopeptides A and B of baboon (Papio anubis, Papio anubis),  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:1973-1978 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL "HEAD"  
CC "TAIL" (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F38854; E38854;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE ; 9 FIBRINOPEPTIDE B.  
FT PEPTIDE ; 9  
FT NCN TER ; 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QES 7  
DB 1  
2 QES 4  
  
RESULT 5  
AXPN-HELM  
ID AXPN-HELM STANDARD; PRT: 10 AA.  
AC P21731;  
DT 30-MAY-2000 (Rel. 39, Created);  
DT 30-MAY-2000 (Rel. 39, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Aminopeptidase N (EC 3.4.11.2) (CryIA(C) receptor) (Fragment);  
OS Helicoverpa armigera (Cotton bollworm);  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI TaxID=29059;  
RN [1]  
RP SEQUENCE  
AC TISSUE=Midgut;  
RA Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatpar H.S.;  
RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC  
RT toxin from Helicoverpa armigera".  
RJ Submitted (MAR-1999) to the SWISS-PROT data bank.  
CC -1- FUNCTION: ACTS AS A RECEPTOR FOR B. THURINGIENSIS TOXIN CRYIAC.  
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-[-  
CC Xaa- from a peptide, amide or arylamide. Xaa is preferably Ala, but  
CC may be most amino acids including pro (slow action). When a  
CC terminal hydrophobic residue is followed by a prolyl residue, the  
CC two may be released as an intact Xaa-Pro dipeptide.  
CC -1- COFACTOR: Binds; zinc ion (by similarity).  
CC -1- SIMILARITY: Belongs to peptidase family M1.  
DR INTERPRO: IPR036025; Zn\_MpPeptidase.  
DR PROSITE: PS0142; ZINC\_PROTEASE; PARTIAL.  
KW Hydrolyase; Metalloprotease; Aminopeptidase; Zinc.  
FT NCN TER ; 10  
FT NCN TER ; 10  
SQ SEQUENCE 10 AA; 1033 MW; 050424B87B11F1BB CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 QES 7  
DB 1  
4 QES 7  
  
RESULT 9  
URAL HUMAN  
ID URAL HUMAN STANDARD; PRT: 10 AA.  
AC P22118;  
DT 01-OCT-1993 (Rel. 27, Created);  
DT 01-OCT-1993 (Rel. 27, Last sequence update);  
DT 16-OCT-2001 (Rel. 40, Last annotation update);  
DE Unknown protein from 2D-page of red blood cells (Spot 1) (Fragment);  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE  
AC TISSUE Erythrocyte;  
RX MEDLINE=94147970; PubMed=8313871;  
RA Gelaz G., Hughes G., Prutiger S., Paquet N., Bairoch A.,  
RA Pasquini G., Sanchez J., Tisno J.-D., Appel R.D., Walzer G.,  
RA Balazs L., Harsanyi J., D.F.

RT "Plasma and red blood cell protein maps: update (1991);  
 RL Electrophoresis 14:1223-1231(1993);  
 CC "MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 (P TH-S UNO) AND  
 CC PROTEIN IS: 5.4, ITS MW IS: 23 KDa.  
 DR SWISS-2D PAGE: P3118; HUMAN.  
 FT NON-TER 1 1  
 FT NON-TER 10 10  
 SQ SEQUENCE 10 AA; 979 MW; 724065PIADJ0825 Q8704;  
 Query Match 30.8%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 Q883 7  
 DB 1 Q883 4  
 RESULT 10  
 ID TALL\_PICCA STANDARD; PRT; 9 AA;  
 AC PI7441;  
 DT 01-AUG-1990 (Rel. 15, Created;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transaldolase III (EC 2.2.1.2) (Fragment)  
 OS Pichia jadinii (Yeast) (Candida utilis)  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Pichia.  
 CX NCBI\_TAXID:4933;  
 RN 1;  
 RP SEQUENCE.  
 RX MEDLINE:75145197; PubMed:1032249;  
 RA Tsolis C, Sun S, G;  
 RT Isolation of a peptide containing a phosphoryl transferase  
 RL Arch. Biochem. Biophys. 167:525-533(1993);  
 CC "FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF  
 CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY  
 CC CATALYTIC ACTIVITY: Sedheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate + D-erythrose 4-phosphate + D-fructose 6-phosphate.  
 CC "PATHWAY: Pentose phosphate pathway; non-oxidative part  
 CC "SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.  
 DR Euk. Archaea; Biophys. 178:64-78(1977);  
 DR Interfero; PR001563; Transaldolase.  
 DR PROSITE; PS00958; TRANSALDOLASE 2; PARTIAL.  
 DR PROSITE; PS01054; TRANSALDOLASE 1; PARTIAL.  
 KW Transferrase; Pentose shunt.  
 FT NON-TER 1 1  
 FT NON-TER 3 9  
 SQ SEQUENCE 9 AA; 1009 MW; 725434PIADJ0825 Q8704;  
 Query Match 28.8%; Score 15; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 Q87 3  
 DB 5 Q87 7  
 RESULT 11  
 ID ECEGLTNG STANDARD; PRT; 7 AA;  
 AC E42111;  
 DT 28-FEB-2003 (Rel. 41, Created;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ectocitin 5.  
 OS Eukaryota; Metazoa; Chordata; Cephalopoda; Vertebrata; Mollusca; Bivalvia;  
 CC Apollonia; Apollonia; Anota; Nectarion; Ectocitin; Apollonia;  
 CC Polidysididae; Liliaceae.

CX NCBI\_TaxID:104995;  
 RN 1;  
 RP SEQUENCE  
 RC TISSUE: Skin secretion;  
 RA Mannitz P.A., Bowie G.H., Tyler M., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litor: "Electrical comparison with the skin peptides from Litoria  
 RT rubella".  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC "SUBCELLULAR LOCATION: Secreted.  
 CC "TISSUE SPECIFICITY: Skin  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 7  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 834 MW; 68D05B076C8C5030 Q8C64;  
 Query Match 26.9%; Score 14; DB 1; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 E884 10  
 DB 1 E884 7  
 RESULT 12  
 ID TALL\_PICCA STANDARD; PRT; 9 AA;  
 AC PI7441;  
 DT 01-AUG-1990 (Rel. 15, Created;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transaldolase I (EC 2.2.1.2) (Fragment)  
 OS Pichia jadinii (Yeast) (Candida utilis)  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Pichia.  
 CX NCBI\_TAXID:4903;  
 RN 1;  
 RP SEQUENCE.  
 RX MEDLINE:77110644; PubMed:556324;  
 RA Sun S, G, Solis C, G;  
 RT "Purification of crystallization of transaldolase isozyme I and  
 RT evidence for different genetic origin of isozymes I and II in  
 RT Candida utilis";  
 RL Arch. Biochem. Biophys. 178:64-78(1977);  
 CC "FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF  
 CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY  
 CC CATALYTIC ACTIVITY: Sedheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate + D-erythrose 4-phosphate + D-fructose 6-phosphate.  
 CC "PATHWAY: Pentose phosphate pathway; non-oxidative part  
 CC "SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.  
 DR Euk. Archaea; Biophys. 178:64-78(1977);  
 DR Interfero; PR001563; Transaldolase.  
 DR PROSITE; PS00958; TRANSALDOLASE 2; PARTIAL.  
 DR PROSITE; PS01054; TRANSALDOLASE 1; PARTIAL.  
 KW Transferrase; Pentose shunt.  
 FT NON-TER 1 1  
 FT NON-TER 9 9  
 SQ SEQUENCE 9 AA; 1009 MW; 274F1AF0E81E058 Q8C64;  
 Query Match 26.9%; Score 14; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 Q87 3  
 DB 5 Q87 7  
 RESULT 13  
 ID ECEGLTNG STANDARD; PRT; 7 AA;  
 AC E42111;  
 DT 28-FEB-2003 (Rel. 41, Created;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ectocitin 5.  
 OS Eukaryota; Metazoa; Chordata; Cephalopoda; Vertebrata; Mollusca; Bivalvia;  
 CC Apollonia; Apollonia; Anota; Nectarion; Ectocitin; Apollonia;  
 CC Polidysididae; Liliaceae.





GenCore version: 5.1.6  
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CM protein: Protein search, using sw model

Run on: November: 5, 2003, 17:29:05 : Search time: 46 seconds

Without alignment gaps  
49,251 Million cells (gap=refno)

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1: CSTRGELA 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 430525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 6

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.marine:  
7: sp.mhc:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.rodent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:  
15: sp.virus:  
16: sp.bacterioph:  
17: sp.archaea:

Pred. No. is the number of results predicted by GeneCore to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID
1	17	32.7	10	15 Q85598
2	17	32.7	10	15 Q85563
3	17	32.7	10	15 Q85619
4	16	30.8	8	5 Q94695
5	16	30.8	10	4 Q9JNG2
6	16	30.8	10	6 Q87342
7	16	30.8	10	11 Q8JL15
8	15	28.6	8	11 P70243
9	15	28.8	9	4 Q9UG64
10	15	28.8	9	12 Q9Q150
11	15	28.8	9	13 Q8ALY7
12	15	28.8	10	2 Q50812
13	15	28.8	10	4 Q50493
14	15	28.6	10	8 Q9G362
15	15	28.6	10	10 Q94158
16	15	28.8	10	11 Q9QVK9

Continued

17	14	26.9	7	13 Q8JC20
18	14	26.9	8	4 Q16428
19	14	26.9	8	5 Q9TWH6
20	14	26.9	8	6 Q9MTD5
21	14	26.9	9	6 Q8MCT7
22	14	26.9	9	6 Q8MCT8
23	14	26.9	9	11 Q9CZAR
24	14	26.9	10	2 Q95N1
25	14	26.9	10	2 Q95719
26	14	26.9	10	4 Q8NER0
27	14	26.9	10	6 Q8M78
28	14	26.9	10	15 Q9QXJ0
29	13	25.0	8	4 Q9GQF9
30	13	25.0	8	4 Q15890
31	13	25.0	8	13 Q90ZV5
32	13	25.0	8	15 Q85562
33	13	25.0	9	2 Q51349
34	13	25.0	9	11 Q8514
35	13	25.0	9	11 Q9JF4
36	13	25.0	9	15 Q85723
37	13	25.0	10	2 Q47475
38	13	25.0	10	6 Q97R47
39	13	25.0	10	10 Q8L7F5
40	12	23.1	7	11 Q8348C
41	12	23.1	8	2 Q989E0
42	12	23.1	8	7 Q29810
43	12	23.1	9	2 Q47556
44	12	23.1	9	4 Q96P97
45	12	23.1	9	6 Q8HZY2

## ALIGNMENTS

RESULT 1  
Q85598  
ID Q85598 PRELIM:NARY; PRT; 10 AA.  
AC Q85598 (TREMURel. 01, Created:  
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)  
DT 01-DEC 2001 (TREMURel. 19, Last annotation update)  
DE Moloney murine sarcoma virus (S-train HT) env/mos 5' junction  
(Fragment)  
OS Moloney murine leukemia virus  
OC Viruses, Retroviruses, Retroviridae; Gammaretrovirus.  
CX NCBI:TaxId:11801  
RN 11  
PP SEQUENCE FROM N.A.  
RX MEDLINE:91164305; PubMed:6300424;  
FA Donoshue D, Hunter T.  
RT "Recombination functions of variants of Moloney murine sarcoma virus:  
Generation and divergence of a mammalian transforming gene."  
J. Virol. 45:607-617(1983).  
DR EMBL: K0104; AAA46492.1; .  
FT NCN TER 10  
SQ SEQUENCE 10 AA; 1081 MW; 736CFCEBA77185A4 CRC64;  
Query Match: 32.7%; Score 17; DB 15; Length 10;  
Best Local Similarity 75.0%; Pred. No. 7.6e+03;  
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY : CSTR 4  
Db 7 CSOT 10  
RESULT 2  
Q85563  
ID Q85563 PRELIM:NARY; PRT; 10 AA.  
AC Q85563 (TREMURel. 01, Created:  
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)  
DT 01-DEC 2001 (TREMURel. 19, Last annotation update)  
DE Moloney murine sarcoma virus (S-train HT) env/mos 5' junction  
(Fragment)  
OS Moloney murine leukemia virus  
OC Viruses, Retroviruses, Retroviridae; Gammaretrovirus.  
CX NCBI:TaxId:11801  
RN 11  
PP SEQUENCE FROM N.A.  
RX MEDLINE:91164305; PubMed:6300424;  
FA Donoshue D, Hunter T.  
RT "Recombination functions of variants of Moloney murine sarcoma virus:  
Generation and divergence of a mammalian transforming gene."  
J. Virol. 45:607-617(1983).  
DR EMBL: K0104; AAA46492.1; .  
FT NCN TER 10  
SQ SEQUENCE 10 AA; 1081 MW; 736CFCEBA77185A4 CRC64;

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DE Env mms fusion protein (fragment)
OS Meloney murine leukemia virus
OC Viruses; Retroviruses; Retroviridae; Gammaretrovirinae
CX NCBI_TaxID:11811;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE:82196891; PubMed:6251735;
RA Donoghue D.J., Hunter T.;
RT A generalized method of subcloning DNA fragments by restriction site
RT re-orientation. Application to sequencing the avian terminal region of
RT the transforming gene of Qizdar murine sarcoma virus.
RL J Virol. 45:607-617(1983).
DR EMBL: K01157; AAA46491.1;
FT N-TER 10
SQ SEQUENCE 10 AA; 1062 MW; 196CF7BEA771B5B4 CRC64.

Query Match 32.7%; Score 17; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 7 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 7 CUST 10

RESULT 3
Q95619 PRELIMINARY; PRT; 10 AA.
AC Q95619
DT 01-MAY-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-FEB-2003 (TrEMBLrel. 19, Last annotation update)
DE Meloney murine sarcoma virus (strain 10) envelope glycoprotein
DE (fragment)
OS Meloney murine leukemia virus
OC Viruses; Retroviruses; Retroviridae; Gammaretrovirinae
CX NCBI_TaxID:11811;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE:84144404; PubMed:6100414;
RA Donoghue D.J., Hunter T.;
RT "Generation and divergence of a mammalian transforming gene"
RT re-orientation and divergence of a mammalian transforming gene.
RL EMBL: K01155; AAA44941.1;
FT N-TER 10
SQ SEQUENCE 10 AA; 1081 MW; 196CF7BEA771B5B4 CRC64.

Query Match 32.7%; Score 17; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 7 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 7 CUST 10

RESULT 4
Q94495 PRELIMINARY; PRT; 4 AA.
AC Q94495
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Avian (fragment)
OS Avian

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OS Physatum polycephalum (silene fold)
OC Eukaryota; Mycetozoa; Myxogastromycetidae; Physarida;
OC Physarum
CX NCBI_TaxID:5791;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE:96182101; PubMed:9620700;
RA Benard M., Laget C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum."
PL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL: M73459; AAC03706.1;
FT N-TER 8
SQ SEQUENCE 8 AA; 878 MW; F40C62CA8187B16 CRC64;

Query Match 30.8%; Score 16; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EGE 8
DB 2 EGE 4

RESULT 5
Q9CNS0 PRELIMINARY; PRT; 10 AA.
AC Q9CNS0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Canalicular multispecific organic anion transporter (fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
CX NCBI_TaxID:2606;
RN 1
RP SEQUENCE FROM N.A.
RA Tanaka T., Uchiumi T., Kinoshita E., Inokuchi A., Toh S., Wada M.,
RA Nomoto M., Kondo K., Kuwano M.;
RT "Sequence analysis and functional characterization of the 5' flanking
RT region of the human canalicular multispecific organic anion
RT transporter-mediated resistance protein 2 (CMOAT/MRP2) gene."
RL Submitted (APR1999) to the EMBL/GenBank/CCDS databases.
DR EMBL: AB044410; AA044494.1;
FT N-TER 10
SQ SEQUENCE 10 AA; 1219 MW; 16FL4P44B3C13R CRC64;

Query Match 30.8%; Score 16; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 12e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 9 CUST 9

RESULT 6
Q9TS42 PRELIMINARY; PRT; 10 AA.
AC Q9TS42
DT 01-MAY-2003 (TrEMBLrel. 13, Created)
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-COR-2002 (TrEMBLrel. 21, Last annotation update)
DE CESTRACOL RECEPTOR peptide (fragment)
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Artiodactyla; Suidae; Sus
CX NCBI_TaxID:4923;
RN 1
RP SEQUENCE 10 AA; 119 MW; 16FL4P44B3C13R CRC64;

```

```

RX MEMPRO-912911287; PubMed=20646287;
RA Thiele H R , Campbell P W , Jakob T J
RT "The protein driven dissociation of oestradiol-receptor complex as a
PT preparative tool: Isolation of a 32 KDa fragment from porcine uteri
RD and assignment of C-terminal origin by partial sequencing."
RS Biochem J 276:159-174(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 992 MW; D95E047B1451B7ED CRC64;

Query Match 30.8%; Score 16; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TQSG 7
DB 5 TNEG 8

RESULT 7
QY015 PRELIMINARY; PRT; 10 AA
AC QY015
DT 01-OCT-2000 (TREMUREL15, Created)
DT 01-OCT-2000 (TREMUREL15, Last sequence update)
DT 01-OCT-2000 (TREMUREL15, Last annotation update)
DE Melanocortin type 1 receptor NMR fragment
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID:10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J
EX YNGLIN2002C876; PubMed:1023181;
RA Adachi S, Morita K, Kim D-K, Ohtsuka H, Iijima T, Ito A, Ito Y, Ma,
RA Kikuchi Y.
PT "Involvement of mit-transcription factor in expression of alpha
PT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice."
RL J Biol Chem 275:16418-16425(2000).
RR EMBL: AF174816; AAF37231;
RW Receptor
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1148 MW; 9A8B-AAC724B071753A;

Query Match 30.8%; Score 16; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQSG 6
DB 2 STOR 5

RESULT 8
PQ024 PRELIMINARY; PRT; 4 AA
AC PQ024
DT 01-FEB-1997 (TREMUREL12, Created)
DT 01-FEB-1997 (TREMUREL12, Last sequence update)
DT 01-DEC-2001 (TREMUREL19, Last annotation update)
DE Skeletal muscle specific calcium channel fragment
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID:10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=129;
EX YNGLIN2002C876; PubMed:1023181;
RA Adachi S, Morita K, Kim D-K, Ohtsuka H, Iijima T, Ito A, Ito Y, Ma,
RA Kikuchi Y.
PT "Involvement of mit-transcription factor in expression of alpha
PT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice."
RL J Biol Chem 275:16418-16425(2000).
RR EMBL: AF174816; AAF37231;
RW Receptor
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1148 MW; 9A8B-AAC724B071753A;

Query Match 30.8%; Score 16; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQSG 6
DB 2 STOR 5

RESULT 9
QY064 PRELIMINARY; PRT; 9 AA
AC QY064
DT 01-MAY-2000 (TREMUREL13, Created)
DT 01-MAY-2000 (TREMUREL13, Last sequence update)
DT 01-MAY-2000 (TREMUREL13, Last annotation update)
DE D334105.1 (Remainder of gene in sequence ALC23513) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI TaxID:9606;
RN 1
RP SEQUENCE FROM N.A.
RA LLOYD D J
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RR EMBL: AL078460; CAB517511;
RW Exon
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 9 AA; 1125 MW; 8154A2CB0B5E0411 CRC64;

Query Match 30.8%; Score 15; DB 4; Length 9;
Best Local Similarity 42.9%; Pred. No. 6.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TQSG 10
DB 2 TREYEV 8

RESULT 10
QY035 PRELIMINARY; PRT; 9 AA
AC QY035
DT 01-NOV-1998 (TREMUREL18, Created)
DT 01-NOV-1998 (TREMUREL18, Last sequence update)
DT 01-DEC-2001 (TREMUREL19, Last annotation update)
DE Polyprotein fragment
OS Hepatitis G virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group
OX NCBI TaxID:45255;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=SG3419;
RX MEDLINE-99266893; PubMed=10345862;
RA Wong S B C, Chan S H, Ren S C.
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT predominance of group 2a and the Asian group 3 variant."
RL J Virol 73:1545-1551(1999).
RR EMBL: AF076065; AAC12711;
RW GBV-C/HGV group
FT NON TER 9
FT NON TER 9
SQ SEQUENCE 9 AA; 489 MW; D95CA5A5BE9CDDDD CRC64;

Query Match 30.8%; Score 15; DB 12; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TQSG 4
DB 1

```

```

DB          5 GSS 8

RESULT 11
ID QNAME?      PRELIMINARY;      PRT: 10 AA
AC G9A032
DT 01-MAR-2001 (TRENBERG) 01, Created:
DT 01-MAR-2001 (TRENBERG) 21, Last sequence update:
DT 01-MAR-2001 (TRENBERG) 21, Last annotation update:
DE Cytocrome P450 aromatase (frag-nc)
GN CYP11A
OS Carassius auratus (Goldfish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Cyprinodontidae; Cyprinodontes;
OC Cyprinodontidae; Carassius;
CX NCB: TaxID=7957;
RN 11
RP SEQUENCE FROM N.A.
RA Tschudikova A.V., Kishida M., Wada K., Gaiard D.V.
RT "Protein characteristics of two CYP19 genes differentially expressed
RT in the brain and ovary of teleost fish."
PL J. Steroid Biochem. Mol. Biol. 80:1-12(2001).
DR EMBL: AF248895; AAK32616.1;
DR EMBL: AF248996; AAK32617.1;
FT NON TER 9
SQ SEQUENCE 9 AA; 961 MW; C49E76C775B187C4P 0.

Query Match 28.8%; Score 19; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8; 0; 1; 0; 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CY 7 GEL 9
DB 3 GEL 5

RESULT 12
ID QNAME?      PRELIMINARY;      PRT: 10 AA
AC G9C32
DT 01-NOV-1996 (TRENBERG) 01, Created:
DT 01-NOV-1996 (TRENBERG) 01, Last sequence update:
DT 01-NOV-1996 (TRENBERG) 01, Last annotation update:
DE Mycobacterium indicus
GX NCB: TaxID=1243;
RN 12
RP SEQUENCE FROM N.A.
RA Smith R.P.
RT Submitted (APR 1996) to the EMBL database (1996)
RL Submitted (APR 1996) to the EMBL database (1996)
DR EMBL: J05482; AAK60975.1;
SQ SEQUENCE 10 AA; 1137 MW; 5B3F37B5E456C7F54P 0.

Query Match 28.8%; Score 19; DB 12; Length 10;
Best Local Similarity 75.0%; Pred. No. 8; 0; 0; 0; 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CY 6 BSEL 9
DB 7 BSEL 10

RESULT 13
ID QNAME?      PRELIMINARY;      PRT: 10 AA
AC G9C40
DT 01-NOV-1996 (TRENBERG) 01, Created:
DT 01-NOV-1996 (TRENBERG) 01, Last sequence update:
DT 01-NOV-1996 (TRENBERG) 01, Last annotation update:
DE Mycobacterium indicus
GX NCB: TaxID=1243;
RN 13
RP SEQUENCE FROM N.A.
RA Smith R.P.
RT Submitted (APR 1996) to the EMBL database (1996)
RL Submitted (APR 1996) to the EMBL database (1996)
DR EMBL: J05482; AAK60975.1;
SQ SEQUENCE 10 AA; 1137 MW; 5B3F37B5E456C7F54P 0.

Query Match 28.8%; Score 19; DB 13; Length 10;
Best Local Similarity 75.0%; Pred. No. 8; 0; 0; 0; 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

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DT 01-JUL-1997 (TRENBERG) 04, Created:
DT 01-JUL-1997 (TRENBERG) 04, Last sequence update:
DT 01-DEC-2001 (TRENBERG) 19, Last annotation update:
DE MUD: alt XS (Fragment)
GN MCD: INC 45;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo
OX NCB: TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Sugawara M., Toyoshima T., Takeda S., Imota T., Kato K., Wada C.,
RT "Genomic DNA containing the insertion that is seen in the alternative
RT transcripts of MCD1."
DR Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB063802; BAA20388.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1161 MW; 9A6E507B1AB2CB05 CRC64;

Query Match 28.8%; Score 15; DB 4; Length 10;
Best Local Similarity 42.9%; Pred. No. 28-04; 3;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

CY 2 SEVERGE 8
DB 3 SEVERGE 9

RESULT 14
ID QNAME?      PRELIMINARY;      PRT: 10 AA
AC Q9G162
DT 01-MAR-2001 (TRENBERG) 16, Created:
DT 01-MAR-2001 (TRENBERG) 16, Last sequence update:
DT 01-OCT-2003 (TRENBERG) 22, Last annotation update:
DE Cytochrome c oxidase subunit 1 (fragment)
GN CCI.
OS Acetabosaura capra.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Anodontia; Agamidae; Dracoidea;
OC Acetabosaura;
CX NCB: TaxID 52216;
RN 11
RP SEQUENCE FROM N.A.
RA Vasey J.R., Schulte J.A., Papenfuss T.J.,
RT "Repetitive sequence may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs."
RL Mol. Biol. Evol. 14(1):19(1997).
RN 12
RP SEQUENCE FROM N.A.
RA Vasey J.R., Schulte J.A., Papenfuss T.J.,
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:237-256(2000).
DR EMBL: AF28498; AAK30711.1;
KW Mitochondrion
FT NON TER 13
SQ SEQUENCE 10 AA; 1115 MW; 8334E273641B1 CRC64;

Query Match 28.8%; Score 15; DB 4; Length 10;

```

Best Loc.: Similarity 75.0%; Pred. No. 20-04, 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Ov 2 STTC 5  
Db 2 STTC 5

# RESULT 15

Q941S6 PRELIMINARY; PRT: 10 AA.  
AC Q941S6  
DT 01-DEC-2001 (TEMBUREL 19, Created)  
ST 01-DEC-2001 (TEMBUREL 19, Last sequence update)  
CT 01-DEC-2001 (TEMBUREL 19, Last annotation update)  
FE Non-specific lipid transfer protein (Fragment)  
OS Pinus taeda (loblolly pine)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferales; Pinaceae; Pinus  
CX NCBI TaxID 33527  
RN 1;  
RF SEQUENCE FROM N.A.  
RC STRAIN PTLT94 1305;  
EA Jones D.F.;  
RT "Genetic mapping of the lipid transfer protein gene family in Pinus  
radiata and Pinus taeda";  
RL Submitted (MAR-2001) to the EMBL/GenBank/CCP databases.  
LR EMBL; AY029012; AA040261.1;  
FT NON-TER 10  
SQ SEQUENCE 10 AA; 1099 MW; 282C1E3B4H1AEV (P0664).

## Query Match

Best Local Similarity 28.8%; Score 15; DB 10; Length 10  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Ov 1 CTT 3  
Db 4 CTT 6

Search completed: November 5, 2003, 17:34:39  
Job time: 1.29 secs

GenCore version 5.1.6  
Copyright (c) 1993-2003 Compugen Ltd.

ON protein protein search, using sw model

Run on: November 5, 2003, 17:41:00, Search time 17.411 seconds  
Path of alignment: 40 618 Million cell updates/sec

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1 GSGTVEGEIA 10

Scoring table: BLOSUM-62

Gapop 12.0, Gapext 0.5

Searched: 1107861 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 101426

Maximum DB seq length: 2

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseg 19Jun03:  
1: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
2: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
3: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
4: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
5: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
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22: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
23: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT  
24: /SIDS1/gcgdata/geneseq/geneseg emb: AAL195 IAT

pred. No. is the number of results predicted by the database a  
score greater than or equal to the score of the best hit printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	21 AAB20473	Anti-body peptide
2	52	100.0	10	21 AAB25310	Anti-body peptide
3	52	100.0	10	22 AAU16615	Anti-body peptide
4	52	100.0	10	22 AAB51019	Anti-body peptide
5	52	100.0	10	23 AAB20473	Anti-body peptide
6	43	75.0	8	21 AAB20473	Anti-body peptide
7	43	75.0	8	21 AAB25310	Anti-body peptide
8	43	75.0	8	22 AAU16615	Anti-body peptide
9	43	75.0	8	22 AAB51019	Anti-body peptide

10	39	75.0	8	23 AAB20218	Human IgE immunoge
11	31	59.6	6	21 AAB25931	P2 mimotope peptid
12	31	59.6	6	22 AAU16615	Peptide 22sh deriv
13	31	59.6	6	23 AAB20230	Human IgE immunoge
14	27	51.9	9	24 AAB84333	HLA protein 121P2A
15	27	51.9	9	24 AAB84360	HLA protein 121P2A
16	27	51.9	9	24 AAB85789	HLA protein 121P2A
17	27	51.9	9	24 AAB85838	HLA protein 121P2A
18	27	51.9	9	24 AAB85855	HLA protein 121P2A
19	27	51.9	9	24 AAB86135	HLA protein 121P2A
20	27	51.9	9	24 AAB86502	HLA protein 121P2A
21	27	51.9	9	24 AAB86568	HLA protein 121P2A
22	27	51.9	9	24 AAB86784	HLA protein 121P2A
23	27	51.9	9	24 AAB86859	HLA protein 121P2A
24	27	51.9	9	24 AAB86895	HLA protein 121P2A
25	27	51.9	9	24 AAB87052	HLA protein 121P2A
26	27	51.9	9	24 AAB87155	HLA protein 121P2A
27	27	51.9	9	24 AAB87223	HLA protein 121P2A
28	27	51.9	9	24 AAB87334	HLA protein 121P2A
29	27	51.9	9	24 AAB87527	HLA protein 121P2A
30	27	51.9	9	24 AAB87867	HLA protein 121P2A
31	27	51.9	9	24 AAB87868	HLA protein 121P2A
32	27	51.9	9	24 AAB87940	HLA protein 121P2A
33	27	51.9	9	24 AAB87941	HLA protein 121P2A
34	27	51.9	9	24 AAB88162	HLA protein 121P2A
35	27	51.9	9	24 AAB88228	HLA protein 121P2A
36	27	51.9	9	24 AAB88335	HLA protein 121P2A
37	27	51.9	9	24 AAB88558	HLA protein 121P2A
38	27	51.9	9	24 AAB88635	HLA protein 121P2A
39	27	51.9	9	24 AAB88721	HLA protein 121P2A
40	27	51.9	9	24 AAB88722	HLA protein 121P2A
41	27	51.9	9	24 AAB89053	HLA protein 121P2A
42	27	51.9	9	24 AAB89102	HLA protein 121P2A
43	27	51.9	9	24 AAB89230	HLA protein 121P2A
44	27	51.9	9	24 AAB89273	HLA protein 121P2A
45	27	51.9	9	24 AAB89745	HLA protein 121P2A

ALIGNMENTS

RESULT 1

AAB20873

ID AAB20873 standard, peptide; 10 AA.

XX

AC AAB20873

XX

DT 13 (100.00%) (full entry)

XX

DE Anti-body peptide; mimotope sequence SEQ ID NO:11.

XX

KW Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;

KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;

KW malaria; cyclosporin; anti-allergic; neurotropic; neuroprotective;

KW proenzymes; Alzheimer's disease; allergy.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

PI Modified state

PT 10

XX /note: "amdated"

XX

PN W0200350073-A1

XX

PD 31-01-2000

XX

PF 20-FEB-2000, 2000W0-EP01457

XX

PR 25-FEB-1999, 99W0-000405

PR 25-FEB-1999, 99W0-000408

PR 25-FEB-1999, 99W0-000412

PR 25-FEB-1999, 99W0-000416

XX



PA TACAMAC ACAMBIUS RES LTD.  
 FA (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 PI FRIEDR M. JENSEN T;  
 XX WPI: 2001521967/57;  
 DR WPI: 2001521967/57;  
 XX A linkage comprising an immunogenic conjugate useful for treatment of IgE  
 PT mediated diseases  
 PS Example 4: Page 21; 48pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins, IgG, Fab, etc.)  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier vehicle  
 CC protein, for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE-mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope/tantigen to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AA016612 AA016913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX Sequence 10 AA;  
 SQ

Query Match: 100.0%; Score 52; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTTQGEELA 10  
 DB : CSTTQGEELA 10  
 1 1111111111  
 1 1111111111

RESULT 4  
 AA051029  
 ID AA051029 standard; Peptide; 10 AA;  
 XX AA051029;  
 XX 21 MAR 2000 (first entry);  
 XX IGE Peptide #1  
 XX Vaccine, immunoglobulin E; IgE; anti-allergy  
 XX Mammalia;  
 XX WO200004716-A2;  
 XX 14 DEC 2000;  
 XX 26 JUN 2000; 2000WO EP05364;  
 XX 08 JUN 1999; 9935-0013327;  
 XX (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Prieels J;  
 XX WPI: 2001601527/10;  
 XX New vaccine comprising allergy peptides intended to protect patients  
 PT useful for boosting an anti-allergy response in susceptible individuals  
 XX susceptible to an allergic response.  
 PS Claim 1: Page 21; 66pp; English.

XX The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 CC such peptide from IgE. The composition is useful as a vaccine or for  
 CC manufacturing a medicament for the prophylaxis or treatment of allergy  
 CC in particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.  
 XX Sequence 10 AA;  
 SQ

Query Match: 100.0%; Score 52; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTTQGEELA 10  
 DB : CSTTQGEELA 10  
 1 1111111111  
 1 1111111111

RESULT 5  
 ABJ00229  
 ID ABJ00229 standard; Peptide; 10 AA;  
 XX ABJ00229;  
 XX 02-SEP-2000 (first entry)  
 XX Human IgE immunogenic peptide SEQ ID NO: 13;  
 XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 XX vaccine; antiallergic.  
 XX Horse sapiens.  
 XX WO200216409-A2;  
 XX 28-FEB-2002  
 XX 17-AUG 2001; 2001WOEP09576;  
 XX 22-AUG 2000; 2000GH-020717;  
 XX (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX DEPT : PEPTIDE THERAPEUTICS LTD.  
 XX Friedr M. Jensen S; Funnell WG; Vinals Bassels VC;  
 XX WPI: 2001601474/57;  
 XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier  
 XX Claim 4: Page 9; 48pp; English.  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX Sequence 10 AA;  
 SQ

Query Match: 100.0%; Score 52; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTTQGEELA 10  
 DB : CSTTQGEELA 10  
 1 1111111111  
 1 1111111111

RESULT 6





AAU:6633  
 ID AAU:6633 standard; Peptide: 8 AA.  
 AC AAU16533,  
 XX  
 DT 07 NOV-2001 (first entry)  
 XX  
 DE Peptide P2 derived from Cepsilon2 region of human IgE.  
 XX  
 KW Human linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 CS Homo sapiens.  
 XX  
 EN WO2000145945-A2.  
 PD 28-JUN 2001.  
 XX  
 PF 21-DEC-2000; 2000WO-GB04935.  
 XX  
 ER 31-DEC-1999; 99GB-0030233.  
 PR 22-FEB 2000; 2000GB-0040396.  
 ER 22-AUG-2000; 2000GB-0029787.  
 ER 22-AUG 2000; 2000GB-0029708.  
 XX  
 FA JACAM; ACAMIS RES LTD.  
 PA (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 DI Philip N. Johnson T;  
 XX  
 ER WP: 2001-521967/57.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases.  
 XX  
 PS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier using a  
 CC protein; for use in a pharmaceutical composition of a vaccine. The  
 CC invention describes peptides derived from C-mutations of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE), which are used to produce conjugates of epitopes and carrier  
 CC compositions of the invention are useful in the treatment of a  
 CC condition for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16532 AAU16533 represent peptides derived from C-mutations of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 75.0%; Score 19; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 STTQEGEL 9  
 DB : STTQEGEL 9  
 |||||  
 RESULT 9  
 ABJ00219  
 ID ABJ00219 standard; Peptide: 8 AA.  
 XX  
 AC ABJ00219;  
 XX  
 DT 02 SEP 2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 2.  
 XX  
 KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; antiallergic.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200016409-A2.  
 PD 28-FEB 2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EP09576.  
 XX  
 PR 22-AUG-2000; 2000GB-0020717.  
 XX  
 PA (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PST); PEPTIDE THERAPEUTICS LTD.  
 XX  
 DI Friede M, Mason S, Cornwell WG, Vinals Bassols YC;  
 PT

XX  
 DE IgE peptide #2.  
 XX  
 KW Vaccine; immunoglobulin E; IgE; anti allergy.  
 XX  
 OS Maternalia.  
 XX  
 EN WO200014716-A2.  
 PD 14-DEC 2000.  
 XX  
 PF 06-JUN-2000; 2000WO-BE05164.  
 XX  
 PR 08-JUN-1999; 99GB-0013127.  
 XX  
 PA (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 DI Priele's J;  
 XX  
 ER WP: 2001-091150/10.  
 XX  
 PT New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual.  
 PT susceptible to an allergic response.  
 XX  
 PS Claim 5; Page 20; 26pp; English.  
 XX  
 CC The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 CC such peptide from IgE. The composition is useful as a vaccine or for  
 CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual, susceptible to an allergic response.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 75.0%; Score 39; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 STTQEGEL 9  
 DB : STTQEGEL 9  
 |||||  
 RESULT 10  
 ABJ00219  
 ID ABJ00219 standard; Peptide: 8 AA.  
 XX  
 AC ABJ00219;  
 XX  
 DT 02 SEP 2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 2.  
 XX  
 KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; antiallergic.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200016409-A2.  
 PD 28-FEB 2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EP09576.  
 XX  
 PR 22-AUG-2000; 2000GB-0020717.  
 XX  
 PA (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PST); PEPTIDE THERAPEUTICS LTD.  
 XX  
 DI Friede M, Mason S, Cornwell WG, Vinals Bassols YC;  
 PT



CC (e.g., nucleomolecules, polymers, dendrimers, proteins, proteins to be used  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g., a peptide) to a carrier using a  
 CC protein for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimetopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC adjuvant for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC Amino acid AA11693 represent peptides derived from or mimetopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 CC  
 CC Sequence 6 AA:  
 CC  
 CC Query Match 59.6%; Score 11; DB 24; Length 6;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 CC QY 3 TQEGE 8  
 CC DB 1 TQEGE 6  
 CC  
 CC RESULT 17  
 CC AEP00236  
 CC ID AEP00236 standard; Peptide; 6 AA.  
 CC XX AEP00236  
 CC AC AEP00236  
 CC DT 02 SEP 2002 (first entry)  
 CC LE Human IgE immunogenic peptide SEQ ID NO. 14  
 CC XX Immunogen: human IgE; immunoglobulin E; allotype: none other linkage:  
 CC XX vaccine; antiallergic.  
 CC CS Homo sapiens.  
 CC XX WC006016409-A2.  
 CC PN 28-FEB-2002.  
 CC XX 17 AUG 2002; 2002WO EP09596  
 CC XX 20 AUG 2002; 2002EP 010007.  
 CC PA (SMK) SWITZERLAND HERCAY BIOLOGICALS  
 CC XX (EP09596) PEPTIDE PHARMACEUTICS LTD.  
 CC P1 Fritsch N., Mann G., Turnell W.S., Vithaisalai V.,  
 CC DR WPT; 2002 489644/52.  
 CC XX Conjugate for use in vaccine for treatment of allergic diseases  
 CC PT disulfide bridge cyclized peptide and immunomodulation  
 CC XX Claim 4; Page 9; 45pp; English.  
 CC  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.  
 CC  
 CC Sequence 6 AA:  
 CC  
 CC Query Match 52.6%; Score 10; DB 24; Length 6;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 TQEGE 8  
 CC DB 1 TQEGE 6  
 CC  
 CC RESULT 17  
 CC AEP00236  
 CC ID AEP00236 standard; Peptide; 6 AA.  
 CC XX AEP00236  
 CC AC AEP00236  
 CC DT 02 SEP 2002 (first entry)  
 CC LE Human IgE immunogenic peptide SEQ ID NO. 14  
 CC XX Immunogen: human IgE; immunoglobulin E; allotype: none other linkage:  
 CC XX vaccine; antiallergic.  
 CC CS Homo sapiens.  
 CC XX WC006016409-A2.  
 CC PN 28-FEB-2002.  
 CC XX 17 AUG 2002; 2002WO EP09596  
 CC XX 20 AUG 2002; 2002EP 010007.  
 CC PA (SMK) SWITZERLAND HERCAY BIOLOGICALS  
 CC XX (EP09596) PEPTIDE PHARMACEUTICS LTD.  
 CC P1 Fritsch N., Mann G., Turnell W.S., Vithaisalai V.,  
 CC DR WPT; 2002 489644/52.  
 CC XX Conjugate for use in vaccine for treatment of allergic diseases  
 CC PT disulfide bridge cyclized peptide and immunomodulation  
 CC XX Claim 4; Page 9; 45pp; English.  
 CC  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.  
 CC  
 CC Sequence 6 AA:  
 CC  
 CC Query Match 52.6%; Score 10; DB 24; Length 6;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 TQEGE 8  
 CC DB 1 TQEGE 6  
 CC  
 CC RESULT 17  
 CC AEP00236  
 CC ID AEP00236 standard; Peptide; 6 AA.  
 CC XX AEP00236  
 CC AC AEP00236  
 CC DT 02 SEP 2002 (first entry)  
 CC LE Human IgE immunogenic peptide SEQ ID NO. 14  
 CC XX Immunogen: human IgE; immunoglobulin E; allotype: none other linkage:  
 CC XX vaccine; antiallergic.  
 CC CS Homo sapiens.  
 CC XX WC006016409-A2.  
 CC PN 28-FEB-2002.  
 CC XX 17 AUG 2002; 2002WO EP09596  
 CC XX 20 AUG 2002; 2002EP 010007.  
 CC PA (SMK) SWITZERLAND HERCAY BIOLOGICALS  
 CC XX (EP09596) PEPTIDE PHARMACEUTICS LTD.  
 CC P1 Fritsch N., Mann G., Turnell W.S., Vithaisalai V.,  
 CC DR WPT; 2002 489644/52.  
 CC XX Conjugate for use in vaccine for treatment of allergic diseases  
 CC PT disulfide bridge cyclized peptide and immunomodulation  
 CC XX Claim 4; Page 9; 45pp; English.  
 CC  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.  
 CC  
 CC Sequence 6 AA:  
 CC  
 CC Query Match 51.9%; Score 27; DB 24; Length 9;  
 CC Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 CC Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 TQEGE 8  
 CC DB 1 TQEGE 6  
 CC  
 CC RESULT 14  
 CC AEP00236  
 CC ID AEP00236 standard; Peptide; 9 AA.  
 CC XX AEP00236  
 CC AC AEP00236  
 CC DT 28 MAR 2003 (first entry)  
 CC LE Human protein 121P2A3; Peptide 4688.  
 CC XX  
 CC KW Human; 121P2A3; cytoskeletal; immunostimulant; vaccine; SSH;  
 CC KW humoral; immune response; cellular immune response;  
 CC KW suppression subtractive hybridisation; HLA; human leukocyte antigen  
 CC XX  
 CC OS Homo sapiens  
 CC XX WC0200293068 A2.  
 CC XX 24 OCT 2002.  
 CC PF 09 APR 2002; 2002WO US11359.  
 CC PR 10-APR-2001; 2001US-282739P.  
 CC PR 25-APR-2001; 2001US-286630P.  
 CC PR 22-JUN-2001; 2001US-300331P.  
 CC XX (AGEN) AGENSYS INC.  
 CC P1 Challita old PM, Raitano AB, Paris M, Hubert RS, Mitchell SC,  
 CC P1 Afar DM, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A,  
 CC DR WPT; 2001-032956/08.  
 CC  
 CC New composition comprising a substance that modulates the status of  
 CC 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 CC responses or in assessing the status of 121P2A3 gene products in normal  
 CC versus cancerous tissues.  
 CC  
 CC Claim 1; Page 14; 34pp; English.  
 CC  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in AEP0023644 - AEP0023655 represent peptides from the 121P2A3 variants of  
 CC the invention.

Job time : 33.333 secs

```

RESULT 15
ABP#4540
ID  ABP#4540 standard: peptide, 9 AA
XX  ABP#4540
XX
XX  24-NAR 2001 (first entry)
XX
XX  HLA Protein L112A1 peptide #915
XX
XX  Human IL12p33, cyclostatin immunostimulant, variant, 35H,
XX  human immune response, cellular immune response
XX  Suppression subtractive hybridization (SSH) HLA, human leukocyte antigen
XX
XX  Homo sapiens
XX
XX  W52002H3065 A21
XX
XX  24-OCT 2002
XX
XX  06-APR 2002; 2002WO-US11359
XX
XX  10-APR-2001; 2001US-282739P
XX  26-MAR 2001; 2001US 286632P
XX  22-JUN 2001; 2001US-300133P
XX
XX  AGENT 1 AGENTSYS INC
XX
XX  Chaitin-Leid JW, Raitano AB, Paris V, Hupert P, Mitchell D,
XX  Atar LH, Saffian D, Morrison K, Morrison KK, Gao W, Goldsmiths A
XX
XX  WI: 2003-092956/28
XX
XX  New composition comprising a substance that modulates the status of
XX  L12p33 polypeptides, useful for eliciting humoral or cellular immune
XX  responses or in assessing the status of L12p33 gene products in normal
XX  versus cancerous tissues
XX
XX  Claim 1: page 145; 362pp; English
XX
XX  The invention relates to a novel composition comprising a substance that
XX  modulates the status of a protein, L12p33, the gene status of the
XX  invention has cytostatic and immunomodulatory activity, and is useful as a
XX  vaccine. The L12p33 proteins and polypeptide subunits are useful for
XX  eliciting humoral or cellular immune responses, and are useful for
XX  useful for characterizing cytotoxicity, and for identifying and small
XX  locus, as tools that can be used in identifying and small
XX  in the chromosomal region that encodes L12p33, and is useful to
XX  mutant phenotype, and in assessing the status of L12p33 gene
XX  products in normal versus cancerous tissues. The protein are useful
XX  for generating and characterizing domain-specific vaccines, for
XX  identifying agents or cellular factors that bind to L12p33, and
XX  particular structure domain, and in various, benign, and/or harmless
XX  contexts, including cancer vaccines. The antibodies are useful as reagents
XX  with the product are useful in passive or active immunization, and in
XX  imaging methodologies for the management of cancer. The sequences shown
XX  in ABP#4540 ABP#5595 represent peptides from the L12p33 variants of
XX  the invention
XX
XX  Sequence 9 AA
XX
XX  Query Match 51.9% Score 27, 28-34; 1st 100%
XX  Best Local Similarity 83.3% Pref 100% 2nd 100%
XX  Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0
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XX  2 TPESE
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Computer Ltd.

OM: protein - protein search, using sw model  
Run on: November 5, 2003, 17:34:45 / Search time 21 seconds  
(without alignment)  
81,785 Million cell updates/sec

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1: STGEGRSLA 10

Scoring table: ELCSMA2

Gapex 12.0, Gapext 0.5

Searched: 644279 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 5116

Minimum DP seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 5: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 6: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 7: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 8: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 9: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 10: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 11: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 12: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
- 13: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt
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- 18: /sgn2\_6/prodata/2/pubpaar/US09\_PUBCOMB.ppt

Proc. No. is the number of results (positivity of the search)  
score greater than or equal to the score of the best alignment  
and is derived by analysis of the first 45 summaries

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	75.0	8	12	US-10-082-014-274
2	39	75.0	8	12	US-10-082-014-274
3	39	75.0	9	12	US-10-082-014-274
4	39	75.0	9	12	US-10-082-014-274
5	25	48.1	9	9	US-09-812-122-122
6	25	48.1	9	10	US-09-812-122-122
7	23	44.2	9	9	US-09-812-122-122
8	23	44.2	9	12	US-10-082-014-274
9	23	44.2	9	12	US-09-812-122-122
10	23	44.2	9	12	US-09-812-122-122
11	23	44.2	10	12	US-09-812-122-122
12	23	44.2	10	12	US-09-812-122-122
13	23	44.2	10	12	US-09-812-122-122
14	23	44.2	10	12	US-09-812-122-122
15	22	42.3	9	11	US-09-809-638-62

16	22	42.3	9	11	US-09-809-638-62
17	22	42.3	9	11	US-09-809-638-62
18	22	42.3	10	11	US-09-809-638-62
19	22	42.3	10	11	US-09-809-638-62
20	22	42.3	10	11	US-09-809-638-62
21	22	42.3	10	11	US-09-809-638-62
22	21	40.4	7	9	US-09-989-789-1221
23	21	40.4	7	11	US-09-989-789-1221
24	21	40.4	7	11	US-09-989-789-1221
25	21	40.4	7	11	US-09-989-789-1221
26	21	40.4	7	11	US-09-989-789-1221
27	21	40.4	7	11	US-09-989-789-1221
28	21	40.4	9	9	US-09-989-789-1221
29	21	40.4	9	12	US-10-082-014-274
30	21	40.4	9	12	US-10-082-014-274
31	21	40.4	9	12	US-09-942-052-429
32	21	40.4	9	12	US-09-942-052-429
33	21	40.4	9	12	US-09-942-052-429
34	21	40.4	10	9	US-09-942-052-429
35	21	40.4	10	10	US-09-942-052-429
36	21	40.4	10	11	US-09-942-052-429
37	21	40.4	10	11	US-09-942-052-429
38	21	40.4	10	11	US-09-942-052-429
39	21	40.4	10	11	US-09-942-052-429
40	21	40.4	10	11	US-09-942-052-429
41	21	40.4	10	11	US-09-942-052-429
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45	21	40.4	10	12	US-09-942-052-429

ALIGNMENTS

RESULT 1  
US-10-082-014-274  
; Sequence 274, Application US/10082014  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N TERMINAL C  
; FILE REFERENCE: J01-130 0 4564/65124  
; CURRENT APPLICATION NUMBER: US/10/082-014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/910,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: PatAlign version 3.1  
; SEQ ID NO: 274  
; LENGTH: 8  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-10-082-014-274

Query Match 75.0% Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred No. 5.8e+05;  
Matches #: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 STGEGRSL 9  
||| |||  
Db : STGEGRSL 8

RESULT 2  
US-10-372-076-128  
; Sequence 128, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10372076  
CURRENT FILING DATE: 2003-02-21  
PRIOR FILING DATE: 10/082,294  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 128  
LENGTH: 8  
TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-372-076-128

Query Match 75.0% Score 39; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 1 STORED 8

RESULT 3  
US-10-372-076-128  
Sequence 137, Application US/10082076  
Patent No. US2003018589A1  
GENERAL INFORMATION:  
APPLICANT: Biotech, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS PARTICLES STABILIZED WITH AN N-TERMINAL CY  
FILE REFERENCE: 10372076  
CURRENT APPLICATION NUMBER: US/10372076  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/930,915  
PRIOR FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 283  
LENGTH: 9  
TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-372-076-128

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 1 STORED 8

RESULT 4  
US-10-372-076-128  
Sequence 137, Application US/10372076  
Patent No. US2003019864A1  
GENERAL INFORMATION:  
APPLICANT: Biotech, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS PARTICLES STABILIZED WITH AN N-TERMINAL CY  
FILE REFERENCE: 10372076  
CURRENT APPLICATION NUMBER: US/10372076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/082,294  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 137  
LENGTH: 9

TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-372-076-137

Query Match 75.0% Score 39; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 1 STORED 8

RESULT 5  
US-09-832-132-12  
Sequence 12, Application US/09832182  
Patent No. US2003002979A1  
GENERAL INFORMATION:  
APPLICANT: Resnicoff, David Abraham, and Mariana Resnicoff  
TITLE OF INVENTION: Method of Inducing Resistance to Tumor Growth  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US2003002979A1  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/832,382  
FILING DATE: 11-APR-2001  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/564,641  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legatid  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: TCU 2137  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-832-132-12  
Query Match 49.1% Score 25; DB 9; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 STORED 7  
DB 1 STORED 9

RESULT 6  
US-09-835-133-3  
Sequence 3, Application US/09835853  
Patent No. US2003016513A1  
GENERAL INFORMATION:  
APPLICANT: BASENGA, Renato L.  
APPLICANT: RESNICOFF, Mariana  
APPLICANT: BEANS, David  
TITLE OF INVENTION: HIV PARTICLES AND METHODS OF USE

Query Match 49.1% Score 25; DB 9; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 STORED 7  
DB 1 STORED 9

1 NUMBER OF SEQUENCES: 23  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: HALE and DORR LLP  
 4 STREET: 1455 Pennsylvania Avenue, N.W.  
 5 CITY: Washington  
 6 STATE: D.C.  
 7 COUNTRY: USA  
 8 ZIP: 20004  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC-DOS/MS-DOS  
 13 SOFTWARE: Parent In Release #1.0, Version #1.0  
 14 CURRENT APPLICATION DATA:  
 15 APPLICATION NUMBER: US/09/835,859  
 16 FILING DATE:  
 17 CLASSIFICATION:  
 18 PRIOR APPLICATION DATA:  
 19 APPLICATION NUMBER: US 08/704,344  
 20 FILING DATE: 28-AUG-1996  
 21 ATTORNEY/AGENT INFORMATION:  
 22 NAME: WIXON, Henry N.  
 23 REGISTRATION NUMBER: 32,273  
 24 REFERENCE/DOCKET NUMBER: 104222-196  
 25 TELECOMMUNICATION INFORMATION:  
 26 TELEPHONE: (202) 942-8459  
 27 TELEFAX: (202) 942-8484  
 28 INFORMATION FOR SEQ ID NO: 3:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 9 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: single  
 33 TOPOLOGY: linear  
 34 MOLECULE TYPE: peptide  
 35 HYPOTHECA: NO  
 36 ANTI-SENSE: NO  
 37 US 09-835 853 3

Query Match: 49.2%; Score 23; DB 9; Length 9;  
 Best Local Similarity: 57.1%; Pred. No. 5,8e+05;  
 Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSTT 9  
 DB 1 CSTT 9

RESULT 9  
 1 US-09-832 713-92  
 2 Sequence 92, Application US/0981273  
 3 Publication No. US2002009924A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: ESTELL, David A.  
 6 APPLICANT: Chen, Yiyou  
 7 APPLICANT: Murray, Christopher J.  
 8 APPLICANT: Tjeltjema, Pilar  
 9 TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 10 FILE REFERENCE: GC617-2  
 11 CURRENT APPLICATION NUMBER: US/09/831,129  
 12 CURRENT FILING DATE: 2001-04-11  
 13 PRIOR APPLICATION NUMBER: US 60/137,149  
 14 PRIOR FILING DATE: 2000-04-14  
 15 NUMBER OF SEQ ID NOS: 117  
 16 SOFTWARE: Pas-SEQ for Windows Version 4.0  
 17 SEQ ID NO 92  
 18 LENGTH: 9  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: peptides screened from a phage display random  
 23 OTHER INFORMATION: peptide library  
 24 US-09-832 713-92

Query Match: 44.2%; Score 23; DB 9; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 5,8e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTT 4  
 DB 1 CSTT 4

RESULT 8  
 1 US-10-303 331-92  
 2 Sequence 92, Application US/1030331  
 3 Publication No. US2003052976A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Janssen, Giselle G.  
 6 APPLICANT: Murray, Christopher J.  
 7 APPLICANT: Kinetzky, Deborah S.  
 8 TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 9 FILE REFERENCE: GC617-3  
 10 CURRENT APPLICATION NUMBER: US/10/303,231  
 11 CURRENT FILING DATE: 2002-11-25  
 12 PRIOR APPLICATION NUMBER: US 09/842,723  
 13 PRIOR FILING DATE: 2002-04-11  
 14 PRIOR APPLICATION NUMBER: US 60/197,259  
 15 PRIOR FILING DATE: 2000-04-14  
 16 NUMBER OF SEQ ID NOS: 125  
 17 SOFTWARE: PasSEQ for Windows Version 4.0  
 18 SEQ ID NO 92  
 19 LENGTH: 9  
 20 TYPE: PPT  
 21 ORGANISM: Artificial Sequence  
 22 FEATURE:  
 23 OTHER INFORMATION: peptides screened from a phage display random  
 24 OTHER INFORMATION: peptide library  
 25 US-10-303 331-92

Query Match: 44.2%; Score 23; DB 12; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 5,8e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTT 4  
 DB 1 CSTT 4

RESULT 9  
 1 US-09-831 39-119  
 2 Sequence 119, Application US/0981319  
 3 Publication No. US20030175960A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureci, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof  
 9 FILE REFERENCE: JUC 5622.1  
 10 CURRENT APPLICATION NUMBER: US/09/831,039  
 11 CURRENT FILING DATE: 2001-04-12  
 12 PRIOR APPLICATION NUMBER: US 09/459,455  
 13 PRIOR FILING DATE: 1999-09-30  
 14 PRIOR APPLICATION NUMBER: US 09/344,340  
 15 PRIOR FILING DATE: 1999-06-25  
 16 PRIOR APPLICATION NUMBER: US 09/105,839  
 17 PRIOR FILING DATE: 1999-06-26  
 18 PRIOR APPLICATION NUMBER: US 08/051,130  
 19 PRIOR FILING DATE: 1997-05-05  
 20 NUMBER OF SEQ ID NOS: 143  
 21 SEQ ID NO 119  
 22 LENGTH: 9  
 23 TYPE: PPT  
 24 ORGANISM: Homo sapiens  
 25 US-09-831 39-119

Query Match: 44.2%; Score 23; DB 12; Length 9;



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Best Local Similarity 55.68, Score 41, DB 12, Length 10,
Matches 5, Conservative 1, Mismatches 3, Indels 0, Gaps 0;

QY 2 STTQFDELA 10
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DB 1 AIPMEARELA 9

RESULT 10
US-09-572-270A-241
; Sequence 241, Application US/09572270A
; Publication No. US20030145168A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter-complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09572270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 241:
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in (CAM2 OR CAL1) AND (AM3 AND
US-09-572-270A-241
Best Local Similarity 44.28, Score 23, DB 12, Length 10;
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 1 CSTTQE F
   | | | |
DB 2 CTTTKE 7

RESULT 11
US-09-572-270A-935
; Sequence 935, Application US/09572270A
; Publication No. US20030145168A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter-complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09572270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 935:
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in F1622.5, at 27.36 and may interact with
US-09-572-270A-935
Best Local Similarity 44.28, Score 23, DB 12, Length 10;
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 1 CSTT 4
   | | |
DB 4 CSTT 7

RESULT 14
US-10-364-414-12
; Sequence 12, Application US/10364414
; Publication No. US20030195250A1
; GENERAL INFORMATION:
; APPLICANT: CAGRP, Eike
; APPLICANT: KNUH, Alexander
; APPLICANT: GLO, Iluyi
; APPLICANT: Genetic, Sashu
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: US/09572270A
; CURRENT APPLICATION NUMBER: US/10364414
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/465,428
; PRIOR FILING DATE: 2002-04-13
; NUMBER OF SEQ ID NOS: 11
```

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Best Local Similarity 55.68, Score 41, DB 12, Length 10,
Matches 5, Conservative 1, Mismatches 3, Indels 0, Gaps 0;

QY 2 STTQFDELA 10
   | | | |
DB 1 AIPMEARELA 9

RESULT 10
US-10-377-277-114
; Sequence 114, Application US/10377277
; Publication No. US20030185444A1
; GENERAL INFORMATION:
; APPLICANT: Takeda, Golem
; APPLICANT: Sashu, Golem
; APPLICANT: Pfeundscher, Michael
; APPLICANT: Ramenec, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Detecting
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From SSX Gene and
; FILE REFERENCE: US/09572270A
; CURRENT APPLICATION NUMBER: US/10377277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09344117
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/101,873
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 08/851,136
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 114:
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-377-277-114
Best Local Similarity 44.28, Score 23, DB 12, Length 10;
Matches 5, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 2 STTQFDELA 10
   | | | |
DB 1 AIPMEARELA 9

RESULT 11
US-09-572-270A-935
; Sequence 935, Application US/09572270A
; Publication No. US20030145168A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter-complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09572270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 935:
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in F1622.5, at 27.36 and may interact with
US-09-572-270A-935
Best Local Similarity 44.28, Score 23, DB 12, Length 10;
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 1 CSTTQE F
   | | | |
DB 2 CTTTKE 7

RESULT 14
US-10-364-414-12
; Sequence 12, Application US/10364414
; Publication No. US20030195250A1
; GENERAL INFORMATION:
; APPLICANT: CAGRP, Eike
; APPLICANT: KNUH, Alexander
; APPLICANT: GLO, Iluyi
; APPLICANT: Genetic, Sashu
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: US/09572270A
; CURRENT APPLICATION NUMBER: US/10364414
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/465,428
; PRIOR FILING DATE: 2002-04-13
; NUMBER OF SEQ ID NOS: 11
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1 SOFTWARE: Patent in version 3.2
2 SEQ ID NO: 10
3 LENGTH: 10
4 TYPE: PRT
5 ORGANISM: Homo sapiens
6 US 10-164 614-12

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Query Match: 44.2% Score 211 SB 127 Length 10,
Best Local Similarity 55.6% Pred. No. 5,80,021
Matches 5: Conservative 1; Mismatches 3; Inp-Is 0; Sup 0;

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QY 2 STQCEHLE 10
DB : ATPMEAFLE 9

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RESULT 15
US-09-909-618-61
1 Sequence 61: Application US/09009519
2 Publication No. US20030059895A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Paris
5 APPLICANT: Mia M. Chailita-Bid
6 APPLICANT: Steve Chappell Mitchell
7 APPLICANT: Ramie E.H. Atar
8 APPLICANT: Arthur H. Raitano
9 APPLICANT: Ava Jakobovits
10 TITLE OF INVENTION: 124P508: A TISSUE SPECIFIC PROTEIN
11 TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
12 FILE REFERENCE: 129.35US01
13 CURRENT APPLICATION NUMBER: US/09/603,618
14 CURRENT FILING DATE: 2001-03-14
15 NUMBER OF SEQ ID NOS: 746
16 SOFTWARE: FastSeq for Windows Version 4.7
17 SEQ ID NO: 61
18 LENGTH: 9
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-909-618-61

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Query Match: 42.3% Score 207 SB 117 Length 10
Best Local Similarity 80.0% Pred. No. 5,80,009
Matches 4: Conservative 1; Mismatches 3; Inp-Is 0; Sup 0;

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QY 1 EUEIA 10
DB : EUEIA 9

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Search completed: November 5, 2003, 11:14:27
Job time: 1.24 secs

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Alt.	Del.	Score	Query Match	Length	DB	ID	Description
1		34	48	1	9	3	US-08-054 441 3
2		35	49	1	9	4	US-08-049 440 10
3		35	49	1	9	4	US-09-014 440 10
4		35	49	1	9	4	US-09-138 440 10
5		35	49	1	9	4	US-09-144 047 10
6		35	49	1	9	4	US-08-144 511A 9
7		35	49	1	10	2	US-08-144 511A 9
8		35	49	1	10	3	US-08-181 662 29
9		35	49	1	10	4	US-09-1664 235 29
10		35	49	1	10	4	US-08-274 028 9
11		35	49	1	9	3	US-09-258 754 143
12		35	49	1	9	2	US-09-342 107 143
13		35	49	1	7	2	US-08-369 504 9
14		35	49	1	7	3	US-09-128 467 9
15		35	49	1	9	1	US-08-615 191 10
16		35	49	1	9	1	US-08-191 131A 24
17		35	49	1	9	2	US-08-290 268 19
18		35	49	1	9	2	US-08-386 338 39
19		35	49	1	9	4	US-09-161 740 8
20		35	49	1	10	2	US-05-764 644 133
21		35	49	1	10	3	US-05-793 425 133
22		35	49	1	10	3	US-08-371 225 135
23		35	49	1	10	3	US-08-374 225 135
24		35	49	1	10	3	US-09-244 298A 12
25		35	49	1	10	3	US-09-311 96 21
26		35	49	1	10	3	US-09-311 738 8
27		35	49	1	10	3	US-09-316 738 133
28		35	49	1	10	4	US-09-461 607 133
29		35	49	1	10	4	US-09-540 80 133

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NUMBER OF SEQ ID NOS: 132  
 SEQ ID NO 119  
 LENGTH: 2  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-914-088-24

Query Match 44.2% Score 23 DB 4 Length 10  
 Best Local Similarity 55.6% Pred No. 2.3e+02  
 Matches 5 Conservative 1 Mismatches 1 Indels 0 Gaps 0

QY 2 STTQ 5  
 DB 1 ATNFAELA 3

RESULT 6  
 US-08-441-513A-9  
 Sequence 9, Application US/08441513A  
 Patent No. 5981480  
 GENERAL INFORMATION:  
 APPLICANT: Utef, Roman  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Winslow, John W.  
 TITLE OF INVENTION: Patropic Neurotrophic Factors

NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 SEQID TYPE: 1.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winntatic (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/441513A  
 FILING DATE: 15-May-1995

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/25917  
 FILING DATE: 01-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Turcotte, P.D., T-00141  
 REGISTRATION NUMBER: 36,709  
 REFERENCE NUMBER: 802000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-225-8674  
 TELEFAX: 650-225-9881

INFORMATION FOR SEQ ID NO: 1  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-441-513A-9

Query Match 44.2% Score 23 DB 4 Length 10  
 Best Local Similarity 55.6% Pred No. 2.3e+02  
 Matches 5 Conservative 1 Mismatches 1 Indels 0 Gaps 0

QY 2 STTQ 5  
 DB 1 ATNFAELA 3

RESULT 7  
 US-08-581-662-29  
 Sequence 29, Application US/08581662  
 Patent No. 612125  
 GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang  
 TITLE OF INVENTION: Treatment of Balance Impairments  
 FILE REFERENCE: P09F1  
 CURRENT APPLICATION NUMBER: US/08/581,662  
 CURRENT FILING DATE: 1995 12 29  
 NUMBER OF SEQ ID NOS: 36  
 SEQ ID NO 29  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-581-662-29

Query Match 44.2% Score 23 DB 3 Length 10  
 Best Local Similarity 40.3% Pred No. 2.3e+02  
 Matches 4 Conservative 0 Mismatches 1 Indels 0 Gaps 0

QY 1 CSTTQ 5  
 DB 2 CRTTQ 6

RESULT 8  
 US-09-664-295-29  
 Sequence 29, Application US/09664295  
 Patent No. 6429196  
 GENERAL INFORMATION:  
 APPLICANT: Gao, Wei-Qiang  
 TITLE OF INVENTION: Treatment of Balance Impairments  
 FILE REFERENCE: GENENT.051C1  
 CURRENT APPLICATION NUMBER: US/09/664,295  
 CURRENT FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: US 08/581,662  
 PRIOR FILING DATE: 1995 12-29  
 NUMBER OF SEQ ID NOS: 37  
 SEQ ID NO 29  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-664-295-29

Query Match 44.2% Score 23 DB 4 Length 10  
 Best Local Similarity 40.3% Pred No. 2.3e+02  
 Matches 4 Conservative 0 Mismatches 1 Indels 0 Gaps 0

QY 1 CSTTQ 5  
 DB 2 CRTTQ 6

RESULT 9  
 US-08-794-049-7  
 Sequence 29, Application US/08794049  
 Patent No. 6503728  
 GENERAL INFORMATION:  
 APPLICANT: Utef, Roman  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Winslow, John W.  
 TITLE OF INVENTION: Patropic Neurotrophic Factors  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 SEQID TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winntatic (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/794,049

? FILING DATE: 01-Feb-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/253939  
 ? FILING DATE: 03 JUN 1994  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: TORCHIA, PH.D., Timothy E.  
 ? REGISTRATION NUMBER: 36,700  
 ? REFERENCE/DOCKET NUMBER: P09080  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 800/225-8674  
 ? TELEFAX: 800/352-9891  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 10 amino acids  
 ? TYPE: Amino Acid  
 ? TOPOLOGY: linear  
 ?  
 US 09 914 088 24

Query Match 44.2% Score 23 DB 4 Length 10  
 Best Local Similarity 80.0% Pred No 2.5e+05  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CDTQ 5  
 Db 2 CDTQ 4

RESULT 12  
 US 09 914 088 24  
 ? Sequence 143, Application US/032539-4  
 ? Patent No. 6174687  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RUSGALLI, EKKI  
 ? APPLICANT: PASQUALINI, RENALDO  
 ? APPLICANT: RIGOTTE, DANIEL  
 ? TITLE OF INVENTION: Methods of identifying and removing nucleic acids using  
 ? TITLE OF INVENTION: Membrane Dipeptides  
 ? FILE REFERENCE: P. 17, 3443  
 ? CURRENT APPLICATION NUMBER: US/09-914-088-24  
 ? FILING DATE: 1999-02-26  
 ? EARLIER APPLICATION NUMBER: 09/145,111  
 ? EARLIER FILING DATE: 1998-03-13  
 ? NUMBER OF SEQ ID NOS: 452  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 143  
 ? LENGTH: 4  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence  
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 US-09-914-088-24

Query Match 42.3% Score 22 DB 4 Length 10  
 Best Local Similarity 80.0% Pred No 2.5e+05  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CDTQ 5  
 Db 1 CDTQ 4

RESULT 11  
 US 09 914 088 24  
 ? Sequence 143, Application US/090421-2  
 ? Patent No. 6232187  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RUSGALLI, EKKI  
 ? APPLICANT: PASQUALINI, RENALDO  
 ? TITLE OF INVENTION: Molecules that bind to viral nucleic acid  
 ? TITLE OF INVENTION: Issues  
 ? FILE REFERENCE: P. 17, 2892  
 ? CURRENT APPLICATION NUMBER: US/09-914-088-24

? CURRENT FILING DATE: 1998 03-13  
 ? NUMBER OF SEQ ID NOS: 436  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 143  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 US-09-914-088-24

Query Match 42.3% Score 22 DB 4 Length 9  
 Best Local Similarity 80.0% Pred No 2.5e+05  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CDTQ 5  
 Db 1 CDTQ 5

RESULT 12  
 US-08-869-506-9  
 ? Sequence 9, Application US/08869506  
 ? Patent No. 5827710  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Uchida, Kohji  
 ? APPLICANT: Matsukawa, Hirokazu  
 ? APPLICANT: Matsuo, Yushi  
 ? APPLICANT: Fujita, Teyosi  
 ? TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
 ? TITLE OF INVENTION: LACTATE DEHYDROGENASE  
 ? NUMBER OF SEQUENCES: 11  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: NIXON & VANDERHAVE P.C.  
 ? STREET: 1100 N. 5827710th Glete Rd. 8th floor  
 ? CITY: Arlington  
 ? STATE: VA  
 ? COUNTRY: USA  
 ? ZIP: 22201-4741  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/869,506  
 ? FILING DATE: 05-JUN-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 7397/1994  
 ? FILING DATE: 29 MAR 1996  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Crawford, Arthur R.  
 ? REGISTRATION NUMBER: 25,327  
 ? REFERENCE/DOCKET NUMBER: 159-41  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 703-816-4000  
 ? TELEFAX: 703-816-4100  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STANDARDS:  
 ? TOPOLOGY: linear  
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 US-08-869-506-9

Query Match 40.4% Score 21 DB 2 Length 7  
 Best Local Similarity 100.0% Pred No 2.5e+05  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CDTQ 5  
 Db 1 CDTQ 4

```

1  ADDRESS:  OBLON, SPIVAK, MCCLELLAND, KAISER & NEUSTADT,
2  ADDRESSEE:  P.C.
3  STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
4  CITY:  ARLINGTON
5  STATE:  VA
6  COUNTRY:  USA
7  ZIP:  22202
8  COMPUTER READABLE FORM:
9  MEDIUM TYPE:  Floppy disk
10  COMPUTER:  IBM PC compatible
11  OPERATING SYSTEM:  PC DOS/MS-DOS
12  SOFTWARE:  Patent In Release #1.0, Version #1.30
13  CURRENT APPLICATION DATA:
14  APPLICATION NUMBER:  US/08/615,181
15  FILING DATE:  04 APR 1996
16  CLASSIFICATION:  424
17  PRIOR APPLICATION DATA:
18  APPLICATION NUMBER:  PCT/JP94/01756
19  FILING DATE:  19 OCT 1994
20  PRIOR APPLICATION DATA:
21  APPLICATION NUMBER:  JP 261302/1993
22  FILING DATE:  19 OCT 1993
23  ATTORNEY/AGENT INFORMATION:
24  NAME:  OBLON, NORMAN F.
25  REGISTRATION NUMBER:  24,618
26  REFERENCE/DOCKET NUMBER:  10-736-0 PCT
27  TELECOMMUNICATION INFORMATION:
28  TELEPHONE:  703-413-3000
29  TELEFAX:  703-413-2220
30  INFORMATION FOR SEQ ID NO. 10:
31  SEQUENCE CHARACTERISTICS:
32  LENGTH:  9 amino acids
33  TYPE:  amino acid
34  STRANDEDNESS:  single
35  TOPOLOGY:  linear
36  MOLECULE TYPE:  peptide
37  ORIGINAL SOURCE:
38  ORGANISM:  HUMAN IMMUNODEFICIENCY VIRUS
39  US-09-914-088-24
40
41  Query Match      40.4%  Score 21:  DB 1:  Length 9;
42  Best Local Similarity  66.7%  Prod. No. 2.5e+05;
43  Matches      4;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;
44
45  QY      4  QSEQEL 9
46      |  |  |
47  DB      4  TEEAEL 9
48
49  RESULT 14
50  US-09-914-088-24
51  Sequence 10, Application US/08/615,181
52  Patent No. 576666
53  GENERAL INFORMATION:
54  APPLICANT:  Calenoff, Emanuel
55  TITLE OF INVENTION:  Immunogenic Cancer Proteins and Peptides
56  TITLE OF INVENTION:  and Method of Use
57  NUMBER OF SEQUENCES:  16
58  CORRESPONDENCE ADDRESS:
59  ADDRESSEE:  Arnold, White & Durkee
60  STREET:  321 N. 5763164th Clark Street, Suite 800
61  CITY:  Chicago
62  STATE:  IL
63  COUNTRY:  USA
64  ZIP:  60610
65  COMPUTER READABLE FORM:
66  MEDIUM TYPE:  Floppy disk
67  COMPUTER:  IBM PC compatible
68  OPERATING SYSTEM:  PC DOS/MS-DOS
69  SOFTWARE:  Patent In Release #1.0, Version #1.25
70  CURRENT APPLICATION DATA:
71  APPLICATION NUMBER:  US/08/615,181
72  FILING DATE:  11 JAN 1994

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1 CLASSIFICATION: 416
2
3 ATTORNEY/AGENT INFORMATION:
4 NAME: No. 576364dруп, Thomas H
5 REGISTRATION NUMBER: 43,368
6 REFERENCE/DOCKET NUMBER: DW10102
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 412-744-0030
9 TELEFAX: 412-755-4489
10
11 INFORMATION FOR SEQ ID NO: 36:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 3 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 TECHNOLOGY: chemical
17 MOLECULE TYPE: peptide
18 FEATURE:
19 NAME/KEY: Xaa
20 LOCATION: 5
21 IDENTIFICATION METHOD: Phosphorylated Threonine
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23 US-08-191-338A-16
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25 Query Match 40.4% Score 212 DB 17, 19, 19, 19, 19
26 Best Local Similarity 57.1% Pfam No. 2, 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100
27 Matches: 4; Conservative 2; Variations 1; Mismatches 1; Gaps 0;
28
29 QY 3 TROPHIN 9
30 ILK 1
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GenCore version: 5.1.6  
Copyright 1993-2003 Compugen Ltd.

OX protein - protein search, using SW model

Run on: November 5, 2003, 18:41:05, Search time: 0.0 seconds  
Without alignment  
62,889 Modified cells updated/used

Title: US 09 914-088-26

Perfect score: 66

Sequence: 1 CSQKWLSDPT 11

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 28108 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 1106

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 751:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	34.8	10	2 A49187	gonadotropin-releasing hormone 111 - sea lamprey
2	21	31.8	11	2 PT0273	Ig heavy chain CRD
3	20	30.3	10	1 RH503	penicillinase B1
4	20	30.3	10	1 RH504	penicillinase B2
5	20	30.3	10	1 RH505	penicillinase B3
6	20	30.3	10	1 RH506	penicillinase B4
7	20	30.3	10	1 A61124	penicillinase B5
8	20	30.3	10	2 B46240	penicillinase B6
9	20	30.3	10	2 A46240	penicillinase B7
10	20	30.3	10	2 A21114	penicillinase B8
11	19	28.8	10	2 PQ0177	gonadotropin-releasing hormone 111 - sea lamprey
12	19	28.8	10	2 A60547	gonadotropin-releasing hormone 111 - sea lamprey
13	19	28.8	11	2 C59151	protein tyrosine kinase
14	19	28.8	11	2 T17041	cytochrome-c oxidase
15	18	27.3	6	2 S2981	Na+/K+-exchanging ATPase
16	18	27.3	7	2 PH602	Ig B chain V-D-Jr
17	18	27.3	10	2 PT0289	Ig heavy chain CRD
18	18	27.3	11	2 S3275	lysozyme
19	17	25.8	8	2 XGH02	alpha-1-glycoprotein
20	16	24.2	7	2 PT0576	T-cell receptor beta chain
21	16	24.2	8	2 T14576	hypothetical protein
22	16	24.2	9	2 A43843	cell surface adhesion molecule
23	16	24.2	9	2 PT0241	Ig heavy chain CRD
24	16	24.2	10	2 S27573	cytochrome-c oxidase
25	16	24.2	10	2 T17054	cytochrome-c oxidase
26	16	24.2	11	2 T17018	cytochrome-c oxidase
27	15	22.7	5	2 PT0672	T-cell receptor beta chain
28	15	22.7	7	2 S33567	tubulin beta-3 chain
29	15	22.7	7	4 A58725	penicillinase B9

30	15	22.7	8	2 S59622	metallothionein 18
31	15	22.7	9	2 A60108	exotoxin A - Srept
32	15	22.7	9	2 PT0324	Ig heavy chain CRD
33	15	22.7	9	2 A37227	macrophage chemotaxis factor
34	15	22.7	9	2 PT0562	T-cell receptor beta chain
35	15	22.7	10	2 T40332	trypsinogen - Bac
36	15	22.7	10	2 T17035	cytochrome-c oxidase
37	15	22.7	10	2 T17035	cytochrome-c oxidase
38	15	22.7	10	2 T17035	cytochrome-c oxidase
39	15	22.7	10	2 T17035	cytochrome-c oxidase
40	15	22.7	10	2 T17035	cytochrome-c oxidase
41	15	22.7	10	2 T17035	cytochrome-c oxidase
42	15	22.7	10	2 T17035	cytochrome-c oxidase
43	15	22.7	11	2 A33571	follicle-stimulating hormone
44	15	22.7	11	2 B41946	T-cell receptor gamma chain
45	15	22.7	11	2 S53436	beta-D-galactosidase

ALIGNMENTS

RESULT 1

A49187  
gonadotropin-releasing hormone 111 - sea lamprey  
C:Species: Petromyzon marinus (sea lamprey)  
C:Date: 19-Dec-1993 #sequence\_revision: 18-Nov-1994 #text\_change: 03-Mar-1995  
C:Accession: A49187  
R:Owner: S.A. Chiang, Y.C. Lovas, S. Conlon, J.M.  
E:Endocrinology 132, 1125-1131, 1993  
A:Title: Primary structure and biological activity of a third gonadotropin-releasing hormone receptor from sea lamprey  
A:Reference number: A49187; MUI:9178316; PMID:8440174  
A:Accession: A49187  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SOW>  
A:Experimental source: brain  
A:Note: sequence extracted from NCBI backbone (NCBI:126381)

Query Match: 34.8%; Score 23; DB 2; Length 10;  
Best Local Similarity: 50.0%; Pred. No. 6.9e+02;  
Matches: 3; Conservative: 1; Mismatches: 2; Indels: 0; Gaps: 0;

QY 4 KHWLSD 9  
DB 1 EHWSD 6

RESULT 2

PT0273  
Ig heavy chain CRD region (clone 1-109A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Sep-1993 #sequence\_revision: 30-Sep-1993 #text\_change: 16-Aug-1996  
C:Accession: PT0273  
R:Yamada, M.; Wasserman, B.; Reichard, B.A.; Share, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: P10222; MUI:91108137; PMID:1895102  
A:Accession: PT0273  
A:Molecule type: DNA  
A:Residues: 1-11 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match: 31.8%; Score 21; DB 2; Length 11;  
Best Local Similarity: 37.5%; Pred. No. 1.6e+03;  
Matches: 3; Conservative: 1; Mismatches: 4; Indels: 0; Gaps: 0;

QY 3 QKWLSDR 10  
DB 1 ESRKSPDF 8

RESULT 3

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Query #0: SELECT ... FROM ... WHERE ...  
      DB 17 Length 10;  
      Executed at: 2019-08-16 15:34  
      Pred No. 2,24+0;
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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
1  
1 QHW 3

Db

RESULT 8

Gonadoliberin 11 - spiny dogfish  
N-Alternate names: gonadotropin-releasing hormone  
C:Species: *Squalus acanthias* (spiny dogfish)  
C:Date: 06 Jan 1999 #sequence\_revision 02 Jan 1999 #text\_change 14 Jan 2003  
C:Accession: B46030

R:Lovejoy, D.A.; Fischer, W.H.; Nganvorachon, S.; Craig, A.; Nukushnik, C.S.; Peter, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A:Title: Distinct sequence of gonadotropin releasing hormone (GRH) in dogfish brain pro  
A:Reference number: A46030; MUID:92335300; PMID:1631133

A:Accession: B46030

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-10 <CON>

C:Superfamily: gonadoliberin

C:Keywords: hormone; pyroglutamic acid

F:10/Modified site: pyroglutamate carboxylic acid (pin) #status experimental

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
1  
1 QHW 3

Db

RESULT 9

Gonadoliberin 1 - spiny dogfish  
N-Alternate names: gonadotropin-releasing hormone  
C:Species: *Squalus acanthias* (spiny dogfish)  
C:Date: 06 Jan 1999 #sequence\_revision 06 Jan 1999 #text\_change 14 Dec 1998  
C:Accession: A46030

R:Lovejoy, D.A.; Fischer, W.H.; Nganvorachon, S.; Craig, A.; Nukushnik, C.S.; Peter, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A:Title: Distinct sequence of gonadotropin releasing hormone (GRH) in dogfish brain pro  
A:Reference number: A46030; MUID:92335300; PMID:1631133

A:Accession: A46030

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-10 <CON>

C:Keywords: hormone; pyroglutamic acid

F:10/Modified site: pyroglutamate carboxylic acid (pin) #status experimental

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
1  
1 QHW 3

Db

RESULT 10

Gonadoliberin - chum salmon  
C:Species: *Oncorhynchus keta* (chum salmon)  
C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 14 Jan 1999  
C:Accession: A21114

R:Stewart, R.; Eiden, L.; Brownstein, W.; Finkbeiner, S.; Eiden, L.; Finkbeiner, W.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

A:Title: Characterization of a teleost gonadotropin releasing hormone  
A:Reference number: A21114; MUID:8319-140; PMID:644047

A:Accession: A21114

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-10 <SHE>

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
1  
1 QHW 3

Db

RESULT 11

neuroedin 11 - laughing frog  
C:Species: *Rana ridibunda* (laughing frog)  
C:Date: 23 Nov 1991 #sequence\_revision 23 Nov 1991 #text\_change 11-Jan-2003  
C:Accession: P00172

R:Conlon, J.M.; O'Hare, F.; Vaudry, H.  
Biochem. Biophys. Res. Commun. 178, 526-530, 1991

A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that  
A:Reference number: P00172; MUID:91315477; PMID:1859413

A:Accession: P00172

A:Molecule type: protein

A:Residues: 1-10 <CON>

A:Experimental source: brain

C:Superfamily: gastrin releasing peptide

C:Keywords: amidated carboxyl end

F:10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 28.8%; Score 19; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHW 6  
1  
3 HW 4

Db

RESULT 12

neuroedin 11 - bovine  
C:Species: *Bos primigenius taurus* (cattle)  
C:Date: 14 May 1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
C:Accession: A60647

R:DeMaire, S.; Trifiro, G.M.; Chouinard, L.; Cecyre, D.; Dessureault, J.; Mercier, F.  
Peptides 17, 355-360, 1999

A:Title: Structure identification, subcellular localization and secretion of bovine ad  
A:Reference number: A60647; MUID:99311342; PMID:2755976

A:Accession: A60647

A:Molecule type: protein

A:Residues: 1-10 <SHE>

A:Note: this neuropeptide was purified from secretory granules of cells in the adrenal  
C:Superfamily: gastrin releasing peptide

C:Keywords: adrenal gland; neuropeptide

Query Match 28.8%; Score 19; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHW 6  
1  
3 HW 4

Db

RESULT 13

protein-tyrosine kinase (EC 2.7.1.112) - jack bean (fragment)  
C:Species: *Canavalia ensiformis* (jack bean)  
C:Date: 07 Dec 1999 #sequence\_revision 07 Dec 1999 #text\_change 04 Feb 2003  
C:Accession: C59151

R:Oliveira, A.B.A.; Machado, G.L.T.; Gomes, V.M.; Xavier-Neto, G.; Pereira, A.C.P.; Vie

Job time : 20 secs

Protein Pegg, Lett, 6, 15-21, 1999  
 A>Title: Duck brain seed coat contains a protein with complete sequence homology to bovin  
 A/Reference number: A59151  
 A/Accession: C59151  
 A/Molecule type: protein  
 A/Residues: 111 <MAC>  
 C/Keywords: ATP; phosphotransferase; tyrosine specific protein kinase

Query Match 28.8% Score 19, 100.0, length 11  
 Best local similarity 60.0% Pref. Res. 1.5, 0.33,  
 Matches 3, Conservative 0; Mismatch 2, Gaps 0;

QY 3 CQHW 7  
 DB 1 CQWL -

RESULT 14  
 T17081  
 Cytochrome c oxidase (EC 1.9.3.1) chain 1, Pityrospiralus (strain mitochondion (fragmen  
 A/Species: mitochondion Pityrospiralus radzi  
 C/Dates: 15 Oct-1999 #sequence\_revision: 15 Oct-1997 #text\_revision: 24 Oct-1999  
 C/Accession: T17081  
 R/Macey, C.R.; Larson, A.; Anandeva, S.B.; Papenhus, E.M.  
 C/Mol. Evol., 44, 660-674, 1997  
 A>Title: Evolutionary shifts in three major structural components of the mitochondrial gen  
 A/Reference number: Z18674; X0101971; X10101972  
 A/Accession: T17081  
 A>Status: preliminary, translated from B25982718  
 A/Molecule type: DNA  
 A/Residues: 1-11 <MAC>  
 A/Cross-references: EMBL:U92691; NID:1974144, 1974145, 1974146, 1974147, 1974148, 1974149, 1974150, 1974151, 1974152, 1974153, 1974154, 1974155, 1974156, 1974157, 1974158, 1974159, 1974160, 1974161, 1974162, 1974163, 1974164, 1974165, 1974166, 1974167, 1974168, 1974169, 1974170, 1974171, 1974172, 1974173, 1974174, 1974175, 1974176, 1974177, 1974178, 1974179, 1974180, 1974181, 1974182, 1974183, 1974184, 1974185, 1974186, 1974187, 1974188, 1974189, 1974190, 1974191, 1974192, 1974193, 1974194, 1974195, 1974196, 1974197, 1974198, 1974199, 1974200, 1974201, 1974202, 1974203, 1974204, 1974205, 1974206, 1974207, 1974208, 1974209, 1974210, 1974211, 1974212, 1974213, 1974214, 1974215, 1974216, 1974217, 1974218, 1974219, 1974220, 1974221, 1974222, 1974223, 1974224, 1974225, 1974226, 1974227, 1974228, 1974229, 1974230, 1974231, 1974232, 1974233, 1974234, 1974235, 1974236, 1974237, 1974238, 1974239, 1974240, 1974241, 1974242, 1974243, 1974244, 1974245, 1974246, 1974247, 1974248, 1974249, 1974250, 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OM protein - protein search, using sw mode.

Run on: November 5, 2003, 18:17:24 / Search time: 11 seconds  
(without alignment)  
47,027 Million cell updates/sec

Title: US-09-914-088-26  
Perfect score: 66  
Sequence: 1 (SQHWLSDRF 11)

Scoring table: BLOSUM62  
Gapop 10.0 / Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	23	34.8	10	1 GON3_PETMA	P13546 Petromyzon
2	20	30.3	9	1 COW_CONVE	P19347 Conus ventr
3	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
4	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
5	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
6	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
7	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
8	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
9	20	30.3	10	1 GON3_PETMA	P19347 Conus ventr
10	19	28.4	10	1 GON3_PETMA	P19347 Conus ventr
11	18	27.3	11	1 GON3_PETMA	P19347 Conus ventr
12	18	27.3	11	1 GON3_PETMA	P19347 Conus ventr
13	17	24.8	5	1 GUR2_HUMAN	P19347 Conus ventr
14	17	25.8	10	1 MP2_MOUSE	P19347 Conus ventr
15	16	24.3	10	1 FAR5_MOUSE	P19347 Conus ventr
16	15	22.7	8	1 FAR3_HUMAN	P19347 Conus ventr
17	14	21.2	7	1 BRP1_HUMAN	P19347 Conus ventr
18	13	19.7	5	1 UCL1_MOUSE	P19347 Conus ventr
19	13	19.7	6	1 E101_HUMAN	P19347 Conus ventr
20	13	19.7	7	1 FAR2_MOUSE	P19347 Conus ventr
21	13	19.7	8	1 CKN1_MOUSE	P19347 Conus ventr
22	13	19.7	9	1 OXYT_RATU	P19347 Conus ventr
23	13	19.7	10	1 BP2_MOUSE	P19347 Conus ventr
24	13	19.7	10	1 BP2_MOUSE	P19347 Conus ventr
25	13	19.7	10	1 CABR_HUMAN	P19347 Conus ventr
26	13	19.7	10	1 URAG_HUMAN	P19347 Conus ventr
27	13	19.7	11	1 CAV1_MOUSE	P19347 Conus ventr
28	13	19.7	11	1 CEP1_HUMAN	P19347 Conus ventr
29	13	19.7	11	1 CXLI_MOUSE	P19347 Conus ventr
30	12	18.2	7	1 TFF1_HUMAN	P19347 Conus ventr
31	12	18.2	8	1 COW2_MOUSE	P19347 Conus ventr
32	12	18.2	8	1 FAR2_MOUSE	P19347 Conus ventr
33	12	18.2	8	1 HTF1_PETMA	P19347 Conus ventr

34	12	18.2	8	1 HTF2_PETMA	P04549 periplaneta
35	12	18.2	8	1 HTF2_PETMA	P25419 tenebric mo
36	12	18.2	9	1 LITO_LITAU	P08945 litorea aur
37	12	18.2	9	1 NEUX_HUMAN	P04277 homo sapien
38	12	18.2	10	1 AEG1_AGRAR	P83465 agrocyphe ae
39	12	18.2	10	1 AKW1_MOUSE	P81626 locusta nig
40	12	18.2	10	1 APE_MOUSE	P80474 capnocyph
41	12	18.2	10	1 HTF1_MOUSE	P18110 rosalea mic
42	12	18.2	10	1 HTF2_MOUSE	P11385 carausius m
43	12	18.2	10	1 TKU1_MOUSE	P40751 urechis uni
44	12	18.2	10	1 TPIS_MOUSE	P19118 nicotiana gl
45	12	18.2	11	1 MGS_MOUSE	P41989 theicomyzon

## ALIGNMENTS

RESULT 1					
GON3_PETMA STANDARD; FRG; 10 AA.					
AC	P10548;				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)				
DE	Malibetan III				
CS	Petromyzon marinus (Sea lamprey)				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;				
CC	Petromyzontiformes; Petromyzontidae; Petromyzon.				
CX	NCBI_TaxID=7757;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Brain;				
RC	MEDLINE=93178316; PubMed=8443174;				
RA	Sower S.A., Chiang Y. C., Lovas S., Conlon J.M.;				
RT	"Primary structure and biological activity of a third gonadotropin releasing hormone from lamprey brain";				
RL	Endocrinology 112:1125-1131(1993).				
CC	!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.				
CC	!- SUBCELLULAR LOCATION: Secreted.				
CC	!- SIMILARITY: Belongs to the GNRH family.				
DR	Interpro: IPR002012; GNRH.				
DR	Pfam: PF00446; GNRH; 1.				
DR	PROSITE: PS00473; GNRH; 1.				
KW	Hormone; Amidation; Hypothalamus; Pyroglutamic acid				
FT	MDL:163 1 13 PYROGLUTAMIC ACID.				
FT	MDL:163 1 13 AMIDATION				
SQ	SEQUENCE 10 AA: 1277 MW: 28453623AA1F5A3 CRC64:				
Query Match 34.8% Score 23; DB 1; Length 10;					
Best Local Similarity 50.0%; Pred. No. 2.1e+02;					
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY 4 KHWLSD 9					
Eh 1 QHWSHD E					
RESULT 2					
COW_CONVE STANDARD; FRG; 9 AA.					
AC	P30477;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Contryphan-Vn.				
CS	Conus ventricosus (Mediterranean cone).				
CC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;				
CC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;				
CC	Neogastropoda; Conidae; Conidae; Conus.				
CX	NCBI_TaxID=117741;				

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RN 11
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE: Ventricle;
RX MEDLINE: 21547785; PubMed: 1688955;
RA Yassinia G.B., Schinina M.B., Asencio P., Pollicella P.,
RT "Contryphan-Vn: a novel peptide from the venom of the Mexican mean
RT snail Gonys ventriosus."
RQ Biochem. Biophys. Res. Commun. 289:908-913(2002).
CC 1 SUBCELLULAR LOCATION: Secreted.
CC 1 TISSUE SPECIFICITY: Expressed by the venom duct.
CC 1 MASS SPECTROMETRY: MW=1038.6; METHOD: MALDI
CC 1 SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxicity: Amidation; Diamine acid.
FT DISULFID 1 9
FT MOD RES 5 5 D-TRYPTOPHAN.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1031 MW; 80386743236768RA (JGI)
Query Match 10.3%; Score 20; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1; Gaps 0;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 1 CSCRW 6
DB 3 CPKRW 9
RESULT 3
CONS ALIMI STANDARD; PRT; 10 AA.
AC P12411 P23407;
DT 01 FEB 1991 (Rev. 17, Last sequence update);
DT 24 FEB 2003 (Rev. 41, Last annotation update);
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1);
DE "Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1);
DE (Gonadoliberin 1);
OS Alligator mississippiensis (American alligator);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Actinopterygii; Cyprinodontiformes; Poeciliidae; Poeciliinae;
OS N-RI TaxID 8445;
RN 11
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE: 9152138; PubMed: 182082;
RA Lavey D.A., Fischer W.H., Parker D.E., McVey J.E., Park M.,
RA Lavey N., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis)
RT (Gonadoliberin 1);
RQ Biochem. Biophys. Res. Commun. 161:1991;
CC 1 FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1) (LR RH)
DE (Gonadoliberin 1);
OS Clupea pallasi (Pacific herring);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
CC Clupea;
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
RN 11
RP SEQUENCE, AND FUNCTION.
RC TISSUE: Brain, and pituitary;
RX MEDLINE: 2014353; PubMed: 1065929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring."
RQ Endocrinology 141:525-532(2002).
CC 1 FUNCTION: Stimulates the secretion of gonadotropins.
CC 1 SUBCELLULAR LOCATION: Secreted.
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
DR InterPro: IPR005512: GNRH.
DR Pfam: PF00446: GNRH.

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AC P06677;
DT 01 NOV 1997 (Rev. 35, Created);
DT 01 NOV 1997 (Rev. 35, Last sequence update);
DT 28 FEB 2003 (Rev. 41, Last annotation update);
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1);
DE (Gonadoliberin 1);
OS Chelysoma productum;
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterozoa;
OS Phlebobranchia; Corellidae; Chelyosoma;
CC NCB TaxID=71177;
RN 11
RP SEQUENCE.
RX MEDLINE: 9411567; PubMed: 8814821;
RA Powell J.F.F., Reska Skinner S.M., Prakash M.C., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications."
RQ Proc Natl Acad Sci U S A 93:10461-10464(1996).
CC 1 FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC 1 the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC 1 SUBCELLULAR LOCATION: Secreted.
CC 1 TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC THE GONADS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC 1 MASS SPECTROMETRY: MW=1246.56; METHOD: MALDI.
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
DR InterPro: IPR02012: GNRH.
DR Pfam: PF00446: GNRH.
DR PROSITE: PS00473: GNRH_1.
KW Hormone; Amidation; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A5A3 CRC64;
Query Match 10.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 4 KRW 6
DB 1 QHW 3
RESULT 5
CONS CLUPA STANDARD; PRT; 10 AA.
AC P87347;
DT 16 OCT 2001 (Rev. 41, Created);
DT 28 FEB 2003 (Rev. 41, Last sequence update);
DT 28 FEB 2003 (Rev. 41, Last annotation update);
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1) (LR RH)
DE (Gonadoliberin 1);
OS GNRH1;
OS Clupea pallasi (Pacific herring);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
CC Clupea;
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
RN 11
RP SEQUENCE, AND FUNCTION.
RC TISSUE: Brain, and pituitary;
RX MEDLINE: 2014353; PubMed: 1065929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring."
RQ Endocrinology 141:525-532(2002).
CC 1 FUNCTION: Stimulates the secretion of gonadotropins.
CC 1 SUBCELLULAR LOCATION: Secreted.
CC 1 SIMILARITY: BELONGS TO THE GNRH family.
DR InterPro: IPR005512: GNRH.
DR Pfam: PF00446: GNRH.

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DR PROSITE: P500423; GNRH: 1;
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid;
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID;
FT MOD_RES 10 10 AMIDATION;
SQ SEQUENCE 10 AA: 1105 MW; 244B2F972871F5A1 CPC64;

Query Match 30.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6
DE 1 QHW 1

RESULT 7
GGN2_CHICK
ID -GGN2_CHICK STANDARD; PRT; 10 AA;
AC P20468; PHL750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II; GnRH II; GnRH II)
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI TaxID 71197;
RN 1;
RP SEQUENCE;
RX MEDLINE:9641359; PubMed:8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.G., Fischer W.H.,
Park M., Rivier J.E., Craig A.G., Vinkie G.G., Sherwood N.M.,
"Two new forms of gonadotropin-releasing hormone in a protochordate
and the evolutionary implications";
Proc. Natl. Acad. Sci. U.S.A. 93:10481-10484(1996);
RT "Primary structure of gonadotropin-releasing hormone (GNRH) in
dofish brain provides insight into GNRH evolution.";
Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992);
RL "Primary structure of gonadotropin-releasing hormone from the brain
of a holocarpal ratfish, Hydrolagus colliei";
Gen. Comp. Endocrinol. 92:152-161(1991);
RN SEQUENCE;
RP SPECIES=Chelodactylus; TISSUE=Brain;
RX MEDLINE:9233330; PubMed:1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
Naborniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.,
"Distinct sequence of gonadotropin-releasing hormone (GNRH) in
dofish brain provides insight into GNRH evolution.";
Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992);
RL "Primary structure of gonadotropin-releasing hormone from the brain
of a holocarpal ratfish, Hydrolagus colliei";
Gen. Comp. Endocrinol. 92:152-161(1991);
RN SEQUENCE;
RP SPECIES=H. colliei; TISSUE=Brain;
RX MEDLINE:9334566; PubMed:1678233;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
Lee T.;
"Primary structure of gonadotropin-releasing hormone from the brain
of a holocarpal ratfish, Hydrolagus colliei";
Gen. Comp. Endocrinol. 92:152-161(1991);
RN SEQUENCE;
RP SPECIES=H. colliei; TISSUE=Brain, and Pituitary;
RX MEDLINE:2011455; PubMed:1065099;
RA Carolan J.J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
Chang J.P., Rivier J.E., Sherwood N.M.;
"Primary structure and function of three gonadotropin-releasing
hormones, including a novel form, from an ancient teleost, Herring.";
Endocrinology 141:505-512(2001);
CC 1- FUNCTION: Stimulates the secretion of gonadotropins.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: Belongs to the GNRH family.
DR PIR: A61126; A61126;
DR PIR: B46038; B46038;
DR PIR: B60666; B60666;
DR InterPro: IPR002012; GNRH;
DR Pfam: PF07446; GNRH; 1;
DR PROSITE: PS00473; GNRH; 1;
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID;
FT MOD_RES 10 10 AMIDATION;
SQ SEQUENCE 10 AA: 1254 MW; 284B2E437871F5A3 CRC64;

Query Match 30.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OS Alligator mississippiensis (American alligator);
OS Squalus acanthias (Spiny dogfish);
OS Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and
OS Clupea pallasi (Pacific herring);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
OX NCBI TaxID=9031, 8496, 7997, 7873, 10724;
RN 1;
RP SEQUENCE;
RC SPECIES=Chicken; TISSUE=Hypothalamus;
RX MEDLINE:8422659; PubMed:6427779;
RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
Matsuo H.;
"Identification of the second gonadotropin-releasing hormone in
chicken hypothalamus: evidence that gonadotropin secretion is
probably controlled by two distinct gonadotropin-releasing hormones
in avian species";
Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984);
RL 1;
RN SEQUENCE;
RC SPECIES=Alligator mississippiensis; TISSUE=Brain;
RX MEDLINE:9335338; PubMed:188082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
"Primary structure of two forms of gonadotropin-releasing hormone
from brains of the American alligator (Alligator mississippiensis)";
Regul. Pept. 33:105-116(1991);
RN SEQUENCE;
RP SPECIES=Alligator mississippiensis; TISSUE=Brain;
RX MEDLINE:9233330; PubMed:1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
Naborniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
"Distinct sequence of gonadotropin-releasing hormone (GNRH) in
dofish brain provides insight into GNRH evolution.";
Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992);
RL "Primary structure of gonadotropin-releasing hormone from the brain
of a holocarpal ratfish, Hydrolagus colliei";
Gen. Comp. Endocrinol. 92:152-161(1991);
RN SEQUENCE;
RP SPECIES=H. colliei; TISSUE=Brain;
RX MEDLINE:9334566; PubMed:1678233;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
Lee T.;
"Primary structure of gonadotropin-releasing hormone from the brain
of a holocarpal ratfish, Hydrolagus colliei";
Gen. Comp. Endocrinol. 92:152-161(1991);
RN SEQUENCE;
RP SPECIES=H. colliei; TISSUE=Brain, and Pituitary;
RX MEDLINE:2011455; PubMed:1065099;
RA Carolan J.J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
Chang J.P., Rivier J.E., Sherwood N.M.;
"Primary structure and function of three gonadotropin-releasing
hormones, including a novel form, from an ancient teleost, Herring.";
Endocrinology 141:505-512(2001);
CC 1- FUNCTION: Stimulates the secretion of gonadotropins.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: Belongs to the GNRH family.
DR PIR: A61126; A61126;
DR PIR: B46038; B46038;
DR PIR: B60666; B60666;
DR InterPro: IPR002012; GNRH;
DR Pfam: PF07446; GNRH; 1;
DR PROSITE: PS00473; GNRH; 1;
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID;
FT MOD_RES 10 10 AMIDATION;
SQ SEQUENCE 10 AA: 1254 MW; 284B2E437871F5A3 CRC64;

Query Match 30.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity: 50.0%; Pred. No. 2,26-01;  
Matches: 2; Conservative: 1; Mismatches: 1; Gaps: 0;

QY 4 PFWL 7  
DI 5 ROWL 8

RESULT 15

PAP5 MACRS  
AC PAP5 MACRS STANDARD; PRT: 10 AA;  
DT 28 FEB 2003 (Rel. 4); Created;  
DT 28 FEB 2003 (Rel. 4); Last sequence update;  
DT 28 FEB 2003 (Rel. 4); Last annotation update;  
CE PMEAamide like neuropeptide PEP5 (PAP5ALRPPF amide)  
OS Macrobathrus rosenbergi: Giant fresh water lizard  
CC Eukaryota; Metazoa; Arthropoda; Chiroptera; Malacostraca;  
CC Euryarchontacea; Eucariota; Decapoda; Plecoptera; Curculio;  
CC Palaeomonidae; Palaemonidae; Macrobathrus  
CX NCBI\_TaxID=79674;  
PX 1;  
PY SEQUENCE AND MASS SPECTROMETRY;  
PP TSSUB:Eye stalk; Sarathongkum W.; Jai-esthery S.; Sarathongkum W.;  
PA Sarathongkum W.;  
RT "Novel PMEAamide like neuropeptides from the eye stalk of the giant  
freshwater planor Macrobathrus rosenbergi";  
RL Conf. Biochem. Physiol. 12CB:587-595, 1998;  
CC 1- MASS SPECTROMETRY: MW1243.4; VETRID VAL2;  
CC 1- SIMILARITY: BELONGS TO THE PAP5 (PMEAAMIDE RECEPTOR) LEPTIDE  
FAMILY;  
CC QY: G010007215; Eneuropeptide signaling pathway; 1A;  
KW Neuropeptide; Amidation;  
PT WCD RSC 10 10 AMIDATION;  
SQ SEQUENCE 10 AA, 1244 MW, 9AIA55442720011 15764.

Query Match 24.2%; Score 167; CB 1; Best Local  
Best Local Similarity: 100.0%; Pred. No. 3,000-1;  
Matches: 3; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 9 CRT 1  
DI 1 CRT 3

Search Completed: November 6, 2003, 14:41:04  
Completed: 11:00:00

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 14:41:29 / Search time: 13.560 mds  
(without alignment)  
86.016 Million cells updated/sec

Title: US-09-914-088 26

Perfect score: 66

Sequence: 1 CSQKWSERT 11

Scoring table: ELKSJMa2

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1748

Maximum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summit=8

Database :

SPRMBL 231\*  
1: sp.archaea\*  
2: sp.bacteria\*  
3: sp.fungi\*  
4: sp.human\*  
5: sp.invertebrate\*  
6: sp.marine\*  
7: sp.mhc\*  
8: sp.organalle\*  
9: sp.prage\*  
10: sp.plant\*  
11: sp.todent\*  
12: sp.virus\*  
13: sp.vertbrate\*  
14: sp.unclassified\*  
15: sp.virus\*  
16: sp.bacteriap\*  
17: sp.archaeap\*

Pred. No. is the number of results per identity that have a score greater than or equal to the value of the pred. no. printed, and is derived by analysis of the total number of sequences.

SUMMARY

Result No.	Score	Query Match	Length DB	ID	Description
1	21	31.8	9	Q8W8X4	Q8W8X4 diadema mex
2	21	31.8	11	Q8SKP8	Q8SKP8 streptophorus
3	21	31.8	11	Q8C2A3	Q8C2A3 gallus gall
4	21	31.8	11	Q8I410	Q8I410 mouse mamma
5	20	30.3	8	Q8WGT3	Q8WGT3 lemis haita
6	20	30.3	9	Q8WGE6	Q8WGE6 procambatus
7	20	30.3	10	Q8F9H5	Q8F9H5 halicobacte
8	19	29.8	8	Q8O283	Q8O283 cyctolagus
9	19	29.8	9	Q8AVIC	Q8AVIC varanus gig
10	19	29.8	10	Q8AVG5	Q8AVG5 varanus gri
11	19	29.8	10	Q8SHK1	Q8SHK1 bradypodion
12	19	29.8	10	Q8S5Z8	Q8S5Z8 para muscus
13	19	29.8	10	Q8C184	Q8C184 mus musculus
14	19	29.8	11	Q7Z8A4	Q7Z8A4 meochochris
15	19	29.8	11	Q7Z8A4	Q7Z8A4 meochochris
16	19	29.8	11	Q7Z8A4	Q7Z8A4 meochochris

17	19	29.8	11	8	Q79921	Q79921 phrynoceph
18	18	27.3	8	4	Q1589C	Q1589C homo sapien
19	18	27.3	9	2	Q937C8	Q937C8 escherichia
20	18	27.3	9	2	Q937H9	Q937H9 enterobacte
21	18	27.3	10	2	Q937J5	Q937J5 acinetobact
22	18	27.3	10	8	Q79915	Q79915 leiobolus b
23	18	27.3	10	8	Q8SHQ2	Q8SHQ2 charaalep j
24	18	27.3	10	8	Q9G694	Q9G694 leiobolus g
25	18	27.3	10	15	Q85598	Q85598 moloney mur
26	18	27.3	10	15	Q85563	Q85563 moloney mur
27	18	27.3	10	15	Q85619	Q85619 moloney mur
28	17	25.8	8	11	Q99MNC	Q99MNC mus musculu
29	17	25.8	9	4	Q9H1Z6	Q9H1Z6 homo sapien
30	17	25.8	9	12	P90159	P90159 barley mild
31	17	25.8	10	2	Q47561	Q47561 escherichia
32	17	25.8	10	8	Q9XMB4	Q9XMB4 aegilops ta
33	17	25.8	10	8	Q94VZ6	Q94VZ6 varanus cil
34	17	25.8	10	9	Q9G362	Q9G362 acanthosaur
35	17	25.9	11	2	Q476C6	Q476C6 escherichia
36	16	24.2	8	6	Q95M23	Q95M23 sus scrofa
37	16	24.2	9	2	Q9RSM1	Q9RSM1 staphylococ
38	16	24.2	10	3	Q8TGB8	Q8TGB8 pleurotus o
39	16	24.2	10	6	Q8TU33	Q8TU33 canis faml
40	16	24.2	10	8	Q9T8P3	Q9T8P3 liolaemus a
41	16	24.2	10	8	Q9T8Z9	Q9T8Z9 liolaemus f
42	16	24.2	10	8	Q9T8W5	Q9T8W5 liolaemus r
43	16	24.2	10	8	Q8W916	Q8W916 liolaemus m
44	16	24.2	10	8	Q9T8N7	Q9T8N7 liolaemus o
45	16	24.2	10	8	Q79888	Q79888 basilliscus

# ALIGNMENTS

RESULT 1  
Q8W8X4  
1C Q8W8X4 PRESUMINARY: PR7 9 AA.  
AC Q8W8X4  
BT 01-MAR-2002 (TREVURE), 20, Created)  
BT 01-MAR-2002 (TREVURE), 20, Last sequence update)  
BT 01-MAR-2002 (TREVURE), 20, Last annotation update)  
DB Cytochrome oxidase subunit 1 (Fragment).  
GN CCl1.  
OS Diadema mexicanum.  
OC Mitochondrion.  
CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
CC Echinolida; Euechinoridea; Diadematacea; Diadematoida; Diadematidae;  
CC Diadema  
CX NCBI TaxID=105356;  
RN 11  
FP SEQUENCE FROM N.A.  
RC STRAIN:Q870, and CCl17;  
RX MEDLINE=2132357; PubMed=1430656;  
RA Lessios H.A., Kessing B.D., Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global  
phylogeography of the sea urchin Diadema,"  
RL Evolution 55:965-975(2001).  
[2]  
RN RN  
FP SEQUENCE FROM N.A.  
RC STRAIN:Q870, and CCl17;  
RX MEDLINE=21561594; PubMed=1703875;  
RA Lessios H.A., Garrido M.J., Kessing B.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on  
Caribbean reefs,"  
Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
DR EMBL: AY012920; AAL33843.1;  
DR EMBL: AY012921; AAL33844.1;  
KW Mitochondrion.  
FT NON TIR  
SQ SEQUENCE 9 AA: 1174 MW: 257133B46DDC2D3 CRC64;  
Query Match: 51.8%; Score 21; DB 9; Length 9;  
Best local similarity: 50.3%; Pred. No. 8.3e+85;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HWJLS 8  
DB 1 HWVA 4

RESULT 2  
Q8K8F8 PRELIMINARY; PRT; 11 AA.  
AC Q8K8F8  
DT 01-NOV-2002 (TREMUREL. 21, Created)  
DT 01-NOV-2002 (TREMUREL. 21, Last sequence update)  
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)  
DE Cytochrome c oxidase subunit 1 (fragment)  
GN Cyt.  
OS Cytochrome c oxidase.  
CC Mitochondrion.  
CA Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Iguania; Anseriformes; Agamididae; Agamidinae;  
CC Cytochrome c.  
CX NCBI TaxID=150305;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=1613864; PubMed=11754013;  
RA Melville C., Schulte C.A., Jr., Laine A.,  
RT "A molecular phylogenetic study of *Crotaphytus* in the  
PT Australian lizard genus *Crotaphytus*."  
PL J. Exp. Zool. 291:339-353(2001).  
DR EMBL: AF175623; AAC78791.1;  
KW Mitochondrion.  
FT NON\_TER 1;  
SQ SEQUENCE 11 AA; 1354 MW; A8F747E1264031E CR74;

Query Match 31.8%; Score 21; DB 15; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3e-03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 HWJLS 7  
DB 1 HWK5K 5

RESULT 3  
Q8C735 PRELIMINARY; PRT; 11 AA.  
AC Q8C735  
DT 01-NOV-1996 (TREMUREL. 01, Created)  
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)  
DE Beta-joint gene (fragment)  
GN Gallus gallus (Chicken)  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Gallinae; Gallinae;  
CC Gallus.  
CX NCBI TaxID 9031;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9126850; PubMed=6263304;  
RA Day L.E., Harst A., Lal E.C., Maro M.J., Wood J.L.,  
RT "cDNA and nucleotide sequence of an adult chicken mitochondrial  
beta-globin gene."  
PL Biochemistry 20:2091-2098(1981).  
DR EMBL: V00378; CAA23677.1;  
FT NON\_TER 1;  
SQ SEQUENCE 11 AA; 1372 MW; 2710A0E14000B3 DP74;

Query Match 31.8%; Score 21; DB 15; Length 11;  
Best Local Similarity 40.0%; Pred. No. 3e-03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HWJLS 9  
DB 1 HWK5K 5

Db 3 HWTA 7

RESULT 4  
Q8341C PRELIMINARY; PRT; 11 AA.  
AC Q8341C  
DT 01-NOV-1996 (TREMUREL. 01, Created)  
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)  
DE Superantigen (fragment)  
GN SAG.  
OS Mouse mammary tumor virus.  
CC Viruses; Retroviruses; Retroviridae; Betaretrovirus.  
CX NCBI TaxID=11757;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX STRAIN=Mtv-6;  
RX MEDLINE=9533174; PubMed=7811795;  
RA Cho K., Ferrick C.A., Morris D.W.,  
RT "Structure and biological activity of the subgenomic Mtv-6 endogenous  
RT provirus."  
PL Virology 206:395-403(1995).  
DR EMBL: U37518; AAA6963.1;  
DR InterPro: IPR00213; XMTV\_SAG  
PT Pfam: PF01054; XMTV\_SAG; 1;  
FT NON\_TER 1;  
SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326C6D7 CRC64;

Query Match 31.8%; Score 21; DB 15; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3e-03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QKHWS 8  
DB 5 QCKWJN 10

RESULT 5  
Q8WGD7 PRELIMINARY; PRT; 8 AA.  
AC Q8WGD7  
DT 01-MAR-2002 (TREMUREL. 20, Created)  
DT 01-MAR-2002 (TREMUREL. 20, Last sequence update)  
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)  
DE Cytochrome oxidase subunit 1 (fragment)  
GN Lomus birra.  
OS Mitochondrion.  
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
CC Eumalacostraca; Decapoda; Decapoda; Platysemata; Anomura; Lomodea;  
CX NCBI TaxID=177234;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MORRIS C., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
RA Cunningham C.W.;  
RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
RT evolution to the crab-like form."  
PL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF436035; AAL3161.1;  
KW Mitochondrion.  
FT NON\_TER 1;  
FT NON\_TER 8;  
SQ SEQUENCE 8 AA; 1038 MW; C5B590C733640321 CRC64;

Query Match 30.3%; Score 20; DB 8; Length 8;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 4 KHWL 7  
DB 2 KPWL 5





OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9649533; PubMed=9649533;  
RA Maiga-Trillo E., Zaleska-Rutczynska Z., Molander P., Vences V.,  
R Figueroa F., Sultmann H., Klein J.  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
rt class II B loci."  
R1 Genetics 149:1527-1537(1998).  
DR EXEL:AP049994; AAC41332.1;  
FT NON-TER  
FT NON-TER  
SQ SEQUENCE 11 AA; 1253 YW; 72449701E987.8 (CR064)

Query Match 28.8% Score 19.18 E-01 Length 11  
Best Local Similarity 50.0% P-adj No. 6.0e-03;  
Matches 2; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 WISC 9  
DB : WISE 4

RESULT 15  
Q77884  
ID Q77884 PRELIMINARY FR1 11 AA.  
AC Q77884;  
DT 01-NOV-1998 (CERNB0rel\_08, Create);  
DT 01-NOV-1998 (CERNB0rel\_08, Last sequence updated);  
DT 01-DEC-2001 (CERNB0rel\_19, Last annotation update);  
DE MHC class II B locus 4 (Fragment).  
CS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Fungi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Eupercerygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9649533; PubMed=9649533;  
RA Maiga-Trillo E., Zaleska-Rutczynska Z., Molander P., Vences V.,  
R Figueroa F., Sultmann H., Klein J.  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
rt class II B loci."  
R1 Genetics 149:1527-1537(1998).  
DR EXEL:AP049994; AAC41332.1;  
FT NON-TER  
FT NON-TER  
SQ SEQUENCE 11 AA; 1253 YW; 72449701E987.8 (CR064)

Query Match 28.8% Score 19.18 E-01 Length 11  
Best Local Similarity 50.0% P-adj No. 6.0e-03;  
Matches 2; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 WISC 9  
DB : WISE 4

GenCore version: 5.1.6  
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CM protein - protein search, using sw tool

Run on: November 5, 2003, 18:11:45 / Search time: 49 seconds  
(without alignment)  
43,659 Million cell updates/sec

Title: US-09-914-088-26  
Perfect score: 66  
Sequence: 1 CSQXFLSRT 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 6.0

Searched: 110963 seqs, 1967653 residues

Total number of hits satisfying chosen parameters: 20125

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	21	AA225274
2	66	100.0	11	21	AA225332
3	66	100.0	11	22	AA216567
4	66	100.0	11	22	AA251330
5	66	100.0	11	23	AA202251
6	57	86.4	10	21	AA225269
7	57	86.4	10	21	AA225339
8	57	86.4	10	22	AA216514
9	57	86.4	10	22	AA251325
10	57	86.4	10	23	AA202274
11	57	86.4	10	23	AA202274
12	57	86.4	10	23	AA202274
13	57	86.4	10	23	AA202274
14	57	86.4	10	23	AA202274
15	57	86.4	10	23	AA202274
16	57	86.4	10	23	AA202274
17	57	86.4	10	23	AA202274
18	57	86.4	10	23	AA202274
19	57	86.4	10	23	AA202274
20	57	86.4	10	23	AA202274
21	57	86.4	10	23	AA202274
22	57	86.4	10	23	AA202274
23	57	86.4	10	23	AA202274
24	57	86.4	10	23	AA202274
25	57	86.4	10	23	AA202274
26	57	86.4	10	23	AA202274
27	57	86.4	10	23	AA202274
28	57	86.4	10	23	AA202274
29	57	86.4	10	23	AA202274
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31	57	86.4	10	23	AA202274
32	57	86.4	10	23	AA202274
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35	57	86.4	10	23	AA202274
36	57	86.4	10	23	AA202274
37	57	86.4	10	23	AA202274
38	57	86.4	10	23	AA202274
39	57	86.4	10	23	AA202274
40	57	86.4	10	23	AA202274
41	57	86.4	10	23	AA202274
42	57	86.4	10	23	AA202274
43	57	86.4	10	23	AA202274
44	57	86.4	10	23	AA202274
45	57	86.4	10	23	AA202274

10	57	86.4	10	23	AB200219	Human IgE immunoge
11	48	72.7	8	20	AAV42608	Human IgE peptide
12	48	72.7	8	21	AAV42617	Human IgE mutant #
13	48	72.7	8	21	AAV42620	Human IgE mutant #
14	37	56.1	9	24	AAE35074	Human immunoglobul
15	37	56.1	9	24	ABP96578	Human immunoglobul
16	35	53.0	8	14	AA533325	IgE Kabat residue
17	35	53.0	9	24	AAE35054	Immunoglobulin E (
18	35	53.0	9	24	AAE35063	Human immunoglobul
19	35	53.0	9	24	ABP96567	Human immunoglobul
20	30	45.5	9	17	AAW09128	FIV principal immu
21	30	45.5	9	23	AAE26749	Fibrin binding loo
22	30	45.5	9	24	ABR18853	Human cancer-relat
23	30	45.5	9	24	ABR19200	Human cancer-relat
24	30	45.5	9	24	ABR19431	Human cancer-relat
25	30	45.5	10	24	ABR18995	Human cancer-relat
26	30	45.5	10	24	ABR18960	Human cancer-relat
27	30	45.5	10	24	ABR19294	Human cancer-relat
28	30	45.5	10	24	ABR19341	Human cancer-relat
29	30	45.5	10	24	ABR19520	Human cancer-relat
30	30	45.5	10	24	ABR19521	Human cancer-relat
31	30	45.5	10	24	ABR19533	Human cancer-relat
32	30	45.5	10	24	ABR19725	Human cancer-relat
33	30	45.5	10	24	ABR19752	Human cancer-relat
34	30	45.5	10	24	ABR19764	Human cancer-relat
35	29	43.9	10	18	AAW36713	Thrombopoietin rec
36	29	43.9	10	18	AAW09562	Thrombopoietin rec
37	29	43.9	10	22	AAU25532	Human thrombopoiet
38	29	43.9	10	23	ABR75933	Acetylcholinestera
39	29	43.9	10	23	ABR75938	Acetylcholinestera
40	29	43.9	11	23	ABR44677	Human protective s
41	28	42.4	7	23	AAU81676	Enterokinase recog
42	28	42.4	8	14	AA336117	Hepatitis C virus
43	28	42.4	8	14	AA336118	Hepatitis C virus
44	28	42.4	10	18	AAW36598	Thrombopoietin rec
45	28	42.4	10	18	AAW09547	Thrombopoietin rec

ALIGNMENTS

RESULT:  
AAB20374  
ID AAB20374 standard; peptide; 11 AA.

XX AC AAB20374,  
XX D3-JAN 2001 (first entry)  
XX DE Antiallergy peptide-mimotope sequence SEQ ID NO:12.  
XX KW Immunoglobulin E, IgE; immunogenic; immunogen; Protein D; carrier;  
XX KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
XX KW malaria; cytotoxic; antiallergic; nontropic; neuroprotective;  
XX KW protozoicide; Alzheimer's disease; allergy.  
XX OS Homo sapiens.  
XX PH Key location/Qualifiers  
XX PT Modified site 11 /note= "amidated"

XX PN WC200150377-A1.  
XX PD 31-AUG-2000.  
XX PF 22-FEB-2000, 2000WO-EP01457.  
XX PR 25-FEB-1999, 99GB-0004405.  
XX PR 25-FEB-1999, 99GB-0004408.  
XX PR 25-FEB-1999, 99GB-0004412.  
XX PR 13-AUG-1999, 99GB-0019260.





PA (SMIR) SMITHKLINE BEECHAM BIOLOGICALS.

XX F. J. N. Johnson T;

XX WFI: 2001 521367/57.

XX A linkage comprising an immunogenic conjugate useful in treatment of IgE mediated diseases.

XX Example 4; Page 21; 48pp; English.

XX The present invention relates to linkage methods to be used in the conjugation of compounds (e.g. peptides) to carrier molecules (e.g. macromolecules, polymers, dendrimers, etc.) to provide biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition of a vaccine. The invention describes peptides derived from or mimotopes of the Cεp1/2, Cεp1/3 or Cεp1/4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. Cεp1/2, Cεp1/3 and Cεp1/4 represent peptides derived from Cεp1/2, Cεp1/3 or Cεp1/4 regions of human IgE.

XX Sequence 11 AA;

Query Match: 100.0%; Score 66; DB 21; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQKHWLSQRT 11

DB 1 CSQKHWLSQRT 11

RESULT 4

ABJ00231

ID AAB01010 standard; Peptide; 11 AA;

AC AAB01010;

DT 21 MAR 2001 (first entry)

XX IgE peptide #4;

XX Vaccine; immunoglobulin E; IgE; thio-ether linkage;

XX Mammalia;

XX WC20004716 A2;

XX 14-DEC 2000;

XX 04 JUN 2001; 2000WG-EF06164;

XX 06 JUN 1999; 99GB-5013127;

XX (SMIR) SMITHKLINE BEECHAM BIOLOGICALS;

XX F. J. N. Johnson T;

XX WFI: 2001-521367/57/10;

XX New vaccine comprising allergy peptide conjugate and an immunogenic carrier. The vaccine can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Claim 4; Page 21; 26pp; English.

XX The present invention relates to a composition comprising allergy peptides linked by an inert carrier. The allergy peptides are derived from immunoglobulin E (IgE) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for manufacturing a medicament for the prophylaxis or treatment of allergy. In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.

XX Sequence 11 AA;

Query Match: 100.0%; Score 66; DB 21; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQKHWLSQRT 11

DB 1 CSQKHWLSQRT 11

RESULT 5

ABJ00231

ID AAB01010 standard; Peptide; 11 AA;

AC AAB01010;

DT 02 SEP 2002 (first entry)

XX Human IgE immunogenic peptide SEQ ID NO: 15;

XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;

XX Vaccine; anti-allergic;

XX Homo sapiens;

XX WC200016409 A2;

XX 26-FEB-2002;

XX 17-AUG-2001; 2001WG-EF09576;

XX 22 AUG 2000; 2000GB-0020917;

XX (SMIR) SMITHKLINE BEECHAM BIOLOGICALS;

XX (PEPT) PEPTIDE THERAPEUTICS LTD;

XX F. J. N. Johnson T; Turnell WG; Vinals Bassols VC;

XX WFI: 2002 499642/52;

XX Conjugate for use in vaccine for treatment of allergy, comprises disulphide bridge cyclized peptide and immunogenic carrier.

XX Claim 4; Page 9; 41pp; English.

XX The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulphide bridge cyclised peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Sequence 11 AA;

Query Match: 100.0%; Score 66; DB 21; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQKHWLSQRT 11

DB 1 CSQKHWLSQRT 11

RESULT 6



AAU16634  
 ID AAU16634 standard; Peptide: 10 AA.  
 XX  
 AC AAC16634;  
 XX  
 DI 07 NOV 2002 (first entry)  
 XX  
 DE Peptide P3 derived from Cepsilon2 region of human IgE.  
 XX  
 KW Human linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IGE mediated disease; antibody response  
 XX  
 CS Homo sapiens.  
 XX  
 PN WC2002145745-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 21-DEC-2002; 2005WO-GB04935.  
 XX  
 PP 21-DEC-1999; 99GB-0030233.  
 PR 22-FEB-2003; 2000GB-0004096.  
 PR 22-AUG-2003; 2003GB-0025737.  
 PR 22-AUG-2003; 2003GB-0026738.  
 XX  
 PA (ACAM-1) ACAMBI5 RES LTD.  
 PA (SMIK ; SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Flynn N. Johnson T;  
 XX  
 DR WPI; 2001 521967/47.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IGE mediated diseases .  
 PT  
 PS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from orthotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IGE mediated diseases. The invention allows for controlled conjugation of a peptide with the attachment to a protein so as to form an immunogenic peptide which may be used to raise a protective antibody response in an individual. The compounds AAU16632 AAU16633 represent peptides derived from orthotopes of the Cepsilon2/Cepsilon3/Cepsilon4 regions of human IgE.  
 XX  
 SQ Sequence 10 AA.  
 Query Match 86.4%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0059;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQKHWLSDR 11  
 DI 1 SQKHWLSDR 10  
 RESULT 9  
 AAB5125  
 ID AAB51045 standard; Peptide: 10 AA.  
 XX  
 AC AAB51045;  
 XX  
 DI 21-MAR-2001 (first entry)

XX IGE peptide #3.  
 DE  
 XX Vaccine; immunoglobulin E; IGE; anti-allergy.  
 KW  
 XX Mammalia.  
 OS  
 XX WC2002074716-A2.  
 PN  
 XX 14-DEC-2000.  
 XX  
 PD 06 JUN-2003; 2006WO-EP05164.  
 XX  
 PF 08 JUN-1999; 99GB-0013327.  
 PR  
 XX (SMIK ; SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX Friebe's J;  
 XX  
 DR WPI; 2001-091150/10.  
 XX  
 PP New vaccine comprising allergy peptides linked by an inert carrier, useful for boosting an anti-allergy immune response in an individual susceptible to an allergic response .  
 PR  
 XX Claim 5; Page 20; 26pp; English.  
 PS  
 XX The present invention relates to a composition comprising allergy peptides linked by an inert carrier. The allergy peptides are derived from immunoglobulin E (IgE) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for manufacturing a medicament for the prophylaxis or treatment of allergy. In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
 CC  
 XX SQ Sequence 10 AA;  
 Query Match 86.4%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0059;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQKHWLSDR 11  
 DI 1 SQKHWLSDR 10  
 RESULT 10  
 ABM20213  
 ID ABM20213 standard; Peptide: 10 AA.  
 XX  
 AC ABM20213;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human IGE immunogenic peptide SEQ ID NO: 3.  
 XX  
 KW Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage; vaccine; anti-allergic.  
 KW  
 XX Homo sapiens.  
 CS  
 XX WC200216409-A2.  
 PN  
 XX 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-EP09576.  
 XX  
 PR 22-AUG-2003; 2003GE-0020717.  
 XX  
 PA (SMIK ; SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPTI) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Friebe M, Mason S, Turnell WG, Vinals Bassols YC;







GenCore version 5.1.6  
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new protein - protein search, using a model

Run on: November 5, 2003, 19:43:55 / Search time: 29 seconds  
without all indexes  
2004-03-11 09:43:55 / Indexes: 505

File: JS 09 914-C88-26

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sequence : 009005 009006  
correct score : 66
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Scoring table: PLOSM62  
Gapex 12.0, Gapext 2.5

Searched: 644079 segs, 171749232 residues

Total number of hits satisfying chosen: `parameter`: `value`

Maximum CB	seq	length: 0
Maximum CB	seq	length: 0

[illegible]

Post-processing: Minimum Match: 0%  
Maximum Match: 100%  
Listing first: 45 s

Database : Published Applications AA: •

[illegible]

proved. No. is the number of repetitions performed,  $\bar{X}$  is the mean score,  $\sigma^2$  is the variance,  $\bar{X}^2$  is the square of the mean score,  $\bar{X}^2$  is the square of the mean score greater than or equal to the score of interest, and  $\bar{X}^2$  is the square of the mean score less than or equal to the score of interest.  $\bar{X}^2$  and  $\bar{X}^2$  are derived by analysis of variance, and  $\bar{X}^2$  is derived by analysis of variance.

100

Result No.	Score	Query Match	Length	PE	ID	File Location
1	48	72.7	8	9	US	50.00.000 14. App.
2	48	72.7	8	9	US	50.00.000 17. App.
3	48	72.7	8	9	US	50.00.000 14. App.
4	48	72.7	8	9	US	50.00.000 17. App.
5	48	72.7	8	11	US	50.00.000 17. App.
6	48	72.7	8	11	US	50.00.000 17. App.
7	47	72.7	9	15	US	50.00.000 17. App.
8	35	63.0	9	12	US	50.00.000 17. App.
9	35	63.0	9	15	US	50.00.000 17. App.
10	30	45.5	10	12	US	50.00.000 17. App.
11	29	43.9	10	12	US	50.00.000 17. App.
12	29	43.9	10	12	US	50.00.000 17. App.
13	28	42.4	10	12	US	50.00.000 17. App.
14	28	42.4	10	12	US	50.00.000 17. App.
15	26	39.4	10	12	US	50.00.000 17. App.

16	26	35.4	10	10	US-09-731-378-455	Sequence 455, App
17	26	39.4	10	10	US-09-851-138-193	Sequence 193, App
18	26	39.4	10	12	US-10-093-768-73	Sequence 73, App1
19	26	39.4	10	12	US-10-083-768-112	Sequence 112, App
20	25	37.9	9	12	US-10-034-974-24	Sequence 24, App1
21	25	37.9	9	15	US-10-301-644-9	Sequence 9, App1
22	25	37.9	10	12	US-10-083-768-63	Sequence 63, App1
23	25	37.9	10	12	US-10-083-768-68	Sequence 68, App1
24	25	37.9	10	12	US-10-083-768-122	Sequence 122, App
25	25	37.9	11	15	US-10-012-806A-10	Sequence 10, App1
26	25	37.9	11	15	US-10-012-806A-35	Sequence 35, App1
27	24	36.4	5	9	US-09-517-661-34	Sequence 34, App1
28	24	36.4	7	12	US-10-193-764-20	Sequence 20, App1
29	24	36.4	8	9	US-09-548-164-78	Sequence 78, App1
30	24	36.4	8	9	US-09-548-164-86	Sequence 86, App1
31	24	36.4	8	10	US-09-500-379-78	Sequence 75, App1
32	24	36.4	8	10	US-09-500-379-86	Sequence 86, App1
33	24	36.4	9	12	US-10-177-725-110	Sequence 110, App1
34	24	36.4	9	12	US-10-221-984-4	Sequence 4, App1
35	24	36.4	9	12	US-10-286-457-440	Sequence 440, App
36	24	36.4	3	12	US-10-144-188-53	Sequence 53, App1
37	24	36.4	10	11	US-09-423-683-7	Sequence 7, App1
38	24	36.4	10	11	US-09-423-683-8	Sequence 8, App1
39	24	36.4	10	12	US-10-190-082-565	Sequence 565, App
40	24	36.4	10	12	US-10-083-768-62	Sequence 62, App1
41	24	36.4	10	12	US-10-083-768-120	Sequence 120, App
42	24	36.4	10	12	US-10-083-768-208	Sequence 208, App
43	24	36.4	10	12	US-10-353-929-142	Sequence 142, App
44	24	36.4	10	12	US-10-353-929-154	Sequence 154, App
45	24	36.4	10	12	US-10-203-708-260	Sequence 260, App

## ACKNOWLEDGMENTS

RESULT 1  
US-93-902-97 24  
Sequence 24, Application: US/09802077  
Patent No. US2001030542A.  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paul M.  
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended):  
FILE REFERENCE: PCT/EP2002/0205  
CURRENT APPLICATION NUMBER: US/09/802,077  
CURRENT FILING DATE: 2001-03-08  
PRIORITY APPLICATION NUMBER: US 08/445,612  
PRIORITY FILING DATE: 1998-03-15  
PRIORITY APPLICATION NUMBER: US 06/186,469  
PRIORITY FILING DATE: 1994-01-26  
PRIORITY APPLICATION NUMBER: PCT/US92/06490  
PRIORITY FILING DATE: 1992-02-14  
PRIORITY APPLICATION NUMBER: US 07/879,495  
PRIORITY FILING DATE: 1992-05-07  
PRIORITY APPLICATION NUMBER: US 07/744,768  
PRIORITY FILING DATE: 1991-09-14  
NUMBER OF SEQ ID NOS: 64

Query Match 72.78; Score 48; DB 9; Length 8;  
Best Local Similarity 100.00; Prod No. 5.Re+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100





Db 1 QKHWLSR 2

```

RESULT 6
US-10-214-524-57
; Sequence 57, Application US/09925174
; Publication No. US2003034468A1
; GENERAL INFORMATION:
; APPLICANT: Cardieu, Paula M.
; APPLICANT: Prestia, Leonard G.
; TITLE OF INVENTION: ARTIFICIAL ANTIBODIES AND ANTIBODIES
; FILE REFERENCE: P0718P22C1C1US
; CURRENT APPLICATION NUMBER: US/09925174
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/464,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/475,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06960
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,764
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 57
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-174-57

```

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Query Match 72.7% Score 48; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Cy 3 QKHWLSR 10  
 Db 1 QKHWLSR 8

```

RESULT 7
US-10-214-524-57
; Sequence 17, Application US/10214524
; Publication No. US2003037142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: US 00161 P.1.1
; CURRENT APPLICATION NUMBER: US/10214524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,130
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-57

```

```

Query Match 56.1% Score 37; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Cy 2 SQKHWL 7  
 Db 4 SQKHWL 9

```

RESULT 8
US-10-144-188-52
; Sequence 52, Application US/10144188
; Publication No. US20030370212A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Shi, Weixing
; APPLICANT: Kong, Yan
; APPLICANT: Degraw, Juli
; TITLE OF INVENTION: EX Vivo Panning For Generating Cytotoxic T Lymphocytes Specific
; FILE REFERENCE: P0718P22C1C1US
; CURRENT APPLICATION NUMBER: US/10144188
; PRIOR FILING DATE: 2002-05-11
; PRIOR APPLICATION NUMBER: 60/291,380
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144-188-52

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Query Match 53.0% Score 35; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Cy 6 WLSRDT 11  
 Db 1 WLSRDT 6

```

RESULT 9
US-10-214-524-6
; Sequence 6, Application US/10214524
; Publication No. US2003037142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zheng
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: US 00161 P.1.1
; CURRENT APPLICATION NUMBER: US/10214524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,130
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-6

```

```

Query Match 53.0% Score 35; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Cy 6 WLSRDT 11  
 Db 1 WLSRDT 6

RESULT 10  
 US-10-214-524-6  
 ; Sequence 21, Application US/10044974

Publication No. US20030143156A1  
GENERAL INFORMATION:  
APPLICANT: DYAX CORP.  
INVENTOR: Belitzer, James P.  
APPLICANT: Wescott, Charles R.  
APPLICANT: Satoh, Aakon K.  
TITLE OF INVENTION: FIBRIN BINDING PROPERTIES USEFUL AS INHIBITORS  
FILE REFERENCE: DEX-224.1 PCT: DEX 04.1.0  
CURRENT APPLICATION NUMBER: US/09/014,974  
PRIORITY FILING DATE: 2001-12-21  
PRIORITY APPLICATION NUMBER: US 09/742,419  
PRIORITY FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 1  
LENGTH: 9  
TYPE: 1ST  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fibrin binding loop  
US 10 534-974 21

Query Match 45.58; Score 10; DB 12; Length 10;  
Best Local Similarity 57.19; Pred No. 2.4e+22;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 CSQKHWL 7  
DB 1 CSQENWL 7

RESULT 11  
US-10 053-764-118  
Sequence 118, Application US/09/014,974  
Publication No. US2003015916A1  
GENERAL INFORMATION:  
APPLICANT: Dowder, William J.  
INVENTOR: Barlett, Ronald W.  
INVENTOR: Switzer, Steven E.  
INVENTOR: Buffin, David J.  
INVENTOR: Gates, Christian  
INVENTOR: Haselden, Sherill S.  
INVENTOR: Mattheakis, Jerry J.  
INVENTOR: Schatz, Peter J.  
INVENTOR: Weystrom, Christopher R.  
INVENTOR: Weystrom, Nicholas J.  
ADDRESS: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 1517  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Wisc. #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,974  
FILING DATE: 27-Feb-2003  
ATTORNEY/AGENT INFORMATION:  
NAME: Rubric, Robert T.  
REGISTRATION NUMBER: 16,402  
TELEPHONE: 919-248-1000  
TELEFAX: 919-248-1000  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids

TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 118:  
US-10 093-768-118

Query Match 43.9%; Score 29; DB 12; Length 10;  
Best Local Similarity 44.4%; Pred No. 2.4e+22;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 1 CSQKHWL 9  
DB 1 CSQENWL 9

RESULT 12  
US 08-450-442-45  
Sequence 45, Application US/08/450,842  
Publication No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
INVENTOR: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kt floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/456,419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/010,013  
FILING DATE: 23-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649,482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587,707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 16,700  
REFERENCE/DOCKET NUMBER: 66620103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-442-45

Query Match 43.9%; Score 29; DB 8; Length 11;  
Best Local Similarity 42.9%; Pred No. 2.6e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY 1 QRMWLD 9

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11111
: QKRWLSDR 8

RESULT 2
: US-08-466-151-57
: Sequence 57, Application US/08466151
: Patent No. 6017453
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Fresca, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/466163
: FILING DATE: 06-Jun-1995
: APPLICATION NUMBER: 08/405617
: FILING DATE: 11-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/189899
: FILING DATE: 27-JAN-1994

Query Match 72.7%, Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 3 QKRWLSDR 10
DB 1 QKRWLSDR 8

RESULT 4
: US-08-466-151-57
: Sequence 57, Application US/08466151
: Patent No. 6017453
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Fresca, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/466163
: FILING DATE: 06-Jun-1995
: APPLICATION NUMBER: 08/405617
: FILING DATE: 11-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/189899
: FILING DATE: 27-JAN-1994

US-08-466-151-24
: Query Match 72.7%, Score 48; DB 3; Length 8;
: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 3 QKRWLSDR 10
DB 1 QKRWLSDR 8

RESULT 3
: US-08-466-151-24
: Sequence 24, Application US/08466151
: Patent No. 6017453
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Fresca, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 07/879495
3 FILING DATE: 07-MAY-1992
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 07/744766
6 FILING DATE: 14-AUG-1991
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Svoboda, Craig G.
9 REGISTRATION NUMBER: 19,644
10 REFERENCE/DOCKET NUMBER: PG-140-1001
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 650/226-1483
13 TELEFAX: 650/952-9881
14 INFORMATION FOR SEQ ID NO: 57:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 8 amino acids
17 TYPE: Amino Acid
18 TOPOLOGY: Linear
19 US 08-466-163B-57
20
21 Query Match 72.7% Score 497 DB 1, Length 8;
22 Best Local Similarity 100.0%, Pred. No. 2,5e-05;
23 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24
25 QY 3 QKWLSCR 10
26 DB : QKWLSCR 8
27
28 RESULT 7
29 US 08-764-640-118
30 Sequence 118, Application US/08764640
31 Patent No. 5869451
32 Patent No. 5869451 5837683
33 GENERAL INFORMATION:
34 APPLICANT: Dower, William J.
35 APPLICANT: Barrett, Ronald W.
36 APPLICANT: Cutilia, Steven E.
37 APPLICANT: Gates, Christian
38 APPLICANT: Schatz, Peter J.
39 APPLICANT: Balasubramanian, Palaniappan
40 APPLICANT: Wagstrom, Christopher R.
41 APPLICANT: Hendres, Richard W.
42 APPLICANT: Depence, Randolph B.
43 APPLICANT: Podduluri, Surekha
44 APPLICANT: Yin, Qun
45 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
46 TITLE OF INVENTION: RECEPTOR
47 NUMBER OF SEQUENCES: 244
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Glaxo Wellcome
50 STREET: Five Moore Drive, P.O. Box 13398
51 CITY: Research Triangle Park
52 STATE: NC
53 COUNTRY: USA
54 ZIP: 27709
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: Patent Release #1.0, Version #1.30
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/08764,640
62 FILING DATE: 11-DEC-1996
63 CLASSIFICATION: 514
64 ATTORNEY/AGENT INFORMATION:
65 NAME: Hrubiec, Robert T.
66 REGISTRATION NUMBER: 36,392
67 REFERENCE/DOCKET NUMBER: PK3281
68 TELECOMMUNICATION INFORMATION:
69 TELEPHONE: 919-248-1000
70 INFORMATION FOR SEQ ID NO: 118:
71 SEQUENCE CHARACTERISTICS:
72 LENGTH: 13 amino acids
73 TYPE: amino acid
74 STRANDEDNESS:
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1 TOPOLOGY: linear  
2 MOLECULE TYPE: peptide  
3 US-08 764-640-118

Query Match 43.9% Score 29, DR 1, Length 10;  
Best Local Similarity 44.4% Prec No: 75;  
Matches 4; Conservative 2; Mismatches 3; Gaps 0;

QY : CSQKWLSD 9  
DB : CTRCWLSD 9

RESULT 1

US-08-914 225-118

1 Sequence 118, Application US/08914128A

2 Patent No. 6041913

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Swirl, Steven E.

7 APPLICANT: Duffin, David C.

8 APPLICANT: Gates, Christian

9 APPLICANT: Haselden, Sherill J.

10 APPLICANT: Maitheakis, Sally J.

11 APPLICANT: Schatz, Peter J.

12 APPLICANT: Waghston, Christopher R.

13 APPLICANT: Wrighton, Nicholas J.

14 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

15 NUMBER OF SEQUENCES: 232

16 CORRESPONDENCE ADDRESS:

17 ADDRESSEE: Glaxo Wellcome

18 STREET: Five Moore Drive, P.O. Box 1338

19 CITY: Research Triangle Park

20 STATE: NC

21 COUNTRY: USA

22 ZIP: 27709

23 COMPUTER READABLE FORM:

24 MEDIUM TYPE: Floppy disk

25 COMPUTER: IBM PC compatible

26 OPERATING SYSTEM: PC-DOS/MS-DOS

27 SOFTWARE: Patent in Release #118, Version #1.30

28 CURRENT APPLICATION DATA:

29 APPLICATION NUMBER: US/09/244,298A

30 FILING DATE: 11 DEC 1996

31 CLASSIFICATION: 514

32 ATTORNEY/AGENT INFORMATION:

33 NAME: Hrabiec, Robert T.

34 REGISTRATION NUMBER: 36,392

35 REFERENCE/DOCKET NUMBER: PK1281

36 TELECOMMUNICATION INFORMATION:

37 TELEPHONE: 919-248-1000

38 INFORMATION FOR SEQ ID NO: 118:

39 SEQUENCE CHARACTERISTICS:

40 LENGTH: 10 amino acids

41 TYPE: amino acid

42 STRAIDNESS:

43 TOPOLOGY: linear

44 MOLECULE TYPE: peptide

45 SEQUENCE DESCRIPTION: SEQ ID NO: 118

46 US-08-914 225-119

1 Query Match 43.9% Score 29, DR 1, Length 10;

2 Best Local Similarity 44.4% Prec No: 75;

3 Matches 4; Conservative 2; Mismatches 3; Gaps 0;

QY : CSQKWLSD 9  
DB : CTRCWLSD 9

RESULT 1

US-09-914 244-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Swirl, Steven E.

7 APPLICANT: Gates, Christian

8 APPLICANT: Schatz, Peter J.

9 APPLICANT: Waghston, Christopher R.

10 APPLICANT: Haselden, Richard W.

11 APPLICANT: Wrighton, Nicholas J.

12 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

13 NUMBER OF SEQUENCES: 244

14 CORRESPONDENCE ADDRESS:

15 ADDRESSEE: Glaxo Wellcome

16 STREET: Five Moore Drive, P.O. Box 1338

17 CITY: Research Triangle Park

18 STATE: NC

19 COUNTRY: USA

20 ZIP: 27709

21 COMPUTER READABLE FORM:

22 MEDIUM TYPE: Floppy disk

23 COMPUTER: IBM PC compatible

24 OPERATING SYSTEM: PC-DOS/MS-DOS

25 SOFTWARE: Patent in Release #118, Version #1.30

26 CURRENT APPLICATION DATA:

27 APPLICATION NUMBER: US/09/244,298A

28 FILING DATE: 11 DEC 1996

29 CLASSIFICATION: 514

30 ATTORNEY/AGENT INFORMATION:

31 NAME: Hrabiec, Robert T.

32 REGISTRATION NUMBER: 36,392

33 REFERENCE/DOCKET NUMBER: PK1281

34 TELECOMMUNICATION INFORMATION:

35 TELEPHONE: 919-248-1000

36 INFORMATION FOR SEQ ID NO: 118:

37 SEQUENCE CHARACTERISTICS:

38 LENGTH: 10 amino acids

39 TYPE: amino acid

40 STRAIDNESS:

41 TOPOLOGY: linear

42 MOLECULE TYPE: peptide

43 SEQUENCE DESCRIPTION: SEQ ID NO: 118

44 US-09-914 244-119

1 Query Match 43.9% Score 29, DR 1, Length 10;

2 Best Local Similarity 44.4% Prec No: 75;

3 Matches 4; Conservative 2; Mismatches 3; Gaps 0;

QY : CSQKWLSD 9  
DB : CTRCWLSD 9

RESULT 1

US-09-914 244-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

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10 APPLICANT: Haselden, Richard W.

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12 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

13 NUMBER OF SEQUENCES: 244

14 CORRESPONDENCE ADDRESS:

15 ADDRESSEE: Glaxo Wellcome

16 STREET: Five Moore Drive, P.O. Box 1338

17 CITY: Research Triangle Park

18 STATE: NC

19 COUNTRY: USA

20 ZIP: 27709

21 COMPUTER READABLE FORM:

22 MEDIUM TYPE: Floppy disk

23 COMPUTER: IBM PC compatible

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25 SOFTWARE: Patent in Release #118, Version #1.30

26 CURRENT APPLICATION DATA:

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28 FILING DATE: 11 DEC 1996

29 CLASSIFICATION: 514

30 ATTORNEY/AGENT INFORMATION:

31 NAME: Hrabiec, Robert T.

32 REGISTRATION NUMBER: 36,392

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34 TELECOMMUNICATION INFORMATION:

35 TELEPHONE: 919-248-1000

36 INFORMATION FOR SEQ ID NO: 118:

37 SEQUENCE CHARACTERISTICS:

38 LENGTH: 10 amino acids

39 TYPE: amino acid

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43 SEQUENCE DESCRIPTION: SEQ ID NO: 118

44 US-09-914 244-119

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RESULT 1

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RESULT 1

US-09-914 244-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

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12 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

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21 COMPUTER READABLE FORM:

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25 SOFTWARE: Patent in Release #118, Version #1.30

26 CURRENT APPLICATION DATA:

27 APPLICATION NUMBER: US/09/244,298A

28 FILING DATE: 11 DEC 1996

29 CLASSIFICATION: 514

30 ATTORNEY/AGENT INFORMATION:

31 NAME: Hrabiec, Robert T.

32 REGISTRATION NUMBER: 36,392

33 REFERENCE/DOCKET NUMBER: PK1281

34 TELECOMMUNICATION INFORMATION:

35 TELEPHONE: 919-248-1000

36 INFORMATION FOR SEQ ID NO: 118:

37 SEQUENCE CHARACTERISTICS:

38 LENGTH: 10 amino acids



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Best Local Similarity 44.4%, Pref. No. 751  
Matches 4, Conservative 2, Mismatches 0, Indels 0, Gaps 0

QY : USQ9HMLSD 9

DP : STR2WMLD 9

RESULT 14  
US 08 451-947 45  
Sequence 45, Application US/08451947  
Patent No. 6072006

GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451947  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/426419  
FILING DATE: 19-APR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 06/030614  
FILING DATE: 22-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1995  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, PhD, Timothy E.  
REGISTRATION NUMBER: 36730  
REFERENCE/SECRET NUMBER: P0666P102  
TELEPHONE: 415/942-9881  
TELEFAX: 415/942-9884  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPLOGY: linear

Query Match 43.9%, Score 29, 28 2, Length 11:  
Best Local Similarity 42.9%, Pref. No. 831  
Matches 3, Conservative 4, Mismatches 0, Indels 0, Gaps 0

QY : USQ9HMLSD 9

DP : STR2WMLD 9

RESULT 14  
US 08 451-947 45  
Sequence 45, Application US/08451947  
Patent No. 6072006

GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424-836A  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240187  
FILING DATE: 10-May-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1995  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, PhD, Timothy E.  
REGISTRATION NUMBER: 36730  
REFERENCE/SECRET NUMBER: P0666P102  
TELEPHONE: 415/942-9881  
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TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: Amino Acid  
TOPLOGY: Linear

Query Match 43.9%, Score 29, 28 2, Length 11:  
Best Local Similarity 42.9%, Pref. No. 831  
Matches 3, Conservative 4, Mismatches 0, Indels 0, Gaps 0

QY : USQ9HMLSD 9  
DP : STR2WMLD 9

RESULT 15  
US-08-928-94-45  
Sequence 45, Application US/08928694  
Patent No. 607326  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/528,845
3 FILING DATE: 12-Sep-1997
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/451,941
7 FILING DATE: 26-MAY-1995
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 08/426,615
10 FILING DATE: 19-APR-1995
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 08/030,015
13 FILING DATE: 22-MAR-1993
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 07/645,442
16 FILING DATE: 31-JAN
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 07/587,707
19 FILING DATE: 1993
20 ATTORNEY/AGENT INFORMATION:
21 NAME: TORCHIO, PHD., TIMOTHY E
22 REGISTRATION NUMBER: 36,700
23 REFERENCE/DOCKET NUMBER: PC660,071,000
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 650/225-8674
26 TELEFAX: 650/952-9881
27 INFORMATION FOR SEQ ID NO: 45:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 11 amino acids
30 TYPE: Amino Acid
31 TOPOLOGY: Linear
32 US 08 028 694 45

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```

Query Match: 43.9% Score: 297 DB: 12-11-1997
Best Local Similarity: 42.9% P-Val: No 993
Values: 3, Conservative 4, Variations 5, Gaps 6

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CY 3 QSRWISD 9
DO 111111
1 PRWVSE 7

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Search completed: November 5, 2003, 10:44:33
Job time: 1.27 secs

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